



Db	421	FSDA	CEKTR	PGNTSK	436
Ov	421	FSDA	CEKTR	PGNTSK	436

FT	313	POTENTIAL.
CARBOHYD	313	POTENTIAL.
FT	285	POTENTIAL.
CARBOHYD	222	POTENTIAL.
FT	422	POTENTIAL.

CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA- AND BETA-  
CC SUBUNITS THEMSELVES.

[illegible]

Dd		181	NSVYVEKELPELLEPTCYCLEFKAIHPSLKHSNVSIVOCISSTVYANKMPRGLQYDAQ	240
Oy		181	ENTSYNAKIYKLSPEETTCCLAKAALLTSMIGVSPHCITTYVENELPPENIEVSVO	240
Dd		241	GKSIVLKMPVIASADVLFEAOMLPGYSKSSGSHSDKKRPFCANOVOTCVCSPDHY	300
Oy		241	NQRYVALKMXY-YYANNTEPOWLAHLFNRKNGNHLYKKKOIPDENKTKTCVPON-VF	298
Dd		301	-GTFFPLHQASEGHNTSWSEE-KFDSQHILPFPPIVTAVTMSDTLLVYNC--ODS	356
Oy		299	ONGIYLALRQADSGNNTSWSSEIWF-DTEIOAFLLPFVFIRSLSPFHICYAPROG	357
Dd		357	-T-C-D-GLANEIIEMWTNST-KISEXGPBETLKNLOPLRVYCQOARY-LFRALLN	409
Oy		358	NTPYVDIPLYIELIIFEWTSNAEKIIEKN-TDVATPNLRPLTVYCVKAAHTMDERLN	416
Dd		410	KTSNESEKLCEKTRPGS_426	
Oy		417	KSVFSDAVACEKTRPGN_433	
RESULT	5			
ID	CRF4_HUMAN	STANDARD;	PRT; 325 AA.	
AC	Q08334;			
Dt	01-FEB-1995 (Rel. 31, Created)			
Dt	01-FEB-1995 (Rel. 31, Last sequence update)			
Dt	01-OCT-1996 (Rel. 34, Last annotation update)			
Dn	CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.			
DE	CRFB4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
RN	[1]			
RZ	SEQUENCE FROM N.A.			
RC	TISSUE=FETAL BRAIN;			
CC	MEDLINE; 93300510.			
RA	Lutfulala G., Gardiner K., Uze G.:			
RT	"A new member of the cytokine receptor gene family maps on chromosome			
RT	21 at less than 35 kb from IRMAR".			
RL	Genomics 16:366-373(1993).			
RN	[2]			
RM	SEQUENCE FROM N.A.			
RP	MEDLINE; 96054036.			
RX	Lutfulala G., McInnis M.G., Antonarakis S.E., Uze G.:			
RA	"Structure of the human CRFB4 gene: comparison with its IRMAR			
RT	neighbor."			
RL	J. Mol. Evol. 41:338-344(1995).			
CC	-1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.			
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	-1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
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CC	ial entities requires a license agreement (See http://www.isb-sdb.ch/annou			
CC	or send an email to licenses@isb-sdb.ch).			
CC	-----			
DR	EMBL; Z17227; CAA78933.1;			
DR	EMBL; U08988; AAA86872.1;			
DR	PIR; A47003; A47003.			
DR	HSSP; P13726; IDAN.			
DR	MM; I23689;			
KM	Receptor; Transmembrane; Glycoprotein; Signal.			
FT	SIGNAL	1	19	POTENTIAL
FT	CHAIN	20	325	CYTOKINE RECEPTOR CLASS-II CRF2-4.
FT	DOMAIN	20	220	EXTRACELLULAR (POTENTIAL).
FT	TRANSEM	221	249	POTENTIAL.
FT	DOMAIN	250	325	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	666	74	BY SIMILARITY.



FT DISULFID 188 209 BY SIMILARITY.  
 FT CARBOHYD 49 49 POTENTIAL.  
 FT CARBOHYD 68 68 POTENTIAL.  
 FT CARBOHYD 102 102 POTENTIAL.  
 FT CARBOHYD 161 161 POTENTIAL.  
 FT CARBOHYD 124 124 A-> D (IN REF. 2).  
 FT CONFLICT 269 273 FLGHP -> VGRME (IN REF. 2).  
 FT CONFLICT 274 325 MISSING (IN REF. 2).  
 FT CONFLICT 274 325  
 FT SEQUENCE 325 AA; 37011 MM; 66706C79P8514B23 CMC64;  
 Query Match 8.6%; Score 274; DB 1; Length 325;  
 Best Local Similarity 30.1%; Pred. No. 2,52e-35;  
 Matches 62; Conservative 55; Mismatches 75; Indels 14; Gaps 10;  
 Db 23 PPNVBNMSVNFKNILQWESAPAKNITFTAQY---LSRIFQDKCMNTTLECDSS 78  
 Oy 32 SPQVEVDIIDNFIIRNRDESGVNTFSPDYOKTGMNMIKISGCONITSTFCNRS 91  
 Db 79 LS-K-YGDHTRVRAEFADEHSDWNI--TFCPVDTIIGPGMOVEYLADELHRLAPK 135  
 Oy 92 LKLVYEIKIRIRAE-KENTSSWEVDSEFPKRAQIGPEVHLLEDAKIVIH-ISPQ 149  
 Db 136 IENEYETWTKMKNVNSWTYNYQWKNGTDEKFOITPODFEVLNLEPWTYCYQVGRFL 195  
 Oy 150 T-KDSYMAALDGL--SFYSLILKNSGVERIENITSRKIKYKISPEYTYCLAKYKAL 206  
 Db 196 PDRKAGWSEPV-CEOTTHDETVPS 220  
 Oy 207 LITWIKIGVYS-PVHCIRTVEHELPP 231  
 RESULT 6  
 ID INGS\_HUMAN STANDARD; PRT; 337 AA.  
 AC P38484;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA  
 RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).  
 GN INGR OR INGR1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-LUNG FIBROBLAST;  
 RX MEDLINE; 94170380.  
 RA Sch J., Donnelly R.J., Kotenko S., Maritano T.M., Cook J.R.,  
 Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.,  
 RT Identification and sequence of an accessory factor required for  
 RT activation of the human interferon gamma receptor.  
 RL Cell 76:793-802(1994).  
 RN [2]  
 RP SEQUENCE OF 1-24 FROM N.A.  
 RX MEDLINE; 97067142;  
 RA Rhee S., Ebensperger C., Dembic Z., Pestka S.,  
 RT The structure of the gene for the second chain of the human  
 RT interferon gamma receptor.  
 RL J. Biol. Chem. 271:28947-28952(1996).  
 CC 1-FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR  
 CC SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF  
 CC THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO  
 CC INTERACT WITH GAF, JAK1, AND/OR JAK2.  
 CC 1-SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC 1-SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.  
 CC 1-SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC EMBL; 005875; AAA1695.1;  
 DR EMBL; 005877; AAA1695.1;  
 DR EMBL; 068755; AAC52066.1;  
 DR MIM; 147569;  
 DR PIRAM; PF00041; fn3; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 27  
 FT CHAIN 28 337  
 FT DOMAIN 28 247  
 FT TRANSEM 248 268  
 FT DOMAIN 269 337  
 FT CARBOHYD 56 56  
 FT CARBOHYD 85 85  
 FT CARBOHYD 110 110  
 FT CARBOHYD 137 137  
 FT CARBOHYD 219 219  
 FT CARBOHYD 231 231  
 FT CARBOHYD 231 231  
 FT VARIANT 64 64  
 FT R -> Q.  
 FTid-VAR.002718.  
 SQ SEQUENCE 337 AA; 37834 MM; 18C61B10AD90E509 CRC64;  
 Query Match 5.8%; Score 183; DB 1; Length 337;  
 Best Local Similarity 23.7%; Pred. No. 6.08e-16;  
 Matches 56; Conservative 60; Mismatches 95; Indels 25; Gaps 22;  
 Db 1 MRPTLL-WSLLLLGVFAAAAPDPLSQLPAQHRIKRYNAEYLSPEVALSNSTR 59  
 Oy 1 MAVVLLGATVTLVAVGVWLSAAGG-KNKSPQKVEVDIIDNFIIRNR-S-DSVG 57  
 Db 60 PNVYRQFKYDSKMTFADIMSIGVNCQTQATCECDPTAASPAGFPMDFNVLRLRAEL 119  
 Oy 58 NVFES-FDYQKTE-MONMIR-LS-GQGNITSTCNFSLKLVY--E-EIKIRIRAEK 108  
 Db 120 GALSAVNTWPEFHNTVNTVGPENIEVTPGESLLIRSSPP-D-IA-DTSTAFCY 176  
 Oy 109 ENT-SSWYEVDSFEPKRAQIGPE-VHLEDAKIVIHISPGKDSYMAALDGLSPTYS 166  
 Db 177 VHYWKG-GIQO-VKGFPSNSISLDNLKRSRYCLOVOQLT--NKSNIFFRGH 228  
 Oy 167 LITKNSGVERIENITSRKI-Y-KISPEYTYCLAKYKALTSW-KIGVSPVH 219  
 RESULT 7  
 ID INGR\_HUMAN STANDARD; PRT; 489 AA.  
 AC P15260;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119).  
 GN INGR1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89003065;  
 RA Agnet M., Dembic Z., Merlino G.,  
 RT Molecular cloning and expression of the human interferon-gamma  
 RT receptor.  
 RL Cell 55:273-280(1988).  
 RN [2]  
 RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.  
 RX MEDLINE; 93183911.  
 RA Stueber D., Friedlein A., Fountoulakis M., Lahm H.W., Garotta G.,  
 RT Alignment of disulfide bonds of the extracellular domain of the  
 RT interferon gamma receptor and investigation of their role in  
 RT biological activity.  
 RL Biochemistry 32:2423-2430(1993).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.  
 RX MEDLINE; 95342235.

RA Walter M.R., Windsor W.T., Nagabhushan T.L., Lundell D.J., Lynn C.A.,  
 RA Zaodny P.J., Narula S.K.,  
 RT "Crystal structure of a complex between interferon-gamma and its  
 RT soluble high-affinity receptor."  
 RL Nature 376:230-235(1995).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY.  
 RA MEDLINE: 98035727.  
 RA Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,  
 RA Winkler F.K., Robinson J.A.,  
 RT "Neutralizing epitopes on the extracellular interferon gamma receptor  
 RT (IFNGAMMAR) alpha-chain characterized by homolog scanning mutagenesis  
 RT and X-ray crystal structure of the A6 fab-IFNGAMMAR1-108 complex."  
 RL Mol. Biol. 273:882-897(1997).  
 CC -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE  
 CC INTERFERON-GAMMA DIMER.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PM: PHOSPHORYLATED AT SER/THR RESIDUES.  
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC  
 DR EMBL: J03143; AAA52731.1;  
 DR PIR: A31553; A31553.  
 DR PDB: 1JRH; 25-MAR-98.  
 DR MIM: 107470;  
 DR MIM: 209950;  
 KM Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;  
 KM Immunoglobulin domain; 3D-structure.  
 FT SIGNAL 1 17  
 FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.  
 FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 246 265 POTENTIAL.  
 FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 77 85  
 FT DISULFID 122 167  
 FT DISULFID 195 200  
 FT DISULFID 214 235  
 FT CARBOHYD 34 34 POTENTIAL.  
 FT CARBOHYD 79 79 POTENTIAL.  
 FT CARBOHYD 86 86 POTENTIAL.  
 FT CARBOHYD 179 179 POTENTIAL.  
 FT CARBOHYD 240 240 POTENTIAL.  
 SQ SEQUENCE 489 AA; 54404 MW; DCP9E5740BF47400 CRC64;  
 Query Match 4.4%; Score 140; DB 1; Length 489;  
 Best Local Similarity 25.3%; Pred. No. 9.41e-08;  
 Matches 37; Conservative 38; Mismatches 68; Indels 3; Gaps 3;  
 DB 1 MALLFLPLVMOGVSRAEAGTADLGPSSVPTNTIETSYNMPYVWEYQIMPPVY-F 59  
 OY 3 VLLGATTLVLAAGCPWLSAAL-CKNLKSPQKEVDIIDNFIILNRSDSESVGNVTF 61  
 DB 60 TVEVNVYGVKSEWIDACINISHYCNISDHVGDPSNSLWVYKARVQKESAYAKSEEF 119  
 OY 62 SEDYKGTGDMNKLKSGCNITSTKCNSSKLNYEEIKLIRAKENKTSSWYE-YDSF 120  
 DB 120 AVCRGKIGPPKLDIRKEKQIMDI 145  
 OY 121 TPFKRAQIGPPVPHLEAEKAIYIHI 146

RESULT 8  
 ID IL10R\_MOUSE STANDARD: PRT; 575 AA.

AC 061727;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).  
 GN IL10RA OR IL10R.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X AJ F1; TISSUE=HEMATOPOIETIC;  
 RA MEDLINE: 94068585.  
 RA Ho A.S.-Y., Liu Y., Khan T.A., Hsu D.-H., Bazan J.F., Moore K.W.;  
 RT "A receptor for interleukin 10 is related to interferon receptors."  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).  
 CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC  
 DR EMBL: L12120; AAA16156.1;  
 DR MGD: MGI:96538; IL10RA.  
 KM Receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 575 INTERLEUKIN-10 RECEPTOR.  
 FT DOMAIN 17 241 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 242 262 POTENTIAL.  
 FT DOMAIN 263 575 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 204 225  
 FT DISULFID 50 50 POTENTIAL.  
 FT CARBOHYD 66 66 POTENTIAL.  
 FT CARBOHYD 113 113 POTENTIAL.  
 FT CARBOHYD 182 182 POTENTIAL.  
 FT CARBOHYD 238 238 POTENTIAL.  
 SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F686B7 CRC64;  
 Query Match 4.2%; Score 132; DB 1; Length 575;  
 Best Local Similarity 20.5%; Pred. No. 2.43e-06;  
 Matches 33; Conservative 48; Mismatches 65; Indels 15; Gaps 13;  
 DB 69 WNDHICRAQALSCDLFTTLDLYHSYGRARAVDANSQYSNMTTETRTVD-EVI 127  
 OY 277 WKQIDPCENVKTQC-V--FPQNVFQKI-YLLRVAQSDGNTSMSE-EIKFDEIQAF 331  
 DB 128 LTVDSVTLKAMGIIYGIHPHPRP-ITPAGDEYQVREKDLRYVYISIRKSELMKARR 186  
 OY 332 LIPVFNKRLSDSPHVIYIGAPKQGNPVIQDYLIV-ET-IFWENSN-AERRIERK 388  
 DB 187 VQOEFTFLVPVIGVRFCKVLPV-LESRIKNAE-WSEEOC 225  
 OY 389 IDVTPNPK-PLTV--YCYKARAHNDKINKSSVPSDAVC 426  
 RESULT 9  
 ID IL10B\_HUMAN STANDARD: PRT; 918 AA.  
 AC P40189;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6B-BETA) (INTERLEUKIN  
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130) (ONCOSTATIN M  
 DE RECEPTOR) (CDM130) (CD130 ANTIGEN).  
 GN IL6ST.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-MYELOMA, AND PLACENTA;  
 RX MEDLINE: 91084844.  
 RA Hibi M., Murakami M., Saito M., Hirano T., Tago T., Kishimoto T.,  
 RT "Molecular cloning and expression of an IL-6 signal transducer,  
 RT gp130."  
 RL Cell 63:1149-1157(1990).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.  
 RX MEDLINE: 98169383.  
 RA Bravo J., Staunton D., Heath J.K., Jones E.Y.,  
 RT "Crystal structure of a cytokine-binding region of gp130."  
 RL EMBD J. 17:1665-1674(1998).  
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR  
 CC IL-6, LIF, OSM, CNP, AND IL-11 CAN UTILIZE GP130 FOR INITIATING  
 CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6R (ALPHA CHAIN) COMPLEX,  
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,  
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN  
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
 CC -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES  
 CC EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- DATABASE: NAME-PROW, NOTE-CD guide CD130 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm"  
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 CC -----  
 CC EMBL: M57230; AAA59155.1;  
 DR PIR: A36337; A36337.  
 DR PDB: 1BCU; 26-AUG-98.  
 DR MIM: 600694;  
 DR PFAM: PF00041; fn3; 3.  
 DR PRINTS: PRO0014; FNTPEI1.  
 DR PROSITE: PS00340; RECEPTOR CYTOKINES\_2; 1;  
 DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;  
 KW Repeat; 3D-structure.  
 CC FT SIGNAL 1 22  
 CC FT CHAIN 23 918  
 CC FT DOMAIN 23 619  
 CC FT TRANSMEM 620 641  
 CC FT DOMAIN 642 918  
 CC FT DOMAIN 26 120  
 CC FT DOMAIN 124 222  
 CC FT DOMAIN 223 324  
 CC FT DOMAIN 325 423  
 CC FT DOMAIN 424 517  
 CC FT DOMAIN 518 613  
 CC FT DOMAIN 725 755  
 CC FT DISULFID 134 144  
 CC FT DISULFID 172 182  
 CC FT CARBOHYD 43 43  
 CC FT CARBOHYD 83 83  
 CC FT CARBOHYD 131 131  
 CC FT CARBOHYD 157 157  
 CC FT CARBOHYD 227 227  
 CC FT CARBOHYD 379 379  
 CC FT CARBOHYD 383 383  
 CC FT CARBOHYD 390 390  
 CC FT CARBOHYD 553 553  
 CC FT CARBOHYD 564 564  
 CC FT SEQUENCE 918 AA; 103522 MW; D813F3672DD10D53 CRC64;

Query Match 4.0%; Score 128; DB 1; Length 918;  
 Best Local Similarity 22.9%; Pred. No. 1,19e-05;  
 Matches 19; Conservative 25; Mismatches 36; Indels 3; Gaps 3;  
 DB 231 INSEELSLIKLWTNPISIKSYIILKYNIOYTKDASTWSQIP-EDTASTSFTVODL 289  
 QY 36 VEVDIIDNFIILRW-NRSESGVNTFSFDYKTDGMDNKKISGCONITSTCNFSSLTL 94  
 DB 290 KPTEYVPIRCMKEDGKGYMSD 312  
 QY 95 NYEEIKIRIRAKEKNTSS-WYE 116  
 RESULT 10  
 ID 110R-HUMAN STANDARD; PRT; 578 AA.  
 AC Q13651;  
 DT 15-JUL-1998 (rel. 36, Created)  
 DT 15-JUL-1998 (rel. 36, Last sequence update)  
 DT 15-DEC-1998 (rel. 37, Last annotation update)  
 DE INTERLEUKIN-10 RECEPTOR PRECURSOR (IL-10R).  
 GN IL10RA OR IL10R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-LYMPHOMA;  
 RX MEDLINE: 94165477.  
 RA Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;  
 RT "Expression cloning and characterization of a human IL-10 receptor."  
 RL J. Immunol. 152:1821-1828(1994).  
 CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: SPLEEN, THYMUS, AND PBMC. FAINT EXPRESSION  
 CC IN PANCREAS, SKELETAL MUSCLE, BRAIN, HEART, AND KIDNEY. PLACENTA,  
 CC LUNG, AND LIVER SHOWED INTERMEDIATE LEVELS. MONOCYTES, B CELLS,  
 CC LARGE GRANULAR LYMPHOCYTES, AND T CELLS EXPRESS HIGH LEVELS OF IL-  
 CC 10R.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL: U00672; AAA17896.1;  
 DR MIM: 146933;  
 DR Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Repeat; 3D-structure.  
 CC FT SIGNAL 1 21  
 CC FT CHAIN 22 578  
 CC FT TRANSMEM 226 236  
 CC FT DOMAIN 236 257  
 CC FT DOMAIN 257 578  
 CC FT DISULFID 202 223  
 CC FT CARBOHYD 50 50  
 CC FT CARBOHYD 74 74  
 CC FT CARBOHYD 110 110  
 CC FT CARBOHYD 154 154  
 CC FT CARBOHYD 177 177  
 CC FT CARBOHYD 189 189  
 CC FT SEQUENCE 578 AA; 62903 MW; E81B29064338157C CRC64;  
 Query Match 3.7%; Score 116; DB 1; Length 578;  
 Best Local Similarity 20.9%; Pred. No. 1,17e-03;  
 Matches 49; Conservative 68; Mismatches 96; Indels 21; Gaps 19;  
 DB 1 MLCPTVILALALSLRGSDDHAGTELPSPSVFEEAFPH-H-ILMTPIPNSESTCYE 58  
 QY 5 ILGATTVLVAVGVWVLSAAAGKNLKSPOKV-EVDIIDNFIILRWNRSESGVNTFS 62

DB 59 VALLRYGIESNNSISNCSC-TLS-YDLAVTLDLYHSNGYRARVAVGSRHSNM-TVTN 115  
 OY 63 FYQYTGMDNWKISGCCQITSTKCNFSLSKLNVE-E-IKIRIR-EXENTSSWTEVDS 119  
 DB 116 -TRFVDEYTLTVGSYNLEHNGFLIGKIQDPRKAPAPNDYESTFHSFREYTAIRV 174  
 OY 120 FPFPRKAG-D-PEVHEDEKRAIV-THISPGTDSYVMAALDGI-S-FT-YSLIIMN 172  
 DB 175 PCNFETHKKV-KHENFSLTSGEVEPCVOYKPSVANSNNGMSKECISLT 227  
 OY 173 SSGVEREENITSRKHTYKLP-ETT-YCLKVAALITSMKIGVSPVHCITFT 224

RESULT 11  
 ID IL2R HUMAN STANDARD: 662 AA.

AC P42701. 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN PRECURSOR (IL-12R).  
 GN IL12RB1 OR IL12RB OR IL12R.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 94267217.  
 RA Chua A.O., Chizzonite R., Desai B.B., Trullit T.P., Nunes P.,  
 RA Minetti L.J., Marlier R.R., Presky D.H., Levine J.F., Gately M.R.,  
 RA Gubler U.;  
 RT "Expression cloning of a human IL-12 receptor component. A new member  
 of the cytokine receptor superfamily with strong homology to gp130.";  
 RL J. Immunol. 153:128-136(1994).  
 CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION.  
 CC -1- SUBUNIT: MAY FORM DIMERS OR OLIGOMERS. REQUIRES AN UNIDENTIFIED  
 CC -1- SUBUNIT TO GENERATE A HIGH AFFINITY IL-12R COMPLEX.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: ALTERNATIVE SPLICING MAY GIVE RISE TO A  
 CC SECOND PROTEIN 2 AMINO ACIDS SHORTER.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: U03187; AAA21340.1;  
 DR MIM: 601604;  
 DR PIR: PF00041; fn3; 1;  
 DR PROSITE: PS00340; RECEPTOR\_CYTOKINES\_2; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;  
 Repeat.  
 FT SIGNAL 1 23  
 FT CHAIN 24 662  
 FT DOMAIN 24 545  
 FT TRANSMEM 546 570  
 FT DOMAIN 571 662  
 FT DOMAIN 43 133  
 FT DOMAIN 143 236  
 FT DOMAIN 237 337  
 FT DOMAIN 338 444  
 FT DOMAIN 445 540  
 FT DISULFID 52 62  
 FT CARBOHYD 121 121  
 FT CARBOHYD 329 329  
 FT CARBOHYD 346 346  
 FT CARBOHYD 352 352  
 FT CARBOHYD 442 442  
 FT POTENTIAL.  
 FT INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT FIBRONECTIN TYPE-III.  
 FT FIBRONECTIN TYPE-III.  
 FT FIBRONECTIN TYPE-III.  
 FT FIBRONECTIN TYPE-III.  
 FT FIBRONECTIN TYPE-III.  
 FT BY SIMILARITY.  
 FT POTENTIAL.  
 FT POTENTIAL.  
 FT POTENTIAL.  
 FT POTENTIAL.  
 FT POTENTIAL.  
 FT POTENTIAL.

FT CARBOHYD 456 456 POTENTIAL.  
 FT VARSPLIC 659 662 KAKM -> DE (IN A SHORTER FORM).  
 SQ SEQUENCE 662 AA; 73108 MM; 541A060R62D0A1EF CAC64;  
 Query Match 3.7%; Score 118; DB 1; Length 662;  
 Best Local Similarity 28.4%; Pred. No. 5,54e-04;  
 Matches 23; Conservative 17; Mismatches 35; Indels 6; Gaps 5;  
 DB 146 IKVSLAGLRLMEETPNQVCAEV-OPR-HHTPSSPW-KLDCGPODDDTSC-LCPLE 201  
 OY 36 VEVDIIDNFIIRNRSDESVGNVTFSPDYQTKGMDNWKISGC--QNTTSTKCNFSSLK 93  
 DB 202 NNVAOEPOLRRROLGSGSSW 222  
 OY 94 LVNVEIKRLIRAEKENTSSW 114

RESULT 12  
 ID IL6B RAT STANDARD: 918 AA.

AC P40190. 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN  
 DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).  
 GN IL6ST.  
 OS Rattus norvegicus (rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 93052397.  
 RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;  
 RT "Molecular cloning and characterization of the rat liver IL-6 signal  
 transducing molecule, gp130.";  
 RL Genomics 14:666-672(1992).  
 CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR  
 CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING  
 CC SIGNAL TRANSDUCTION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,  
 CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,  
 CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN  
 CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS  
 CC AND ENDOTHELIAL CELLS.  
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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CC EMBL: M92340; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: A44257; A44257.  
 DR HSSP: P40189; 1BOU.  
 DR PIR: PF00041; fn3; 3.  
 DR PROSITE: PS00340; RECEPTOR\_CYTOKINES\_2; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;  
 Repeat.  
 FT SIGNAL 1 22  
 FT CHAIN 23 918  
 FT DOMAIN 23 618  
 FT TRANSMEM 619 640  
 FT DOMAIN 641 918  
 FT DOMAIN 26 120  
 FT DOMAIN 124 221  
 FT POTENTIAL.  
 FT INTERLEUKIN-6 RECEPTOR BETA CHAIN.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT IG-LIKE C2-TYPE DOMAIN.  
 FT FIBRONECTIN TYPE-III.

FT DOMAIN 222 323 FIBRONECTIN TYPE-III  
 FT DOMAIN 324 422 FIBRONECTIN TYPE-III  
 FT DOMAIN 423 516 FIBRONECTIN TYPE-III  
 FT DOMAIN 517 612 FIBRONECTIN TYPE-III  
 FT DOMAIN 724 754 SER-RICH  
 FT DISULFID 134 144 BY SIMILARITY  
 FT DISULFID 172 181 BY SIMILARITY  
 FT CARBOHYD 43 43 POTENTIAL  
 FT CARBOHYD 61 61 POTENTIAL  
 FT CARBOHYD 83 83 POTENTIAL  
 FT CARBOHYD 131 131 POTENTIAL  
 FT CARBOHYD 157 157 POTENTIAL  
 FT CARBOHYD 205 205 POTENTIAL  
 FT CARBOHYD 226 226 POTENTIAL  
 FT CARBOHYD 382 382 POTENTIAL  
 FT CARBOHYD 389 389 POTENTIAL  
 FT CARBOHYD 477 477 POTENTIAL  
 FT CARBOHYD 552 552 POTENTIAL  
 SQ SEQUENCE 918 AA: 102450 MW: 9E18B6FECF087F7 CRC64:

Query Match 3.7% Score 119; DB 1; Length 918;  
 Best Local Similarity 23.3%; Pred. No. 3,806-04;  
 Matches 21; Conservative 27; Mismatches 36; Indels 6; Gaps 5;

Db 223 PPHLSTNSELSTIKLANVNGSLKSDIOTRTDASTWIOVPL-EDTSPRT 281  
 QY 32 SPOKVEVDIIDD-NFILLR--WNRSD-ESVGNVTFSDYOKGMWIKLSCONITSTKC 87  
 Db 282 SFTVQDLKPFTEYVIRISIKNGKGYMSD 311  
 QY 88 NFSLKLVYEIRIKIRIAKENTSS-WYE 116

RESULT 13  
 ID EPHAS\_MOUSE STANDARD; PRT: 877 AA.

AC 060629;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOG KINASE-1) (BRAIN-SPECIFIC KINASE) (CEK-7)  
 DE EPHAS OR EHK1 OR CEK7 OR BSK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-BRAIN;  
 RX MEDLINE: 94194581.  
 RA Zhou R., Copeland T.D., Kromer L.F., Schulz N.T.;  
 RT Isolation and characterization of Bsk, a growth factor receptor-like tyrosine kinase associated with the limbic system.\*  
 RL J Neurosci. Res. 37:129-143(1994).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: BRAIN.  
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
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 CC EMBL: 007357; AAA17038.1;

DR HSPD; P00523; 2PTK.  
 DR MSD; M61;99654; EPHAS.  
 DR PFAM; PF01404; EPH\_1bd; 1.  
 DR PFAM; PF00536; SAM; 1.  
 DR PFAM; PF00041; fn3; 1.  
 DR PFAM; PF00069; Pkinase; 1.  
 DR PRINTS; PR00014; ENTPETIT.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN; 1.  
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 877  
 FT DOMAIN 27 412 EPHRIN TYPE-A RECEPTOR 5.  
 FT TRANSMEM 413 433 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 434 877 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 305 399 FIBRONECTIN TYPE-III.  
 FT DOMAIN 514 775  
 FT NP\_BIND 520 528 ATP (BY SIMILARITY).  
 FT BINDING 546 546 ATP (BY SIMILARITY).  
 FT ACT\_SITE 639 639 BY SIMILARITY.  
 FT CARBOHYD 266 266 POTENTIAL.  
 FT CARBOHYD 301 301 POTENTIAL.  
 SQ SEQUENCE 877 AA: 97115 MW: 54AD2C864178214 CRC64:

Query Match 3.4% Score 108; DB 1; Length 877;  
 Best Local Similarity 40.0%; Pred. No. 2,116-02;  
 Matches 18; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

Db 338 LEVIRKPEKQETSYTIISKETSTIRAEGLKPSVYVQIRAT 382  
 QY 367 LIVRIEIMENTSNAERIKERK-TDYTVNPKLPYVCVKARAT 410

RESULT 14  
 ID EPHAS\_RAT STANDARD; PRT: 1005 AA.

AC P54757;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOG KINASE-1).  
 DE EPHAS OR EHK1 OR EHK-1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;  
 RX MEDLINE: 94067777.  
 RA Maisonneuve P.C., Barreuzeta N.X., Yancopoulos G.D.;  
 RT EHK-1 and EHK-2: two novel members of the eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression.\*  
 RL Oncogene 8:3277-3288(1993).  
 CC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY  
 CC ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS  
 CC SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.  
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC  
 CC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC  
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 CC  
 CC EMBL: X78689; CAA55357.1;  
 CC DR HSSP: P00523; 2PK.  
 CC DR PFAM: PF01404; EPH\_Lbd. 1.  
 CC DR PFAM: PF00536; SAM. 1.  
 CC DR PFAM: PF00041; In3. 2.  
 CC DR PFAM: PF00069; PKINASE. 1.  
 CC DR PRINTS: PR00014; FNTYPEIII.  
 CC DR PRINTS: PR00109; TYRKINASE.  
 CC DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP\_FALSE\_NEG.  
 CC DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR. 1.  
 CC DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM. 1.  
 CC DR PROSITE: PS00790; RECEPTOR\_TYR\_KIN\_V. 1.  
 CC DR PROSITE: PS00791; RECEPTOR\_TYR\_KIN\_V\_2. 1.  
 CC DR PROSITE: PS01186; EGF\_2; UNKNOWN. 1.  
 CC KW Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 CC Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.  
 CC FT SIGNAL 1  
 CC FT CHAIN 1  
 CC FT DOMAIN 1 1005  
 CC FT TRANSMEM 576 596  
 CC FT DOMAIN 597 1005  
 CC FT DOMAIN 677 938  
 CC FT NP\_BIND 683 691  
 CC FT BINDING 709 709  
 CC FT ACT\_SITE 802 802  
 CC FT CARBOHYD 266 266  
 CC FT CARBOHYD 301 301  
 CC FT CARBOHYD 371 371  
 CC FT CARBOHYD 425 425  
 CC FT CARBOHYD 438 438  
 CC FT CARBOHYD 463 463  
 CC FT VARSPLIC 10 20  
 CC FT VARSPLIC 306 358  
 CC FT VARSPLIC 358 470  
 CC FT VARSPLIC 597 621  
 CC FT CONFLICT 170 170  
 CC FT CONFLICT 566 566  
 CC FT CONFLICT 578 578  
 CC FT CONFLICT 669 669  
 CC FT CONFLICT 708 708  
 CC FT CONFLICT 979 979  
 CC SQ SEQUENCE 1005 AA; 111007 MW; 1AED42C99693C574 CRC64;  
 Query Match 3.4%; Score 107; DB 1; Length 1005;  
 Best Local Similarity 40.0%; Pred. No. 13.00e-02;  
 Matches 18; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

RESULT 15  
 ID UFE1\_YEAST STANDARD; PRT; 346 AA.  
 AC P41834;  
 DT 01-NOV-1995 (rel. 32, Created)  
 DT 01-OCT-1996 (rel. 34, Last sequence update)  
 DT 15-FEB-2000 (rel. 39, Last annotation update)  
 DE UFE1 PROTEIN.  
 GN UFE1 OR YOR075W OR YOR29-26.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;  
 CC Saccharomycetaceae; Saccharomyces.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-AH22;  
 RX MEDLINE: 97074230.  
 RA Downing T.A., Storms R.K.;  
 RT "Molecular analysis of UFE1, a Saccharomyces cerevisiae gene  
 RT essential for spore formation and vegetative growth.";  
 RL Curr. Genet. 30:396-403(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 97357290.  
 RA Lewis M.J., Rayner J.C., Pelham H.R.B.;  
 RT "A novel SNARE complex implicated in vesicle fusion with the  
 RT endoplasmic reticulum.";  
 RL EMBO J. 16:3017-3024(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 97279235.  
 RA Valens M., Bohn C., Daignan-Fornier B., Dang V., Bolotin-Fukuhara M.;  
 RT "The presence of a 54.7 kb fragment of yeast chromosome XV reveals  
 RT the presence of two tRNAs and 24 new open reading frames.";  
 RL Yeast 13:379-390(1997).  
 CC -1- FUNCTION: T-SNARE FOR ENDOPLASMIC RETICULUM. MEDIATES RETROGRADE  
 CC TRANSPORT FROM THE GOLGI COMPLEX TO THE ER.  
 CC -1- SIMILARITY: TO S.POMBE SPC895.04C.  
 CC  
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 CC  
 CC EMBL: L15081; AAC13730.1;  
 CC DR EMBL: U53416; AAB50196.1;  
 CC DR EMBL: Z74983; CAA99268.1;  
 CC DR EMBL: Z70678; CAA94560.1;  
 CC DR SGD: L0002637; UFE1.  
 CC KW Transport; Protein transport; Endoplasmic reticulum; Coiled coil.  
 CC FT DOMAIN 222 321  
 CC FT SEQUENCE 346 AA; 40539 MW; DDC164793510A897 CRC64;  
 Query Match 3.3%; Score 104; DB 1; Length 346;  
 Best Local Similarity 23.0%; Pred. No. 8.47e-02;  
 Matches 17; Conservative 26; Mismatches 26; Indels 5; Gaps 5;  
 DB 91 DMECHLQIQV-FK-KFEELF-NYEMERINLSLKRFQGS-HRMSKILSNKDNKRHYH 146  
 OY 234 NIEVSQNONNYLAKNDYTAANFTFOVWLHAFKRNPNHLYKMKOIPDCENVKTKQVF 293  
 DB 147 PODI-ENGVEERFL 159  
 OY 294 PONVFOKGIYLLRV 307  
 Search completed: Mon Aug 21 10:26:14 2000  
 Job time: 18 secs.

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 \*\*\*\*\*

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MSPrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 21 10:26:31 2000; Maspar time 35.95 Seconds

Tabular output not generated. 840.922 Million cell updates/sec

Title: >US-09-240-675-2

Description: (1-436) from US09240675.pep

Sequence: 3178 1 MMYVLGATTLVAVGVPMV.....KSSVSDAVCEKPKGNTSK 436

Scoring table: PAM 150

Gap 11

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

sptrembl12  
 1:sp\_archaea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human  
 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle  
 9:sp\_plant 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified  
 13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 48.339; Variance 79.116; scale 0.611

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	899	28.3	569 13	Q9YHMO	INTERFERON ALPHA/BETA	5.53e-186
2	284	8.9	349 11	Q61190	CYTOKINE RECEPTOR FAMI	5.09e-37
3	241	7.6	332 11	Q63953	INTERFERON GAMMA RECEPTOR	1.25e-27
4	243	7.6	341 13	Q9YGC8	INTERLEUKIN-10 RECEPTOR	4.66e-28
5	140	4.4	484 4	Q10466	INTERFERON-GAMMA RECEPTOR	1.77e-07
6	123	3.9	26926 4	Q10466	TITIN HEART ISOFORM N	1.52e-04
7	118	3.7	349 5	Q9XK66	Y102AKC.31 PROTEIN	1.01e-03
8	114	3.6	349 5	Q45849	T27C5.5 PROTEIN	4.46e-03
9	114	3.6	198 13	Q9W609	GLYCOPROTEIN 130 PRECURSOR	4.46e-03
10	114	3.6	1493 11	P97798	NEOGENIN (NEOGENIN PRO)	4.46e-03
11	113	3.6	6875 6	Q28733	TITIN (FRAGMENT)	6.43e-02
12	111	3.5	1056 14	Q57161	PURATIVE REPLICASE	1.33e-02
13	112	3.5	1471 5	Q18825	C27B7.7 PROTEIN	9.25e-03
14	108	3.4	505 1	Q93662	CATAPLASE (EC-1.13.1.6)	3.87e-02
15	107	3.4	817 13	Q00784	TITIN (FRAGMENT)	5.50e-02
16	109	3.4	979 2	Q9X155	CLOSTRIDIUM-RELATED PR	2.71e-02
17	104	3.3	666 5	Q9XU75	R11A5.7 PROTEIN	1.56e-01
18	104	3.3	837 14	Q36406	PRIMASE	1.56e-01
19	102	3.2	192 5	Q77232	ADPOFERRITIN-2	3.09e-01
20	101	3.2	215 2	Q45207	VARIABLE OUTER MEMBRAN	4.33e-01

21	102	3.2	1055 14	Q98701	REPLICASE.	3.09e-01
22	102	3.2	1825 5	Q61210	H19M22.1 PROTEIN (FRAG	3.09e-01
23	101	3.2	2606 14	Q36414	LARGE TEGUMENT PROTEIN	4.33e-01
24	103	3.2	6048 5	Q23020	TWITCHIN.	2.20e-01
25	103	3.2	6831 5	Q23550	UNC-22 PROTEIN.	2.20e-01
26	103	3.2	7160 5	Q23551	ZK617.1B PROTEIN.	2.20e-01
27	100	3.1	287 2	Q50549	ESTERASE.	6.05e-01
28	99	3.1	310 2	Q47735	ORF13.	8.43e-01
29	99	3.1	327 3	Q94614	HYPOTHETICAL 36.8 KD P	8.43e-01
30	100	3.1	356 10	Q920N3	T13118.1 PROTEIN.	6.05e-01
31	99	3.1	356 2	P72901	HYPOTHETICAL 41.6 KD P	8.43e-01
32	99	3.1	402 4	Q9Y6V4	KIF3 (FRAGMENT).	8.43e-01
33	98	3.1	449 1	Q27677	CHORISMATE MUTASE.	1.17e+00
34	99	3.1	688 14	Q9WBD4	LARGE T ANTIGEN.	8.43e-01
35	99	3.1	688 14	Q9WAZ2	LARGE T ANTIGEN.	8.43e-01
36	99	3.1	688 14	Q9WMO8	LARGE T ANTIGEN.	8.43e-01
37	99	3.1	688 14	Q9WMO7	LARGE T ANTIGEN.	8.43e-01
38	99	3.1	688 14	Q55871	LARGE T ANTIGEN.	8.43e-01
39	99	3.1	688 14	Q82950	LARGE T ANTIGEN.	8.43e-01
40	99	3.1	688 14	Q42051	LARGE T ANTIGEN.	8.43e-01
41	99	3.1	688 14	Q92721	LARGE T ANTIGEN.	8.43e-01
42	99	3.1	688 14	Q92722	LARGE T ANTIGEN.	8.43e-01
43	99	3.1	688 14	Q55875	LARGE T ANTIGEN.	8.43e-01
44	99	3.1	688 14	P90457	LARGE T ANTIGEN.	8.43e-01
45	99	3.1	688 14	P88898	LARGE T ANTIGEN.	8.43e-01

## ALIGNMENTS

RESULT ID	Q9YHMO	PRELIMINARY	PRT	569 AA.
AC	Q9YHMO			
DT	01-MAY-1999 (Trembl)	10, Created		
DT	01-MAY-1999 (Trembl)	10, Last sequence update		
DT	01-MAY-1999 (Trembl)	10, Last annotation update		
DE	INTERFERON ALPHA/BETA RECEPTOR 1.			
GN	IFNAR1.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;			
OC	Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RA	REBOUL J., GARDINER K., MONNERON D., UZE G., LUPFALLA G.;			
RT	"Comparative genomic analysis of the interferon/interleukin-10			
RT	receptor gene cluster."			
RL	Genome Res. 0:0-0(1999).			
DR	EMBL; AF082664; AAD13669.1;			
KW	RECEPTOR.			
SO	SEQUENCE	569 AA; 64055 MW; F99BC099 CMC32;		

Query Match	28.38	Score 899	DB 13	Length 569
Best Local Similarity	38.48	Pred. No. 5.53e-186		
Matches	163	Conservative	90	Mismatches 149; Indels 23; Gaps 20;
DB	27	AGCTNLKSPDIDIOYVAVNTFTLMVNTTGGT-NVTFSAOYCFDDLOTEPEKELSGC	85	
QY	25	AGGKLNKSPKVEYDIIDNFILRMNSDESQVTFPS--FD-YQ--KTGMDMINKLSGC	79	
DB	86	QNVSHCEDPSAATVYDTHIRIRAREAKSPSSIPFEMIPYELAIGPEALQSI	145	
QY	80	QNTTSRCNFSLLKLVYEIKIRIRAEK-ENMSSVEYDSPFPKRAQIGPEVHLENE	138	
DB	146	NGAKINISPEPNOVRKRM-LISVFKNVIMDNSSNVE-KVRSILPIVDINDIAPET	203	
QY	139	DNAIVHISPGTDSV--MVALDGLSEFTSLIMKNSGVEERIEIYSHKIKYKLSPEP	196	
DB	204	TYLAKVQATVPLED--GGLESPHICIKTRKVDILCPNVRFAINMFFYILMDHNYE	262	
QY	197	TYLAKKALD-LTSMKIGVSPHCKITVE--NELPPEETIEVSQNVONIVLAKMDTYA-	253	
DB	263	HTYTVQVYLTGLYKLNLDYDSSKMWQVSCGENTSKCNLSVYKPTSAFYRYQAMKE	322	



OY 254 NMFPOVOMLHAFKRNKGNHLYKWKQIPDCENVTTCQVFPQVFGKI-YLLRVQASDG 312  
 DB 323 YSSCSLSKDVNDPVPVNEIGPPDVAK-DISDVLHHTKIPPGPGKIMSDLYDSYQI 381  
 OY 313 NNTSPSEETKPTDEIOAFLLPVPFNRSLSDSF-HIYGAPQSGWTPYIOPLYEI 371  
 DB 382 LYKNSSDNEEYVMEKTEKOTIATVSDIAPSTLYCVQVAFS-EA-YNKSSDSRECCIG 439  
 OY 372 IFWENIS-NMER-KIIEKTKDY-TVPLRLKLYTCVAKARHTDEKLKSSVFSADVCEK 428  
 DB 440 TAGCK 444  
 OY 429 TKRGN 433

RESULT 2  
 ID 061190 PRELIMINARY; PRT: 349 AA.  
 AC 061190;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE CYTOKINE RECEPTOR FAMILY 2, MEMBER 4 (CLASS II CYTOKINE RECEPTOR 4).  
 GN IL10RB OR CRF4 OR CR2-4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 RN Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RP SEQUENCE FROM N.A.  
 RA GIBBS V.C., PENNICA D.;  
 RX MEDLINE: 97199375.  
 RT "CRF-4: Isolation of cDNA clones encoding the human and mouse  
 RT protein."  
 RL Gene 186:97-101(1997).  
 DR EMBL: U53636; AAC53062.1;  
 DR MGD: MGI:109380; 1110rb.  
 DR PFAM: PF00041; fn3; 1.  
 SQ SEQUENCE 349 AA; 39774 MW; 4AC1802A CRC32;

Query Match 8.98; Score 284; DB 11; Length 349;  
 Best Local Similarity 28.5%; Pred. No. 5, 09e-37;  
 Matches 59; Conservative 60; Mismatches 73; Indels 15; Gaps 14;

DB 23 PREKVMNSVFNKILNOMEPAFPKNTLFTAQESY-R-S-PQ-DHCKRTASTOQDFSH 78  
 OY 32 SPQKVEVDIIDDNFILKMNNSDESGVNTFSFYQTKGDMNWKISGCONITSTKCNFS 91  
 DB 79 LS-K-VGDTYVRVRAELADEHESEVAV-TFCPEVEDITIGPPEKQISLESILRFSAPQ 135  
 OY 92 LKLNVEEIKLRIRAE-KENTSSMYEVDFTPRKAOIGPEVHLAEKAIYHIS-PG 149  
 DB 136 IENEPTWTLKNIYDSWAYRVOIKNGTNEKFOVSPYDSEVLKMLEPTTYCIIQVQFL 195  
 OY 150 T-KDSYVMALDGL-SFYSLIMKNSGVEERIEYIRHRIKISPETTYCLAKVAML 206  
 DB 196 LQNRGTGSEPT-CERTG-NDEITPS 220  
 OY 207 LYSWKIGVTS-PVHCITKTVENELPP 232

RESULT 3  
 ID 063953 PRELIMINARY; PRT: 332 AA.  
 AC 063953;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).  
 GN IFNGR2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 RN Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94170381.

RA HEMMI S., BOHNI R., STARK G., DI MARCO F., AGUET M.;  
 RT "A novel member of the Interferon receptor family complements  
 RT functionality of the murine Interferon gamma receptor in human  
 RL cells."  
 RL Cell 76:803-810(1994).

RP SEQUENCE FROM N.A.  
 RC STRAIN-129SV/72.  
 RX MEDLINE: 97128072.  
 RA EBENSPERGER C., RIEE S., MUTHUKUMARAN G., LEMBO D., DONNELLY R.,  
 RA PESTKA S., DEMBIC Z.;  
 RT "Genomic organization and promoter analysis of the gene Ifng2,  
 RT encoding the second chain of the mouse Interferon gamma receptor."  
 RL Scand. J. Immunol. 44:599-606(1996).  
 DR EMBL: U69599; AAC52938.1; JOINED.  
 DR EMBL: U69594; AAC52938.1; JOINED.  
 DR EMBL: U69595; AAC52938.1; JOINED.  
 DR EMBL: U69596; AAC52938.1; JOINED.  
 DR EMBL: U69597; AAC52938.1; JOINED.  
 DR EMBL: U69598; AAC52938.1; JOINED.  
 DR EMBL: S69336; AAB30165.1;  
 DR MGD: MGI:107654; Ifng2.  
 DR PFAM: PF00041; fn3; 1.  
 SQ SEQUENCE 332 AA; 37471 MW; 0BF24E9E CRC32;

Query Match 7.68; Score 241; DB 11; Length 332;  
 Best Local Similarity 27.8%; Pred. No. 1, 25e-27;  
 Matches 60; Conservative 56; Mismatches 80; Indels 20; Gaps 16;

DB 10 SLILCLGA-MASSPFSQALAPLRLHLNDEOILTWEPSSNDPRPVYQVEYSF 68  
 OY 10 TLVLAVGPGWVLSAAGRNKNSPOKVEVDIIDDNFILKMNNSDESGV-N-VTFSPDYOK 67  
 DB 69 ID-GSWRLLEPCNCDITETKCDLTGGGRKLPEHPFVFLRLRARGNLTSKWLLEPF 127  
 OY 68 TGMDMWIKL--SGCONITSTKCNFSSL-KLNVEE-IR--LKRAREN-TSMYEVDSEF 120  
 DB 128 QHRENTVGPKNISVTPKSGSLVHFSPF-D-V---FHGATFOYLVWKEKSETOQD 182  
 OY 121 TPRKAOIIPP-EVHLAEADKAIYHISPGTDSYVMALDGLSFYSLIMKNSGVEER 179  
 DB 183 VEGPFSKNSIVLGNLKPVYVCLQTEOILNKRI 218  
 OY 180 IENITSRRI-Y-KLSPETTYCLAKVAML-LTSMKI 212

RESULT 4  
 ID 091C8 PRELIMINARY; PRT: 341 AA.  
 AC 091C8;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)  
 DE INTERLEUKIN-10 RECEPTOR 2.  
 GN IL10R2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
 RN Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 RP SEQUENCE FROM N.A.  
 RA REBOUL J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;  
 RT "Comparative genomic analysis of the Interferon/Interleukin-10  
 RT receptor gene cluster."  
 RL Genome Res. 0:0-0(1999).  
 DR EMBL: AF082667; AAD13678.1;  
 DR EMBL: AF082666; AAD13671.1;  
 KM Receptor.  
 SQ SEQUENCE 341 AA; 39062 MW; 743D3364 CRC32;

Query Match 7.68; Score 243; DB 13; Length 341;  
 Best Local Similarity 26.1%; Pred. No. 4, 66e-28;  
 Matches 54; Conservative 52; Mismatches 86; Indels 15; Gaps 12;

DB 24 PNNARISVNFRRSVLLMDPGVRKGNLSYTVQAKSIFPKQNFNNVT--NLNVTCEQVSS 81

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OY 33 POKVEVDIIDNFILRRKRSDESGVNTFSFDYOKT-GMDWVILSGCONITSKCNSS 91
DB 82 L-SVYGAYLVLRVTEDEHSDM-AVYRFPMDVIGPSSVNVKSESGTILHVDFTGPA 138
OY 92 LKLVNEYIKLRIRAE-KENTSSVYEVDSFPFRKAQGPPEVLEHEDKAIYIHIS-PG 149
DB 139 ADREHDKMSLKQYTGSMYIRLLYKKSNNKVIHIDRKHNSIIISOLEPWTYICVOG- 197
OY 150 T-KDSVWALDGL--SFYISLLINKNSGVVE-RINIYSHKIKYKLSPEPTYCLAKVAA 205
DB 198 VIFEMNKTGERSOELCEQT-HNGVTP 223
OY 206 LITSM-KIGVYSPVHCITTYENELPP 231

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RESULT 5
ID 014936 PRELIMINARY; PRT: 484 AA.
AC 014936;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89003065.
RA AGUET M., DEMBIC Z., MERLIN G.;
RT "Molecular cloning and expression of the human interferon-gamma
RT receptor."
RL Cell 55:273-280(1988).
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE; 97246734.
RA MERLIN G., VAN DER LEEDE B.-J.M., MCKUNE K., KNEZEVIC N.,
RA BANNAWARTH W., ROMODIN N., VIEGAS-PEQUIGNOT E., KIEFER H., AGUET M.,
RA DEMBIC Z.;
RT "The gene for the ligand binding chain of the human interferon gamma
RT receptor."
RL Immunogenetics 45:413-421(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA DEMBIC Z.;
RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL; 019247; AAC52064.1;
DR EMBL; 019241; AAC52064.1; JOINED.
DR EMBL; 019242; AAC52064.1; JOINED.
DR EMBL; 019243; AAC52064.1; JOINED.
DR EMBL; 019244; AAC52064.1; JOINED.
DR EMBL; 019245; AAC52064.1; JOINED.
DR EMBL; 019246; AAC52064.1; JOINED.
SQ SEQUENCE 484 AA; 53818 MW; EEC99DIF CRC32;

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Query Match 4.4%; Score 140; DB 4; Length 484;  
 Best Local Similarity 25.3%; Pred. No. 1.77e-07;  
 Matches 37; Conservative 38; Mismatches 68; Indels 3; Gaps 3;

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DB 1 MALLFLPIYVQGVSRAMGADJGPSSVPPYVTVTSTYMANPIVWEQIMPOVY-F 59
OY 3 VLLGATTLVYAVGPWTLGAA-GGNLKSPOKVEYDIIIDNFIILNRNDESGVNTF 61
DB 60 TVEKNTGVKNSWDICINISHYCNISDVGSPNSLWYKVAARYGOKSSAAVAKSEEF 119
OY 62 SFDIOKGMWIKLISGCONITSKCNSSKLNVYEIKIRAEKENTSSWTE-VDSF 120
DB 120 AVCDGKIGPPKIDIRKEEKIMIDI 145
OY 121 TPFKRAQIGPPEVLEHEDKAIYIH 146

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RESULT 6

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ID 010466 PRELIMINARY; PRT: 26926 AA.
AC 010466;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=HEART.
RA LABELT S., KOLMER B.;
RT "Titins: giant proteins in charge of muscle ultrastructure and
RT elasticity."
RL Science 270:293-296(1995).
RN [2]
RP SEQUENCE OF 22277-25376 FROM N.A.
RX MEDLINE; 92258380.
RA LABELT S., GAUTEL M., LAKEY A., TRINICK J.;
RT "Towards a molecular understanding of titin."
RL EMBO J. 11:1711-1716(1992).
RN [3]
RP SEQUENCE OF 1976-2014 FROM N.A.
RA LABELT S.;
RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RX MEDLINE; 95331314.
RA GAUTEL M., CASTIGLIONE-MORELLI M.A., PEUHL M., MOTTA A., PASTORE A.;
RT "A calmodulin-binding sequence in the C-terminus of human cardiac
RT titin kinase."
RL Eur. J. Biochem. 230:752-759(1995).
CC -1- FUNCTION: THIS GIANT MUSCLE PROTEIN MAY BE INVOLVED IN MUSCLE
CC ASSEMBLY AND IN MAINTAINING THE STRUCTURAL INTEGRITY OF
CC SARCOMERES. MAY HAVE PROTEIN KINASE ACTIVITY.
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS OF THIS PROTEIN ARE
CC PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE
CC DISTRIBUTION. DIFFERENT SIZE TRANSCRIPTS MAY ALSO EXIST WITHIN ANY
CC ONE TISSUE. THE SEQUENCE SHOWN HERE IS THAT OF THE HEART ISOFORM
CC N2-B.
CC -1- TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
CC -1- SIMILARITY: TO THE CATALYTIC DOMAINS OF OTHER SERINE/THREONINE
CC KINASES.
CC -1- SIMILARITY: BELONGS TO IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 112
CC IMMUNOGLOBULIN C2-LIKE DOMAINS AND 132 FIBRONECTIN TYPE III-LIKE
CC DOMAINS.
DR EMBL; X64698; CAA45939.1;
DR EMBL; X83270; CAA58243.1;
DR EMBL; X64697; CAA45938.1;
DR EMBL; X90568; CAA62188.1;
DR EMBL; X64699; CAA45940.1;
DR HSSP; P56276; ITLK.
DR PFAM; PF00041; fn3; 132.
DR PFAM; PF00047; 19; 59.
DR PFAM; PF00069; kinase; 1.
DR PRINTS; PR00014; FMYVEPRTT.
DR PRINTS; PR00726; LEXASERFAS.
KW muscle protein; cytoskeleton; Structural protein; Calmodulin-binding;
KW Serine/threonine-protein kinase; Alternative splicing; Repeat;
KW Immunoglobulin domain; Phosphorylation.
FT DOMAIN 1370 1389 4 X 5 AA TANDEM REPEATS OF R-W-S-P-A.
FT DOMAIN 4429 4614 GLU/LYS/PRO/VAL-RICH.
FT DOMAIN 24731 25070 CATALYTIC.
FT DOMAIN 25030 25056 CALMODULIN-BINDING.
FT MOD_RES 1372 1372 PHOSPHORYLATION (BY PDK) (POTENTIAL).
FT MOD_RES 1377 1377 PHOSPHORYLATION (BY PDK) (POTENTIAL).
FT MOD_RES 1382 1382 PHOSPHORYLATION (BY PDK) (POTENTIAL).
FT MOD_RES 1387 1387 PHOSPHORYLATION (BY PDK) (POTENTIAL).
FT MOD_RES 26171 26171 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 26178 26178 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 26184 26184 PHOSPHORYLATION (POTENTIAL).

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FT MOD.RES 26190 26190 PHOSPHORYLATION (POTENTIAL).  
 FT CONFICT 22277 22277 T->P (IN REF. 2).  
 FT CONFICT 22449 22449 E->G (IN REF. 2).  
 FT CONFICT 22454 22454 T->Q (IN REF. 2).  
 FT CONFICT 23324 23324 S->L (IN REF. 2).  
 SQ SEQUENCE 26926 AA; 2993428 MW; 0214E3A3 CRC32;

Query Match 3.98; Score 123; DB 4; Length 26926;  
 Best Local Similarity 27.18; Pred. No. 1.52e-04;  
 Matches 29; Conservative 34; Mismatches 35; Indels 9; Gaps 8;

DB 21139 VILDMN-VCRIVATVITGPPSKP-KGPIRED-ELKADSVLSMDVNGGEGITCY 21195

OY 4 VILGATTVLVAVGPPVLSAAGKNIKSPQKVEYIIDNFTLRNRSDESYG-NVT-P 61

DB 21196 STKRETSQTNW-KNV-CSSVANT--FKVPNVYKDAEYOFVRAEN 21238

OY 62 SFQYKGTGDMWIKLSGCONITSTKCNFSIKNVYEELIKRIRAK 108

RESULT 7  
 ID 09XX66 PRELIMINARY; PRT: 349 AA.

AC 09XX66  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE Y102A5C.31 PROTEIN.  
 GN Y102A5C.31

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditi; Rhabditidae;  
 OC Rhabditi; Rhabditidae; Rhabditidae; Peleoderinae; Caenorhabditis.

RN [1] Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.

RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94150718.

RA GARDNER A.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RL elegans.";  
 RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.

RN [2] SEQUENCE FROM N.A.

RP MEDLINE: 94150718.

RA WILSON R., AINSKOUGH R., ANDERSON K., BAYNES C., BERRS M.,  
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
 RA CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,  
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLSTON J.,  
 RA THIRRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RL elegans.";  
 RL Nature 368:32-38(1994).  
 DR EMBL: AL031627; CAA20969.1;  
 SQ SEQUENCE 349 AA; 4019 MW; FD45B68 CRC32;

Query Match 3.78; Score 118; DB 5; Length 349;  
 Best Local Similarity 29.88; Pred. No. 1.01e-03;  
 Matches 17; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

DB 6 NSSEYDFPAPYLHFAVEIPHLVASYVIFTPSPMAVKNMMPFLRCSAFL 62

OY 112 SSMYEDSTPRKQIGPPEVHLAEADKAIVIHISPGTKDSVMALDGLSTYSIL 168

RESULT 8  
 ID 045849 PRELIMINARY; PRT: 349 AA.  
 AC 045849  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE T27C5.5 PROTEIN.

GN T27C5.5  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditi; Rhabditidae;  
 OC Rhabditi; Rhabditidae; Rhabditidae; Peleoderinae; Caenorhabditis.  
 RN [1] Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RA CUMMINGS P.;  
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.  
 RN [2] SEQUENCE FROM N.A.  
 RX MEDLINE: 94150718.

RA WILSON R., AINSKOUGH R., ANDERSON K., BAYNES C., BERRS M.,  
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
 RA CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,  
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLSTON J.,  
 RA THIRRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RL elegans.";  
 RL Nature 368:32-38(1994).  
 DR EMBL: 282058; CAB04866.1;  
 DR PFM: PF01604; 7em.5; 1.

SO SEQUENCE 349 AA; 40102 MW; 5FED9517 CRC32;

Query Match 3.68; Score 114; DB 5; Length 349;  
 Best Local Similarity 31.68; Pred. No. 4.46e-03;  
 Matches 18; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

DB 6 NSSEYDFPAPYLHFAVEIPHLVASYVIFTPSPMAVKNMMPFLRCSAFL 62

OY 112 SSMYEDSTPRKQIGPPEVHLAEADKAIVIHISPGTKDSVMALDGLSTYSIL 168

RESULT 9  
 ID 09MCU9 PRELIMINARY; PRT: 918 AA.  
 AC 09MCU9  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE GLYCOPROTEIN 130 PRECURSOR.  
 GN GP130.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 RN [1] SEQUENCE FROM N.A.  
 RP TISSUE-EMERGENCY HEART PRIMARY CULTURE (E7, E8);  
 RC MEDLINE: 99026068.  
 RX GEISSEN M., HELLER S., PENNICA D., ERNSECKER U., ROHRER H.;  
 RA "The specification of sympathetic neurotransmitter phenotype depends  
 RT on gp130 cytokine receptor signaling.";  
 RL Development 125:4791-4801(1998).  
 DR EMBL: AJ011688; CAB42084.1;  
 KW Signal.  
 RT Signal.  
 SQ SEQUENCE 918 AA; 102495 MW; 9DC128C3 CRC32;

Query Match 3.68; Score 114; DB 13; Length 918;  
 Best Local Similarity 25.38; Pred. No. 4.46e-03;  
 Matches 21; Conservative 23; Mismatches 36; Indels 3; Gaps 3;

DB 235 VNSGILPTVYKLSWENQISTVYMEKFNIRIRISSDINWMEVP-EDTASPTSFSSIGL 293

OY 36 VEVDIIDNFTLRN-NRDESYGVNTSEFDYKGTGDMWIKLSGCONITSTKCNFSIKL 94

DB 294 RPYEYVSIRCKMEKEDGVGFSMD 316

OY 95 NYEELIKRIRAKENNTSS-NYE 116



DT 01-JAN-1998 (Tremblrel. 05, last sequence update)  
 DT 01-NOV-1999 (Tremblrel. 12, last annotation update)  
 DE C27B7.7 PROTEIN.  
 GN C27B7.7.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
 OC Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MATTHEWS P.;  
 RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94150718.  
 RA WILSON R., AINSKOUGH R., ANDERSON K., BAYNES C., BERRS M.,  
 RA BONFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,  
 RA CRAWFORD M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIR M., JOHNSTON L.,  
 RA JONES M., KERSHAW J., KIRSTEN J., LAISPER N., LARRELLE P.,  
 RA LIGHTNING J., LLOYD C., MCNURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
 RA SMALLDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
 RA THIERRY-MIEG J., THOMAS R., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans."  
 RL Nature 368:32-38(1994).  
 DR EMBL: Z54236; CAA90982.1;  
 DR PFAM: PF00041; fn3: 7.  
 DR PFAM: PF00047; 19: 1.  
 SO SEQUENCE 1471 AA; 165507 MW; 1D71ECFC CRC32;

Query Match 3.5%; Score 112; DB 5; Length 1471;  
 Best Local Similarity 22.9%; Pred. No. 9.25e-03;  
 Matches 41; Conservative 55; Mismatches 66; Indels 17; Gaps 17;

DB 650 SPPDNKFLVINEANOVYVYNN-T-PNSTEYTGIL-IYTRDLSLSDOKNM-QFVEMN 705  
 QY 230 PPEPNEVSVOYOMTYLAK-WDYTYANMTFOVO-WLHAFILKRN-P-GHMLVK-WMOIPDCE 284  
 DB 706 N-NSTRKFFDLVGLKRTFVRVIRISGNSHADGPASEVEFEYSEVPITDTEVL 764  
 QY 285 NVKTKQCVFQNV-FQ-KGTYLRLVQASDGNNTSFNSEIKFDIELOAFILPPFNIRSL 342  
 DB 765 DDNTHIKFNANVRDPDHSKALGEYR-I-DLAATDVLAHLMKQIEPKS-IKIDEISSM 820  
 QY 343 SD-SFHI-YIGAPKQSGNTPIQDYPILEYIIEFMENTSNAERKIIKKTDTVTYVNLKPL 399

RESULT 14  
 ID 093662; PRELIMINARY; PRT; 505 AA.  
 AC 093662;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, last sequence update)  
 DT 01-NOV-1999 (Tremblrel. 12, last annotation update)  
 DE CATALASE (EC 1.11.1.6).  
 GN CAT.  
 OS Methanosarcina barkeri.  
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;  
 OC Methanosarcina.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-FUSARO (DSMZ 804);  
 RA SHIMA S., NETRUSOV A., SORDEL M., WICKE M., HARTMANN G.C.,  
 RA THAUER R.K.;  
 RT "Purification, characterization and primary structure of a  
 RT monofunctional catalase from Methanosarcina barkeri";  
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.  
 DR HSSP: P00432; 7CAT.  
 DR Oxidoreductase; Peroxidase.  
 SO SEQUENCE 505 AA; 57065 MW; 3155E7F1 CRC32;

Query Match 3.4%; Score 108; DB 1; Length 505;  
 Best Local Similarity 26.0%; Pred. No. 3.87e-02;  
 Matches 13; Conservative 18; Mismatches 17; Indels 2; Gaps 2;

DB 365 PENSYORDGFM-RVDANGSGPNWPNPSFGSPDSYLEPP-FGVGSLA 412  
 QY 294 PGNVFGITILRLVQASDGNNTSFNSEIKFDIELOAFILPPVYNIRSL 343

RESULT 15  
 ID 007784; PRELIMINARY; PRT; 817 AA.  
 AC 007784;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, last sequence update)  
 DT 01-NOV-1999 (Tremblrel. 12, last annotation update)  
 DE TITIN (FRAGMENT).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-HEART MUSCLE;  
 RX MEDLINE: 94043058.  
 RA TAN K.O., SATER G.R., MYERS A.M., ROBSON R.M., HUATT T.W.;  
 RT "Molecular characterization of avian muscle titin";  
 RL J. Biol. Chem. 268:22900-22907(1993).  
 DR EMBL: L19140; AAC38006.1;  
 DR HSSP: P02751; 1TTG.  
 DR PFAM: PF00041; fn3: 6.  
 DR PFAM: PF00047; 19: 1.  
 FT NON\_TER 1  
 FT NON\_TER 817  
 SO SEQUENCE 817 AA; 91388 MW; 3E1369C8 CRC32;

Query Match 3.4%; Score 107; DB 13; Length 817;  
 Best Local Similarity 23.0%; Pred. No. 5.50e-02;  
 Matches 32; Conservative 38; Mismatches 59; Indels 10; Gaps 10;

DB 467 VDKTKNSVDLTWOPPRHDGNGKIIGYLYEYOKVDEEMKRNILPPDSCPEYKYVGTGTE 526  
 QY 38 VDIIDNFIILRMNRN-DESGVNT-FSFYDQKGMNMWILS-GCQNTITSKCFSSLKL 94  
 DB 527 GLTYKFNVAVNAAGESEPA-YYPDP-VEV-KDRLEPPELLIDA-NMAREOHVRAQDILR 582  
 QY 95 NV-YEEIKIRIRAREKETSSMYEVDSETPPRKAOIGPPEVHLEADKAIVIHISPGTKDS 153  
 DB 583 ISAVIKGVPPP-KV-SMK 599  
 QY 154 VMNALDGLSTFTSLIKRN 172

Search completed: Mon Aug 21 10:27:12 2000.  
 Job time : 41 secs.

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 M O S E L L  
 (TM)  
 \*\*\*\*\*

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Mpsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Mon Aug 21 10:24:36 2000; Maspar time 13.95 Seconds  
 Tabular output not generated. 740.422 Million cell updates/sec

Title: >US-09-240-675-2  
 Description: (1-436) from US09240675.pep  
 Perfect Score: 3178  
 Sequence: 1 MMVVLGATLVVAVGPWV.....KSSVFSDAVEKTRKPGTSK 436

Scoring table: PAM 150  
 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 08  
 Listing first 45 summaries

Database: a-geneseq36  
 1:geneseqp

Statistics: Mean 35.309; Variance 151.609; scale 0.233

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	3178	100.0	436	1	R28495	Sequence of a soluble
2	3178	100.0	436	1	R14487	Soluble Interferon- $\alpha$
3	3178	100.0	557	1	R14488	Complete Interferon- $\alpha$
4	3178	100.0	557	1	R11958	Human $\alpha$ -Interferon
5	3178	100.0	557	1	R42635	Human Interferon recep
6	3178	100.0	557	1	R28496	Sequence of a soluble
7	3171	99.8	557	1	R75356	Human IFN receptor
8	3171	99.8	557	1	R71804	Transmembrane Interfe
9	3163	99.5	436	1	R71723	IFN receptor extracell
10	3117	98.1	434	1	R21805	Spliced-deleted interf
11	3025	95.2	496	1	R21806	Spliced-deleted interf
12	274	8.6	332	1	W52296	CRP4 protein.
13	243	7.6	332	1	W79159	IFN- $\gamma$ cytokine recep
14	243	7.6	332	1	W79159	Human IFN- $\gamma$ access
15	183	5.8	337	1	R75783	IFN- $\gamma$ cytokine recep
16	183	5.8	337	1	R75783	Human cytokine recep
17	164	5.2	374	1	W97861	Human cytokine recep
18	152	4.8	211	1	W97864	Human cytokine recep
19	139	4.4	17	1	R47008	IFN- $\alpha$ receptor pos
20	140	4.4	489	1	R07469	Plasmod pabaute human
21	132	4.2	575	1	W41803	Mouse IL-10 receptor
22	131	4.1	245	1	R62023	Soluble human Interfer
23	130	4.1	575	1	R57139	Interleukin-10 recepto

24	128	4.0	329	1	W17859	Rheumatoid arthritis a
25	128	4.0	332	1	W70799	Human gp130-delta-3f6b
26	128	4.0	658	1	R94576	Human gp130 splice var
27	128	4.0	708	1	R85811	gp130 N-terminal fragm
28	128	4.0	708	1	R37804	Human gp130 N-terminal
29	128	4.0	859	1	W70796	Human gp130-Fc-His6 am
30	128	4.0	918	1	R75368	Human gp130 protein
31	128	4.0	918	1	R46233	Human soluble glycopro
32	128	4.0	918	1	R10545	Recombinant human gp13
33	128	4.0	951	1	W70798	Human gp130-C-gamma-1
34	125	3.9	227	1	R14642	Gamma interferon recep
35	125	3.9	231	1	R14641	Gamma interferon recep
36	125	3.9	473	1	R55749	Extracellular domain o
37	125	3.9	942	1	R70113	Gamma-IFN-R-GPB 130 fu
38	119	3.7	210	1	R14643	Gamma Interferon recep
39	116	3.7	578	1	R57138	Interleukin-10 recepto
40	116	3.7	578	1	W41804	Human IL-10 receptor
41	118	3.7	660	1	R69633	Human Interleukin-12 r
42	118	3.7	662	1	R69632	Human Interleukin-12 r
43	118	3.7	662	1	W12772	Human Interleukin-12 b
44	113	3.6	180	1	W00404	Interleukin-6 antago
45	108	3.4	877	1	W71628	Mouse Bsk receptor-11k

## ALIGNMENTS

RESULT	1	R28495	standard; Protein; 436 AA.
ID	CC	R28495	
AC	CC	R28495	
DR	CC	31-MAR-1993	(first entry)
DE	CC	Sequence of a soluble form of the Interferon (IFN) receptor	
DE	CC	with a high affinity for IFN- $\alpha$ and - $\beta$ .	
KW	CC	Interferon receptor; alpha-Interferon; beta-Interferon.	
OS	CC	Synthetic.	
PN	CC	MO9218626-A.	
PD	CC	29-OCT-1992	
PF	CC	17-APR-1991; WO-F00318	
PR	CC	17-APR-1991; WO-F00318	
PA	CC	(EUBI-) LAB EURO BIOTECHNOLOGIE.	
PI	CC	Eid P, Gresser I, Luttalla G, Meyer F, Mogensen KE,	
PI	CC	Tovey M, Uze G;	
DR	CC	WPI; 92-382110/46.	
DR	CC	N-PSDB: 030532.	
PT	CC	Water soluble polypeptide(s) strongly bind Interferon(s) $\alpha$ and	
PT	CC	$\beta$ and $\beta$ - useful as immunosuppressants, for treating auto-immune	
PT	CC	diseases and transplant rejection	
PS	CC	Claim 2; Fig 1; 58pp; English.	
CC	CC	DNA encoding the water-soluble polypeptide with a high affinity for	
CC	CC	IFN- $\alpha$ and - $\beta$ is isolated by PCR, using appropriate	
CC	CC	oligonucleotides as primers and cloned cDNA as template. For example,	
CC	CC	bacteriophage lambda ZAP, containing the entire coding sequence of	
CC	CC	the IFN- $\alpha$ and - $\beta$ receptor (Q30533), was incubated with oligos	
CC	CC	Q30534 and Q30535. R28496 represents the complete receptor. R28495	
CC	CC	lacks the transmembrane and cytoplasmic domains. Both forms bind	
CC	CC	IFN in the same way as antibodies so are immunosuppressants e.g. for	
CC	CC	treating autoimmune diseases and graft rejection. They lack the	
CC	CC	toxic side-effects of known immunosuppressants such as steroids.	
CC	CC	Sequence 436 AA.	

Query Match: 100.0%; Score 3178; DB 1; Length 436;  
 Best local similarity: 100.0%; Pred. No. 4.64e-300;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB	1	MMVVLGATLVVAVGPWVLSAAGGKNKSPQKVEVDIIDDPIILRMRSDESVNVT	60
DB	1	MMVVLGATLVVAVGPWVLSAAGGKNKSPQKVEVDIIDDPIILRMRSDESVNVT	60
DB	61	FSDYDQKTDGNNIKSGCNITSTKCNSSKLNTVEETKLRKEKNTSSMYEDSF	120
DB	61	FSDYDQKTDGNNIKSGCNITSTKCNSSKLNTVEETKLRKEKNTSSMYEDSF	120
DB	121	TPPKAIGPPEVHEAEKRAIYHISPGKDSVMAALDLSPTYSLLTKNKGVEERT	160

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OY 121 TPRKAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSTFYSLILMKSSGVEERI 180
DB 181 ENISRKIKYKLSPEYTYCLAKAALITSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
OY 181 ENISRKIKYKLSPEYTYCLAKAALITSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
DB 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTTCQVFPQNVFOR 300
OY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTTCQVFPQNVFOR 300
DB 301 GIVILRQASDGNNTSFSEIEKFDTEIOAFLLPPVFNINLSDFSFIHYIGAPROSGNTP 360
OY 301 GIVILRQASDGNNTSFSEIEKFDTEIOAFLLPPVFNINLSDFSFIHYIGAPROSGNTP 360
DB 361 VIQDYPILYEIIIFWENTSMARKIIIEKTDVTYNLKLPLVYCYKARAHPTDEKLNTSSV 420
OY 361 VIQDYPILYEIIIFWENTSMARKIIIEKTDVTYNLKLPLVYCYKARAHPTDEKLNTSSV 420
DB 421 FSDAVCEKTRKGNNTSK 436
OY 421 FSDAVCEKTRKGNNTSK 436

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## RESULT 2

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ID R14487 standard; Protein; 436 AA.
AC R14487;
DE 16-JAN-1992 (first entry)
DT Soluble interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eid P. Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tover MG, Uze G;
PI WPI; 91-319778/44.
DR N-PSDB; Q14239.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Claim 2; Page 45; 52pp; French.
CC The transmembrane and cytoplasmic domains of the native IFN receptor
CC have been deleted to obtain a soluble, circulating form of the
CC receptor. Potentially immunogenic epitopes have thus been eliminated.
CC Derivatives obtained by substitution or deletion of this sequence
CC are also claimed as are hybrid molecules comprising the soluble
CC receptor (or deriv.) and an immunoglobulin such as IgG1.
CC See also Q14240.
SQ Sequence 436 AA;

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Query Match 100.0%; Score 3178; DB 1; Length 436;
Best Local Similarity 100.0%; Pred. No. 4.64e-300;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MMVVLGATLVLVAVGPVWLSAAGGKNLKSPOKVEVDIIDNFIIRNRSDSEGVNT 60
OY 1 MMVVLGATLVLVAVGPVWLSAAGGKNLKSPOKVEVDIIDNFIIRNRSDSEGVNT 60
DB 61 FSPDYQKTGMDNWKISGCONITSTKCNFSLKINLYEEIKLIRAEKENTSSWYEDSF 120
OY 61 FSPDYQKTGMDNWKISGCONITSTKCNFSLKINLYEEIKLIRAEKENTSSWYEDSF 120
DB 121 TPRKAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSTFYSLILMKSSGVEERI 180
OY 121 TPRKAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSTFYSLILMKSSGVEERI 180
DB 181 ENISRKIKYKLSPEYTYCLAKAALITSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
OY 181 ENISRKIKYKLSPEYTYCLAKAALITSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
DB 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTTCQVFPQNVFOR 300
OY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTTCQVFPQNVFOR 300

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OY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTTCQVFPQNVFOR 300
DB 301 GIVILRQASDGNNTSFSEIEKFDTEIOAFLLPPVFNINLSDFSFIHYIGAPROSGNTP 360
OY 301 GIVILRQASDGNNTSFSEIEKFDTEIOAFLLPPVFNINLSDFSFIHYIGAPROSGNTP 360
DB 361 VIQDYPILYEIIIFWENTSMARKIIIEKTDVTYNLKLPLVYCYKARAHPTDEKLNTSSV 420
OY 361 VIQDYPILYEIIIFWENTSMARKIIIEKTDVTYNLKLPLVYCYKARAHPTDEKLNTSSV 420
DB 421 FSDAVCEKTRKGNNTSK 436
OY 421 FSDAVCEKTRKGNNTSK 436

```

## RESULT 3

```

ID R14488 standard; Protein; 557 AA.
AC R14488;
DE 16-JAN-1992 (first entry)
DT Complete interferon-alpha/beta receptor.
KW IFN; autoimmune disease; graft rejection; histocompatibility.
OS Homo sapiens.
PN FR2657881-A.
PD 09-AUG-1991.
PF 05-FEB-1990; 001298.
PR 05-FEB-1990; FR-001298.
PA (EUBI-) LAB EURO BIOTECHNO.
PI Eid P. Gresser I, Lutfalla G, Meyer F, Mogensen KE;
PI Tover MG, Uze G;
PI WPI; 91-319778/44.
DR N-PSDB; Q14240.
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,
PT aplastic anemia, diabetes mellitus, rheumatoid arthritis, etc.
PS Disclosure; Page 47; 52pp; French.
CC The invention covers derivatives of the interferon-alpha and/or beta
CC receptor obtained by deleting the transmembrane and cytoplasmic domains
CC of the native receptor or by substitution. Potentially immunogenic
CC epitopes are eliminated and the deriv. can be secreted from
CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta
CC and can be used to treat autoimmune diseases or to inhibit graft
CC rejection. See also Q14239.
SQ Sequence 557 AA;

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Query Match 100.0%; Score 3178; DB 1; Length 557;
Best Local Similarity 100.0%; Pred. No. 4.64e-300;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

DB 1 MMVVLGATLVLVAVGPVWLSAAGGKNLKSPOKVEVDIIDNFIIRNRSDSEGVNT 60
OY 1 MMVVLGATLVLVAVGPVWLSAAGGKNLKSPOKVEVDIIDNFIIRNRSDSEGVNT 60
DB 61 FSPDYQKTGMDNWKISGCONITSTKCNFSLKINLYEEIKLIRAEKENTSSWYEDSF 120
OY 61 FSPDYQKTGMDNWKISGCONITSTKCNFSLKINLYEEIKLIRAEKENTSSWYEDSF 120
DB 121 TPRKAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSTFYSLILMKSSGVEERI 180
OY 121 TPRKAOIGPEVHLEADKAIVIHISPGTKDSVMALDGLSTFYSLILMKSSGVEERI 180
DB 181 ENISRKIKYKLSPEYTYCLAKAALITSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
OY 181 ENISRKIKYKLSPEYTYCLAKAALITSMKIGVYSPVHCIKTTVENELPPENIEVSQ 240
DB 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTTCQVFPQNVFOR 300
OY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENVTTCQVFPQNVFOR 300

```



Db 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLLPPVFNIRSLSDSFHYIIGAPKOSGNT 360  
 OY 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLLPPVFNIRSLSDSFHYIIGAPKOSGNT 360  
 Db 361 VIODPLIYEIIFMENTSNAERKIIIEKTDVTPNPKPLTYCYCARAHMDEKLNKSSV 420  
 OY 361 VIODPLIYEIIFMENTSNAERKIIIEKTDVTPNPKPLTYCYCARAHMDEKLNKSSV 420  
 Db 421 FSDAVCEKTKRGNTSK 436  
 OY 421 FSDAVCEKTKRGNTSK 436

RESULT 4  
 ID R1958 standard; Protein 557 AA.  
 AC R1958:  
 DT 18-JUL-1991 (first entry)  
 DE Human alpha-interferon receptor protein.  
 KW Human alpha IFN, IFN agonists; antiviral; anti tumour agent;  
 OS Homo sapiens.  
 FH Key  
 FT peptide  
 FT 1. 27  
 FT Location/Qualifiers  
 PN WO9105862-A.  
 PD 02-MAY-1991.  
 PF 19-OCT-1990; F00758.  
 PR 20-OCT-1989; FR-013770.  
 PA (CNRS) CNRS CENT NAT RECH SCI.  
 PI Mogensen KE, Uze G, Lutfalla G, Gresser I;  
 DR WPI: 91-148740/20.  
 DR N-PSDB: Q11701.  
 PT New human alpha-interferon receptor protein - useful for testing  
 PS Interferon agonists and in treatment or diagnosis  
 PS Disclosure: fig 4; 30pp; French.  
 CC This recombinant human alpha-interferon (IFN) receptor protein is  
 CC useful for the testing of IFN agonists and for treatment and diag-  
 CC nosis of viral diseases and tumours. Antibodies raised against  
 CC this protein can be used for blocking the receptor when required,  
 CC eg where overexpression of alpha-IFN is harmful. The Abs are  
 CC also useful for eg drug targeting. Variants of the protein,  
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted  
 CC between residues 479 and 480, are also useful.  
 SO Sequence 557 AA.

Query Match 100.0%; Score 3178; DB 1; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 4,64e-300;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMYVLLGATTLVLAAGPWTLSAAGKRLKSPQKVEVDIIDDNFILRNRSDESVCNT 60  
 OY 1 MMYVLLGATTLVLAAGPWTLSAAGKRLKSPQKVEVDIIDDNFILRNRSDESVCNT 60  
 Db 61 FSDYOKTGDMNFKISGCONITSTKCNFSLKLNVEEIKLRIRAEKENTSSMYEVSF 120  
 OY 61 FSDYOKTGDMNFKISGCONITSTKCNFSLKLNVEEIKLRIRAEKENTSSMYEVSF 120  
 Db 121 TPRKAOIGPEVHLEAEDKAIYIHISPGKDSVMALDGLSTYSLLIMKSSGVEERI 180  
 OY 121 TPRKAOIGPEVHLEAEDKAIYIHISPGKDSVMALDGLSTYSLLIMKSSGVEERI 180  
 Db 181 ENYSRHKIKYKSPETTYCLAKVAALLTSMKIGVSPVHCITTYVENELPPENIEVSQ 240  
 OY 181 ENYSRHKIKYKSPETTYCLAKVAALLTSMKIGVSPVHCITTYVENELPPENIEVSQ 240  
 Db 241 NONTYAKMDYTYANNFTFOVOMLHAFKRNPGNHLTKMKOIPDCEVNTKTCVFPONVOK 300  
 OY 241 NONTYAKMDYTYANNFTFOVOMLHAFKRNPGNHLTKMKOIPDCEVNTKTCVFPONVOK 300  
 Db 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLLPPVFNIRSLSDSFHYIIGAPKOSGNT 360  
 OY 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLLPPVFNIRSLSDSFHYIIGAPKOSGNT 360

Db 361 VIODPLIYEIIFMENTSNAERKIIIEKTDVTPNPKPLTYCYCARAHMDEKLNKSSV 420  
 OY 361 VIODPLIYEIIFMENTSNAERKIIIEKTDVTPNPKPLTYCYCARAHMDEKLNKSSV 420  
 Db 421 FSDAVCEKTKRGNTSK 436  
 OY 421 FSDAVCEKTKRGNTSK 436

RESULT 5  
 ID R42635 standard; Protein 557 AA.  
 AC R42635:  
 DT 20-APR-1994 (first entry)  
 DE Human interferon receptor  
 KW IFN-R; extracellular domain; monoclonal antibody; viral infection;  
 KW cell proliferation; allograft rejection; systemic lupus erythematosus;  
 KW psoriasis; multiple sclerosis; Behcet's disease; aplastic anaemia;  
 KW immunodeficiency; measles virus; Interferon-alpha-beta.  
 OS Homo sapiens.  
 FH Key  
 FT domain  
 FT 1. 436  
 FT Location/Qualifiers  
 PN BP-563487-A.  
 PD 06-OCT-1993.  
 PF 31-MAR-1992; 400902.  
 PR 31-MAR-1992; EP-400902.  
 PA (Eurt. Lab. EURO BIOTECHNOLOGIE SA.  
 PI Benoit P, Maguette D, Meyer F, Plavec I, Torey MG;  
 DR WPI: 93-312951/40.  
 DR P-PSDB: R42635.  
 PT Monoclonal antibody to human interferon type-I receptor - having  
 PT neutralising activity against human type I interferon, used for  
 PS therapy and diagnosis  
 PS Disclosure: fig 3; 21pp; English.  
 CC Monoclonal antibodies produced against soluble forms of the human  
 CC interferon alpha-beta receptor based on the full-length human IFN-R  
 CC sequence are claimed. The antibodies are useful for treatment and  
 CC prophylaxis of disorders involving cell proliferation and/or viral  
 CC infection.  
 SO Sequence 557 AA.

Query Match 100.0%; Score 3178; DB 1; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 4,64e-300;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMYVLLGATTLVLAAGPWTLSAAGKRLKSPQKVEVDIIDDNFILRNRSDESVCNT 60  
 OY 1 MMYVLLGATTLVLAAGPWTLSAAGKRLKSPQKVEVDIIDDNFILRNRSDESVCNT 60  
 Db 61 FSDYOKTGDMNFKISGCONITSTKCNFSLKLNVEEIKLRIRAEKENTSSMYEVSF 120  
 OY 61 FSDYOKTGDMNFKISGCONITSTKCNFSLKLNVEEIKLRIRAEKENTSSMYEVSF 120  
 Db 121 TPRKAOIGPEVHLEAEDKAIYIHISPGKDSVMALDGLSTYSLLIMKSSGVEERI 180  
 OY 121 TPRKAOIGPEVHLEAEDKAIYIHISPGKDSVMALDGLSTYSLLIMKSSGVEERI 180  
 Db 181 ENYSRHKIKYKSPETTYCLAKVAALLTSMKIGVSPVHCITTYVENELPPENIEVSQ 240  
 OY 181 ENYSRHKIKYKSPETTYCLAKVAALLTSMKIGVSPVHCITTYVENELPPENIEVSQ 240  
 Db 241 NONTYAKMDYTYANNFTFOVOMLHAFKRNPGNHLTKMKOIPDCEVNTKTCVFPONVOK 300  
 OY 241 NONTYAKMDYTYANNFTFOVOMLHAFKRNPGNHLTKMKOIPDCEVNTKTCVFPONVOK 300  
 Db 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLLPPVFNIRSLSDSFHYIIGAPKOSGNT 360  
 OY 301 GYLLRVOASDGNNTSFSEEEKFDTETIOAFLLPPVFNIRSLSDSFHYIIGAPKOSGNT 360  
 Db 361 VIODPLIYEIIFMENTSNAERKIIIEKTDVTPNPKPLTYCYCARAHMDEKLNKSSV 420  
 OY 361 VIODPLIYEIIFMENTSNAERKIIIEKTDVTPNPKPLTYCYCARAHMDEKLNKSSV 420

OY 361 VIQDYPLIYEIIFMENTSNAERKIIIEKTDVTPNKLPLTVYCYKAAHHTDEKLNKSSV 420  
 DB 421 FSDAVCEKTKPGNTSK 436  
 OY 421 FSDAVCEKTKPGNTSK 436

RESULT 6  
 ID R28496 standard; Protein; 557 AA.  
 AC R28496;  
 DT 31-MAR-1993 (first entry)  
 DE Sequence of a soluble form of the interferon (IFN) receptor with a high affinity for IFN-alpha and -beta  
 KM Interferon receptor; alpha-interferon; beta-interferon  
 OS Synthetic.  
 PN WO9218626-A.  
 PD 29-OCT-1992.  
 PF 17-APR-1991; F00318.  
 PR 17-APR-1991; WO-F00318.  
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.  
 PI Eld P, Gresser I, Luftalla G, Meyer F, Mogensen KE.  
 PI Tovey M, Uze G.  
 DR WPI: 92-382110/46.  
 DR N-PSDB: Q30533.  
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha and beta - useful as: immunosuppressants, for treating, auto-immune diseases and transplant rejection  
 PS Claim 3; Fig 2; 58pp; English.  
 CC DNA encoding the water-soluble polypeptide with a high affinity for IFN-alpha and -beta is isolated by PCR, using appropriate oligonucleotides as primers and cloned cDNA as template. For example, bacteriophage lambda ZAP, containing the entire coding sequence of the IFN-alpha and -beta receptor (Q30533), was incubated with oligos Q30534 and Q30535. R28496 represents the complete receptor. R28495 lacks the transmembrane and cytoplasmic domains. Both forms bind IFN in the same way as antibodies so are immunosuppressants e.g. for treating autoimmune diseases and graft rejection. They lack the toxic side-effects of known immunosuppressants such as steroids.  
 CC Sequence 557 AA;

Query Match 100.0%; Score 3178; DB 1; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 4 64e-300;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVYLLGATTLVAVAGPWLISAAGGNLKSPOKYEVDIIDNFI LRNRSDSEYGNVT 60  
 OY 1 MMVYLLGATTLVAVAGPWLISAAGGNLKSPOKYEVDIIDNFI LRNRSDSEYGNVT 60  
 DB 61 FSDYKGTGDMNIRKISGCONITSTKCNFSLKLNVEEIKIRAKENTSSMYEVSF 120  
 OY 61 FSDYKGTGDMNIRKISGCONITSTKCNFSLKLNVEEIKIRAKENTSSMYEVSF 120  
 DB 121 TPRKAOIGPEVHLAEDEKAIYIHISPGTKDSVMALDGLSTYSLLIRKNSGVEERI 180  
 OY 121 TPRKAOIGPEVHLAEDEKAIYIHISPGTKDSVMALDGLSTYSLLIRKNSGVEERI 180  
 DB 181 ENIYSRHKIYKLSPEYTYCLKVAALLTSWKIGVSPHCIKTVENELPPENIEVSQ 240  
 OY 181 ENIYSRHKIYKLSPEYTYCLKVAALLTSWKIGVSPHCIKTVENELPPENIEVSQ 240  
 DB 241 NQNTYVKMDTYTANMTVOVOMLAFLKRNPNHLYKWKQIPDCENVTTCQVFPONVFK 300  
 OY 241 NQNTYVKMDTYTANMTVOVOMLAFLKRNPNHLYKWKQIPDCENVTTCQVFPONVFK 300  
 DB 301 GIYLLRVOASDGNNTSFWSEIKFDEIOAFLLPPVFNIRSLSDSHIYIGAKOSGNTP 360  
 OY 301 GIYLLRVOASDGNNTSFWSEIKFDEIOAFLLPPVFNIRSLSDSHIYIGAKOSGNTP 360  
 DB 361 VIQDYPLIYEIIFMENTSNAERKIIIEKTDVTPNKLPLTVYCYKAAHHTDEKLNKSSV 420  
 OY 361 VIQDYPLIYEIIFMENTSNAERKIIIEKTDVTPNKLPLTVYCYKAAHHTDEKLNKSSV 420  
 DB 421 FSDAVCEKTKPGNTSK 436

OY 421 FSDAVCEKTKPGNTSK 436

RESULT 7  
 ID R75356 standard; Protein; 557 AA.  
 AC R75356;  
 DT 16-OCT-1995 (first entry)  
 DE Human IFN receptor.  
 KM IFN receptor; Interferon receptor; Interferon-alpha; Interferon-beta; monoclonal antibody; Immunomodulator; AIDS.  
 OS Homo sapiens.  
 FH Key location/Qualifiers  
 FT domain 1, 436  
 FT /label- Extracellular\_domain  
 PN WO9507716-A.  
 PD 23-MAR-1995.  
 PF 16-SEP-1994; E03114.  
 PR 17-SEP-1993; EP-402279.  
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.  
 PI Benizri EJ, Tovey MC.  
 PI WPI: 95-131187/17.  
 DR N-PSDB: Q86458.  
 PT Composn. of monoclonal antibodies against interferon receptor - useful as immunomodulator, eg. for treating AIDS  
 PS Disclosure; Fig. 3A-2B; 105pp; English.  
 CC The amino acid sequence of human interferon class I receptor is given in R75356. A recombinant soluble form of the extracellular domain of this receptor (R1723) has been used to raise immunomodulatory monoclonal antibodies.  
 CC Sequence 557 AA;

Query Match 99.8%; Score 3171; DB 1; Length 557;  
 Best Local Similarity 99.8%; Pred. No. 2 33e-299;  
 Matches 435; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVYLLGATTLVAVAGPWLISAAGGNLKSPOKYEVDIIDNFI LRNRSDSEYGNVT 60  
 OY 1 MMVYLLGATTLVAVAGPWLISAAGGNLKSPOKYEVDIIDNFI LRNRSDSEYGNVT 60  
 DB 61 FSDYKGTGDMNIRKISGCONITSTKCNFSLKLNVEEIKIRAKENTSSMYEVSF 120  
 OY 61 FSDYKGTGDMNIRKISGCONITSTKCNFSLKLNVEEIKIRAKENTSSMYEVSF 120  
 DB 121 TPRKAOIGPEVHLAEDEKAIYIHISPGTKDSVMALDGLSTYSLLIRKNSGVEERI 180  
 OY 121 TPRKAOIGPEVHLAEDEKAIYIHISPGTKDSVMALDGLSTYSLLIRKNSGVEERI 180  
 DB 181 ENIYSRHKIYKLSPEYTYCLKVAALLTSWKIGVSPHCIKTVENELPPENIEVSQ 240  
 OY 181 ENIYSRHKIYKLSPEYTYCLKVAALLTSWKIGVSPHCIKTVENELPPENIEVSQ 240  
 DB 241 NQNTYVKMDTYTANMTVOVOMLAFLKRNPNHLYKWKQIPDCENVTTCQVFPONVFK 300  
 OY 241 NQNTYVKMDTYTANMTVOVOMLAFLKRNPNHLYKWKQIPDCENVTTCQVFPONVFK 300  
 DB 301 GIYLLRVOASDGNNTSFWSEIKFDEIOAFLLPPVFNIRSLSDSHIYIGAKOSGNTP 360  
 OY 301 GIYLLRVOASDGNNTSFWSEIKFDEIOAFLLPPVFNIRSLSDSHIYIGAKOSGNTP 360  
 DB 361 VIQDYPLIYEIIFMENTSNAERKIIIEKTDVTPNKLPLTVYCYKAAHHTDEKLNKSSV 420  
 OY 361 VIQDYPLIYEIIFMENTSNAERKIIIEKTDVTPNKLPLTVYCYKAAHHTDEKLNKSSV 420  
 DB 421 FSDAVCEKTKPGNTSK 436  
 OY 421 FSDAVCEKTKPGNTSK 436  
 RESULT 8  
 ID W21804 standard; Protein; 557 AA.  
 AC W21804;  
 DT 23-SEP-1997 (first entry)

PN AU9475977-A.  
PD 11-MAY-1995.

PF 20-OCT-1994; 075977.  
 PR 24-OCT-1993; IL-107378.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI (ABRA/) ABRAMOYICH C.  
 DR ABRAMOYICH C, Ratovitski E, Revel M;  
 WPI: 95-200634/27.  
 PT New mammalian soluble interferon alpha-receptor forms - used for  
 PT inhibiting, modulating or modifying the activities of interferon(s)  
 PS Example 2; Fig 7; 46pp; English.  
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1  
 CC (W21805) is characterised by a new domain (S) which follows an  
 CC end-deleted extracellular domain when compared to transmembran  
 CC IFNAR (W21804). There is no transmembrane domain. The amino acid  
 CC sequence is predicted from a cDNA clone (see also T73520) obd  
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR  
 CC splice-deleted forms 1 and 2 (see also W21806) probably regulate  
 CC the response of human cells to IFNs, either by acting as IFN  
 CC antagonists or by regulating the activity of the multiple IFN  
 CC subtypes. They can be expressed in host cells and used to inhibit  
 CC modulate or modify the activities of IFNs alpha and beta in cells,  
 CC tissues and organisms, or for diagnostic purposes.  
 SQ Sequence 434 AA;

Query Match 98.1%; Score 3117; DB 1; Length 434;  
 Best Local Similarity 99.5%; Pred. No. 5,966-294;  
 Matches 426; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MAAVLLGATTLVLAAGVFWLSAAAGKRLKSPQKVEVDIIDNFIILMNRSDSVGNT 60  
 QY 1 MAAVLLGATTLVLAAGVFWLSAAAGKRLKSPQKVEVDIIDNFIILMNRSDSVGNT 60  
 Db 61 FSPDYORTGMDNMIKLSGCCNITSTKCNFSSKLNTVEIKLRIRAEKENTSSWEYDSF 120  
 QY 61 FSPDYORTGMDNMIKLSGCCNITSTKCNFSSKLNTVEIKLRIRAEKENTSSWEYDSF 120  
 Db 121 TPFRAOIGPEVHLEADKAIYHISPGTDSVMALDGLSFYSLILMNSSGVERRI 180  
 QY 121 TPFRAOIGPEVHLEADKAIYHISPGTDSVMALDGLSFYSLILMNSSGVERRI 180  
 Db 181 ENTYSRHKIYKLSPEYTYCLKVKAAALTSWKIGYSPVHCIKTYVENELPPENIEVSQ 240  
 QY 181 ENTYSRHKIYKLSPEYTYCLKVKAAALTSWKIGYSPVHCIKTYVENELPPENIEVSQ 240  
 Db 181 ENTYSRHKIYKLSPEYTYCLKVKAAALTSWKIGYSPVHCIKTYVENELPPENIEVSQ 240  
 QY 181 ENTYSRHKIYKLSPEYTYCLKVKAAALTSWKIGYSPVHCIKTYVENELPPENIEVSQ 240  
 Db 241 NONTVLKMDIYANNTFOVOMLAFKRNPNHLYKMKQIPDCENVTTCVFPQNVFOK 300  
 QY 241 NONTVLKMDIYANNTFOVOMLAFKRNPNHLYKMKQIPDCENVTTCVFPQNVFOK 300  
 Db 241 NONTVLKMDIYANNTFOVOMLAFKRNPNHLYKMKQIPDCENVTTCVFPQNVFOK 300  
 QY 241 NONTVLKMDIYANNTFOVOMLAFKRNPNHLYKMKQIPDCENVTTCVFPQNVFOK 300  
 Db 301 GIYLLRVOASGNTSFSESEIKPDTLOAFLLPPVFNIRSLDSFHYIGAPROSGNTP 360  
 QY 301 GIYLLRVOASGNTSFSESEIKPDTLOAFLLPPVFNIRSLDSFHYIGAPROSGNTP 360  
 Db 301 GIYLLRVOASGNTSFSESEIKPDTLOAFLLPPVFNIRSLDSFHYIGAPROSGNTP 360  
 QY 301 GIYLLRVOASGNTSFSESEIKPDTLOAFLLPPVFNIRSLDSFHYIGAPROSGNTP 360  
 Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVNKLPLIYCYKARAHMTDEKLKSSV 420  
 QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVNKLPLIYCYKARAHMTDEKLKSSV 420  
 Db 421 FSDAVCEN 428  
 QY 421 FSDAVCER 428

RESULT 11:  
 ID W21806 standard; Protein: 496 AA.  
 AC W21806;  
 DT 23-SEP-1997 (first entry)  
 DE Spliced-deleted interferon alpha-receptor form 2.  
 KW Interferon alpha-receptor; IFNAR.  
 OS Homo sapiens.  
 FH Key  
 FT domain Location/Qualifiers  
 FT 1..419  
 FT /label= "Extracellular domain  
 FT /note= "comprises amino acid residues 1-413 and  
 FT 422-427 of transmembranal IFNAR"  
 FT domain 420..496

FT /label= Intracellular domain  
 FT /note= "comprises amino acids 481-557 of  
 FT transmembranal IFNAR"  
 PN AU9475977-A.  
 PD 11-MAY-1995.  
 PF 20-OCT-1994; 075977.  
 PR 24-OCT-1993; IL-107378.  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PI (ABRA/) ABRAMOYICH C.  
 DR ABRAMOYICH C, Ratovitski E, Revel M;  
 WPI: 95-200634/27.  
 PT New mammalian soluble interferon alpha-receptor forms - used for  
 PT inhibiting, modulating or modifying the activities of interferon(s)  
 PS Example 3; Fig 7; 46pp; English.  
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2  
 CC (W21806) is characterised by a double deletion when compared to  
 CC transmembranal IFNAR (W21804). The extracellular domain is  
 CC shortened by 6 amino acid residues and is followed by a truncated  
 CC intracellular domain. There is no transmembrane region. The amino  
 CC acid sequence is predicted from a cDNA clone (see also T73521) obd.  
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR  
 CC splice-deleted forms 1 (see also W21805) and 2 may regulate the  
 CC response of human cells to IFNs, either by acting as IFN  
 CC antagonists or by regulating IFN activities. They can be expressed  
 CC in host cells and used to inhibit, modulate or modify the  
 CC activities of IFNs alpha and beta in cells, tissues and organisms,  
 CC or for diagnostic purposes.  
 SQ Sequence 496 AA;

Query Match 95.2%; Score 3025; DB 1; Length 496;  
 Best Local Similarity 97.9%; Pred. No. 9,716-285;  
 Matches 414; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Db 1 MAAVLLGATTLVLAAGVFWLSAAAGKRLKSPQKVEVDIIDNFIILMNRSDSVGNT 60  
 QY 1 MAAVLLGATTLVLAAGVFWLSAAAGKRLKSPQKVEVDIIDNFIILMNRSDSVGNT 60  
 Db 61 FSPDYORTGMDNMIKLSGCCNITSTKCNFSSKLNTVEIKLRIRAEKENTSSWEYDSF 120  
 QY 61 FSPDYORTGMDNMIKLSGCCNITSTKCNFSSKLNTVEIKLRIRAEKENTSSWEYDSF 120  
 Db 121 TPFRAOIGPEVHLEADKAIYHISPGTDSVMALDGLSFYSLILMNSSGVERRI 180  
 QY 121 TPFRAOIGPEVHLEADKAIYHISPGTDSVMALDGLSFYSLILMNSSGVERRI 180  
 Db 181 ENTYSRHKIYKLSPEYTYCLKVKAAALTSWKIGYSPVHCIKTYVENELPPENIEVSQ 240  
 QY 181 ENTYSRHKIYKLSPEYTYCLKVKAAALTSWKIGYSPVHCIKTYVENELPPENIEVSQ 240  
 Db 181 ENTYSRHKIYKLSPEYTYCLKVKAAALTSWKIGYSPVHCIKTYVENELPPENIEVSQ 240  
 QY 181 ENTYSRHKIYKLSPEYTYCLKVKAAALTSWKIGYSPVHCIKTYVENELPPENIEVSQ 240  
 Db 241 NONTVLKMDIYANNTFOVOMLAFKRNPNHLYKMKQIPDCENVTTCVFPQNVFOK 300  
 QY 241 NONTVLKMDIYANNTFOVOMLAFKRNPNHLYKMKQIPDCENVTTCVFPQNVFOK 300  
 Db 241 NONTVLKMDIYANNTFOVOMLAFKRNPNHLYKMKQIPDCENVTTCVFPQNVFOK 300  
 QY 241 NONTVLKMDIYANNTFOVOMLAFKRNPNHLYKMKQIPDCENVTTCVFPQNVFOK 300  
 Db 301 GIYLLRVOASGNTSFSESEIKPDTLOAFLLPPVFNIRSLDSFHYIGAPROSGNTP 360  
 QY 301 GIYLLRVOASGNTSFSESEIKPDTLOAFLLPPVFNIRSLDSFHYIGAPROSGNTP 360  
 Db 301 GIYLLRVOASGNTSFSESEIKPDTLOAFLLPPVFNIRSLDSFHYIGAPROSGNTP 360  
 QY 301 GIYLLRVOASGNTSFSESEIKPDTLOAFLLPPVFNIRSLDSFHYIGAPROSGNTP 360  
 Db 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVNKLPLIYCYKARAHMTDEKDAVCEY 420  
 QY 361 VIQDYPLIYEIIFWENTSNAERKIIIEKTDVTVNKLPLIYCYKARAHMTDEKDAVCEY 420  
 Db 421 FSE 423  
 QY 421 FSD 423

RESULT 12:  
 ID W52296 standard; Protein: 325 AA.  
 AC W52296;  
 DT 23-JUN-1998 (first entry)  
 DE CRP4 protein.  
 KW CRP4; Interleukin-10; IL-10; IL-10 receptor; allograft rejection;  
 KW vaccine; photosensitivity; inflammation; autoimmune disease;

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243. .266
/label= Transmembrane anchor 1

```

cytor7 represents the cytor7 cytokine receptor. cytor7 is a ligand-



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MIRAGE (TM)  
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Msearch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Mon Aug 21 10:27:29 2000; MasPar time 11.12 Seconds  
Tabular output not generated. 600.895 Million cell updates/sec

Title: >US-09-240-675-2  
Description: (1-436) from US09240675.pep  
Perfect Score: 3178  
Sequence: 1 MAAVLLGATTLVLA VAVGPV.....KSSVPSDAVCEKTKPGNTSK 436

Scoring table: PAM 150  
Gap 11

Searched: 152433 segs, 15329240 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:6\_COMB 4:PCT\_COMB 5:backfile1

Statistics: Mean 33.109; Variance 154.176; scale 0.215

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3178	100.0	436	2	US-08-307-Sequence 2, Applicatio	1.47e-277
2	3178	100.0	557	1	US-08-471-Sequence 2, Applicatio	1.47e-277
3	3178	100.0	557	2	US-08-466-Sequence 2, Applicatio	1.47e-277
4	3178	100.0	557	2	US-08-471-Sequence 2, Applicatio	1.47e-277
5	3178	100.0	557	1	US-08-328-Sequence 10, Applicati	1.47e-277
6	3178	100.0	557	2	US-08-307-Sequence 4, Applicatio	1.47e-277
7	3124	98.3	434	1	US-08-328-Sequence 11, Applicati	1.43e-272
8	3032	95.4	496	1	US-08-328-Sequence 12, Applicati	4.55e-264
9	705	22.2	202	4	PCT-US94-1 Sequence 3, Applicatio	6.46e-51
10	640	20.1	200	4	PCT-US94-1 Sequence 4, Applicatio	4.26e-45
11	274	8.6	325	4	US-08-683-Sequence 4, Applicatio	3.46e-13
12	241	7.6	332	4	PCT-US94-1 Sequence 2, Applicatio	1.92e-10
13	243	7.6	553	2	US-08-943-Sequence 20, Applicati	1.31e-10
14	243	7.6	553	2	US-08-943-Sequence 22, Applicati	1.31e-10
15	243	7.6	553	2	US-08-943-Sequence 26, Applicati	1.31e-10
16	243	7.6	553	2	US-08-943-Sequence 26, Applicati	1.31e-10
17	243	7.6	553	2	US-08-943-Sequence 42, Applicati	1.31e-10
18	243	7.6	553	2	US-08-943-Sequence 14, Applicati	1.31e-10
19	243	7.6	553	2	US-08-943-Sequence 32, Applicati	1.31e-10
20	243	7.6	553	2	US-08-943-Sequence 36, Applicati	1.31e-10
21	243	7.6	553	2	US-08-943-Sequence 34, Applicati	1.31e-10
22	243	7.6	553	2	US-08-943-Sequence 28, Applicati	1.31e-10
23	243	7.6	553	2	US-08-943-Sequence 38, Applicati	1.31e-10

24	243	7.6	553	2	US-08-943-Sequence 48, Applicati	1.31e-10
25	243	7.6	553	2	US-08-943-Sequence 44, Applicati	1.31e-10
26	243	7.6	553	2	US-08-943-Sequence 46, Applicati	1.31e-10
27	243	7.6	553	2	US-08-943-Sequence 2, Applicati	1.31e-10
28	243	7.6	553	2	US-08-943-Sequence 18, Applicati	1.31e-10
29	243	7.6	553	2	US-08-943-Sequence 16, Applicati	1.31e-10
30	243	7.6	553	2	US-08-943-Sequence 40, Applicati	1.31e-10
31	243	7.6	553	2	US-08-943-Sequence 56, Applicati	1.31e-10
32	219	6.9	221	2	US-08-943-Sequence 50, Applicati	1.47e-08
33	218	6.9	221	2	US-08-943-Sequence 58, Applicati	1.47e-08
34	216	6.8	221	2	US-08-943-Sequence 54, Applicati	1.47e-08
35	215	6.8	221	2	US-08-943-Sequence 52, Applicati	1.47e-08
36	214	6.7	221	2	US-08-943-Sequence 60, Applicati	1.47e-08
37	212	6.7	221	2	US-08-943-Sequence 8, Applicati	1.47e-08
38	207	6.5	221	2	US-08-943-Sequence 243, Applicat	2.39e-02
39	183	5.8	337	4	PCT-US94-1 Sequence 2, Applicat	2.39e-02
40	164	5.2	574	2	US-08-906-Sequence 243, Applicat	2.39e-02
41	139	4.4	17	2	US-08-488-Sequence 243, Applicat	2.39e-02
42	139	4.4	17	2	US-08-488-Sequence 243, Applicat	2.39e-02
43	139	4.4	17	2	US-08-488-Sequence 243, Applicat	2.39e-02
44	140	4.4	489	5	5221789-1 Sequence 1, Applicatio	2.01e-02
45	140	4.4	489	4	PCT-US93-1 Sequence 1, Applicatio	2.01e-02

## ALIGNMENTS

RESULT 1  
ID US-08-307-588-2 STANDARD: PRT; 436 AA.  
AC xxxxxx  
DE  
XX

Sequence 2, Application US/08307588

Sequence 2, Application US/08307588

Patent No. 5919453

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: TOYER, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Bernhard D.

REGISTRATION NUMBER: 28, 665

REFERENCE/DOCKET NUMBER: 17883/117/GDTL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300







SQ SEQUENCE 557 AA; 63525 MW; 1717510 CN;  
 Query Match 100.0%; Score 3178; DB 2; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1,476-277;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMVVLGATTLVAVAGPWLSAAGKRLKSPQKVEVDIIDNFTLRMRSDSEVGNVT 60  
 1 MMVVLGATTLVAVAGPWLSAAGKRLKSPQKVEVDIIDNFTLRMRSDSEVGNVT 60  
 QY 1 MMVVLGATTLVAVAGPWLSAAGKRLKSPQKVEVDIIDNFTLRMRSDSEVGNVT 60  
 Db 61 FSDYOKTGMDNWKLSGCONITSTKCNFSSLNLNVEEIKLRIRAKENTSSWYEDSF 120  
 61 FSDYOKTGMDNWKLSGCONITSTKCNFSSLNLNVEEIKLRIRAKENTSSWYEDSF 120  
 QY 61 FSDYOKTGMDNWKLSGCONITSTKCNFSSLNLNVEEIKLRIRAKENTSSWYEDSF 120  
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 121 TPRRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180  
 QY 121 TPRRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180  
 Db 181 ENIYSRHKIYKLSPEPTYCLKVAALITSKIGVSPVHCIKTYVENELPPENIEVSQ 240  
 181 ENIYSRHKIYKLSPEPTYCLKVAALITSKIGVSPVHCIKTYVENELPPENIEVSQ 240  
 QY 181 ENIYSRHKIYKLSPEPTYCLKVAALITSKIGVSPVHCIKTYVENELPPENIEVSQ 240  
 Db 241 NONTVLKMDTYTANMTFOVOMLHAFKRNPNHLYKMKOIPDCENYKTCVFPQNVFQK 300  
 241 NONTVLKMDTYTANMTFOVOMLHAFKRNPNHLYKMKOIPDCENYKTCVFPQNVFQK 300  
 QY 241 NONTVLKMDTYTANMTFOVOMLHAFKRNPNHLYKMKOIPDCENYKTCVFPQNVFQK 300  
 Db 301 GIYLLRVQASDGNNTSFWSEIEKFDEIQAFLLPVFNIRSLSDSFHIYIGAPKQSGNTP 360  
 301 GIYLLRVQASDGNNTSFWSEIEKFDEIQAFLLPVFNIRSLSDSFHIYIGAPKQSGNTP 360  
 QY 301 GIYLLRVQASDGNNTSFWSEIEKFDEIQAFLLPVFNIRSLSDSFHIYIGAPKQSGNTP 360  
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 361 VIODYPLIYEIIFWENTSNAEKIIEKTDVYVFNKPLTYVCVKARAHMDEKLKSSV 420  
 QY 361 VIODYPLIYEIIFWENTSNAEKIIEKTDVYVFNKPLTYVCVKARAHMDEKLKSSV 420  
 Db 421 FSDVCEKTRPGNTSK 436  
 421 FSDVCEKTRPGNTSK 436  
 QY 421 FSDVCEKTRPGNTSK 436

RESULT 5  
 ID US-08-328-256-10 STANDARD; PRT: 557 AA.  
 AC xxxxxx  
 DE Sequence 10, Application US/08328256  
 CC Patent No. 5643749  
 CC GENERAL INFORMATION:  
 CC APPLICANT: REVEL, Michel  
 CC APPLICANT: ABRAMOVICH, Carolina  
 CC APPLICANT: RATOVIETSKI, Edward  
 CC TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
 CC NUMBER OF SEQUENCES: 12  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: BROWDY AND NEIMARK  
 CC STREET: 419 Seventh Street, N.W., Suite 300  
 CC CITY: Washington  
 CC STATE: D.C.  
 CC COUNTRY: USA  
 CC ZIP: 20004  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patent Release #1.0, Version #1.30  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/328,256  
 CC FILING DATE: 24-OCT-1994  
 CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: IL 107378  
 CC FILING DATE: 24-OCT-1993  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: BROWDY, Roger L.  
 CC REGISTRATION NUMBER: REVEL-13  
 CC REFERENCE/DOCKET NUMBER: 25,618  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 202-628-5197  
 CC TELEFAX: 202-737-3528  
 CC TELEX: 248633  
 CC INFORMATION FOR SEQ ID NO: 10:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 557 amino acids  
 CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 557 AA; 63525 MW; 1718021 CN;

Query Match 100.0%; Score 3178; DB 1; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 1,476-277;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMVVLGATTLVAVAGPWLSAAGKRLKSPQKVEVDIIDNFTLRMRSDSEVGNVT 60  
 1 MMVVLGATTLVAVAGPWLSAAGKRLKSPQKVEVDIIDNFTLRMRSDSEVGNVT 60  
 QY 1 MMVVLGATTLVAVAGPWLSAAGKRLKSPQKVEVDIIDNFTLRMRSDSEVGNVT 60  
 Db 61 FSDYOKTGMDNWKLSGCONITSTKCNFSSLNLNVEEIKLRIRAKENTSSWYEDSF 120  
 61 FSDYOKTGMDNWKLSGCONITSTKCNFSSLNLNVEEIKLRIRAKENTSSWYEDSF 120  
 QY 61 FSDYOKTGMDNWKLSGCONITSTKCNFSSLNLNVEEIKLRIRAKENTSSWYEDSF 120  
 Db 121 TPRRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180  
 121 TPRRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180  
 QY 121 TPRRKAQIGPPEVHLEAEKAIYIHISPGTKDSVMALDGLSFTYSLLIMKNSSGVEERI 180  
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 181 ENIYSRHKIYKLSPEPTYCLKVAALITSKIGVSPVHCIKTYVENELPPENIEVSQ 240  
 QY 181 ENIYSRHKIYKLSPEPTYCLKVAALITSKIGVSPVHCIKTYVENELPPENIEVSQ 240  
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 241 NONTVLKMDTYTANMTFOVOMLHAFKRNPNHLYKMKOIPDCENYKTCVFPQNVFQK 300  
 QY 241 NONTVLKMDTYTANMTFOVOMLHAFKRNPNHLYKMKOIPDCENYKTCVFPQNVFQK 300  
 Db 301 GIYLLRVQASDGNNTSFWSEIEKFDEIQAFLLPVFNIRSLSDSFHIYIGAPKQSGNTP 360  
 301 GIYLLRVQASDGNNTSFWSEIEKFDEIQAFLLPVFNIRSLSDSFHIYIGAPKQSGNTP 360  
 QY 301 GIYLLRVQASDGNNTSFWSEIEKFDEIQAFLLPVFNIRSLSDSFHIYIGAPKQSGNTP 360  
 Db 361 VIODYPLIYEIIFWENTSNAEKIIEKTDVYVFNKPLTYVCVKARAHMDEKLKSSV 420  
 361 VIODYPLIYEIIFWENTSNAEKIIEKTDVYVFNKPLTYVCVKARAHMDEKLKSSV 420  
 QY 361 VIODYPLIYEIIFWENTSNAEKIIEKTDVYVFNKPLTYVCVKARAHMDEKLKSSV 420  
 Db 421 FSDVCEKTRPGNTSK 436  
 421 FSDVCEKTRPGNTSK 436  
 QY 421 FSDVCEKTRPGNTSK 436

RESULT 6  
 ID US-08-307-588-4 STANDARD; PRT: 557 AA.  
 AC xxxxxx  
 DE Sequence 4, Application US/08307588  
 CC Patent No. 5919453  
 CC GENERAL INFORMATION:  
 CC APPLICANT: BENOIT, Patrick  
 CC APPLICANT: MEYER, Francois  
 CC APPLICANT: MAGUIRE, Deborah  
 CC APPLICANT: PLAVEC, Ivan  
 CC APPLICANT: TOVEY, Michael G.

```

01 RESULT 7
02 ID US -08-328-256-11 STANDARD: PRT: 434 AA.
03 AC xxxxxx
04 DT
05 XX
06 XX
07 DE Sequence 11, Application US/08328256
08 XX
09 CC Sequence 11, Application US/08328256
10 CC Patent No. 5643749
11 CC GENERAL INFORMATION:
12 CC APPLICANT: REVEL, Michel
13 CC APPLICANT: ABRAMOVICH, Carolina
14 CC APPLICANT: RATOVITSKI, Edward
15 CC TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
16 CC TITLE OF INVENTION: PREPARATION AND USE
17 CC NUMBER OF SEQUENCES: 12
18 CC CORRESPONDENCE ADDRESSES:
19 CC ADDRESSEE: BROWDY AND NEIMARK
20 CC STREET: 419 Seventh Street, N.W., Suite 300
21 CC CITY: Washington
22 CC STATE: D.C.
23 CC COUNTRY: USA
24 CC ZIP: 20004
25 CC COMPUTER READABLE FORM:
26 CC MEDIUM TYPE: Floppy disk
27 CC COMPUTER: IBM PC compatible
28 CC OPERATING SYSTEM: PC-DOS/MS-DOS
29 CC SOFTWARE: Patent In Release #1.0, Version #1.30
30 CC CURRENT APPLICATION DATA:
31 CC APPLICATION NUMBER: US/08/328,256
32 CC FILING DATE: 24-OCT-1994
33 CC PRIOR APPLICATION DATA:
34 CC APPLICATION NUMBER: IL 107378
35 CC FILING DATE: 24-OCT-1993
36 CC ATTORNEY/AGENT INFORMATION:
37 CC NAME: BROWDY, Roger L.
38 CC REGISTRATION NUMBER: REVEL-13
39 CC REFERENCE/DOCKET NUMBER: 25,618
40 CC TELECOMMUNICATION INFORMATION:
41 CC TELEPHONE: 202-628-5197
42 CC TELEFAX: 202-737-3528
43 CC TELEX: 248633
44 CC INFORMATION FOR SEQ. ID. NO. 11:
45 CC SEQUENCE CHARACTERISTICS:
46 CC LENGTH: 434 amino acids
47 CC TYPE: amino acid
48 CC STRANDEDNESS: single
49 CC TOPOLOGY: linear
50 CC MOLECULE TYPE: protein
51 CC SEQUENCE 434 AA; 49546 MW; 1042221 CN;
52
53 Query Match 98.3%; Score 3124; DB 1; Length 434;
54 Best Local Similarity 99.8%; Pred. No. 1,43e-272;
55 Matches 427; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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57 Db 1 MAAVLLGATLTVLVAAPVWLSAAGGRNLKSPQKVEVDIIDNFIIRNRSDESGVNT 60
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Query Match          95.4%; Score 3032; DB 1; Length 496;
Best Local Similarity 98.1%; Pred. No. 4,556-264;
Matches 415; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Db      1 MMVLLGATTLVLA VAGFWVL SAAAGKNLKS POKVEVDI IDDFILIMNNS DESVGNT 60
Oy      1 MMVLLGATTLVLA VAGFWVL SAAAGKNLKS POKVEVDI IDDFILIMNNS DESVGNT 60
Db      61 FSPDYQKTGMQNWIKLSCQNTITSTKCNFSSLKLVNTEBEIKLRIRAEKENTSSMYEVSDF 120
Oy      61 FSPDYQKTGMQNWIKLSCQNTITSTKCNFSSLKLVNTEBEIKLRIRAEKENTSSMYEVSDF 120
Db      121 TPFRAQAGPPEVHLAEADKAIVIHISPTGDSVMNALDGLSFTYSLLIMNSSGVEERI 180
Oy      121 TPFRAQAGPPEVHLAEADKAIVIHISPTGDSVMNALDGLSFTYSLLIMNSSGVEERI 180
Db      181 ENYSRHHIYVLSPEPTYCLFVKKALLTSMKIGVYSPHICIKTYVENELAPPENIEVSQ 240
Oy      181 ENYSRHHIYVLSPEPTYCLFVKKALLTSMKIGVYSPHICIKTYVENELAPPENIEVSQ 240
Db      241 NONTYLAQNDYTYANNTEFOVQVLAFLKRNPGNHLTKMKQIPDCENVVTKQCVFPQNVFK 300
Oy      241 NONTYLAQNDYTYANNTEFOVQVLAFLKRNPGNHLTKMKQIPDCENVVTKQCVFPQNVFK 300
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Oy      301 GYILLRVAOSGNNTSFSESEIKPDTEIOALPLPVPFIRLSDSFHYIGAPQOSQNTP 360
Db      361 VIQDPPLIYEIIFEMENTSNAERKIIKEKTDVTVENLKLFLVYCYKARAHITMDESDAVCEY 420
Oy      361 VIQDPPLIYEIIFEMENTSNAERKIIKEKTDVTVENLKLFLVYCYKARAHITMDESLSSV 420
Db      421 FSE 423
Oy      421 FSD 423

RESULT      9          STANDARD;      PRT;      202 AA.
ID          PCT-US94-14277-3
AC          xxxxxx
DE          Sequence 3, Application PC/TUS9414277
CC          GENERAL INFORMATION:
CC          APPLICANT: Agnet, Michel
CC          APPLICANT: Bonini, Ruth
CC          APPLICANT: Hemmi, Silvio
CC          TITLE OF INVENTION: Receptor Subunit Polypeptides
CC          NUMBER OF SEQUENCES: 8
CC          CORRESPONDENCE ADDRESS:
CC          ADDRESSEE: Genentech, Inc.
CC          STREET: 460 Point San Bruno Blvd
CC          CITY: South San Francisco
CC          STATE: California
CC          COUNTRY: USA
CC          ZIP: 94080
CC          COMPUTER READABLE FORM:
CC          MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC          COMPUTER: IBM PC compatible
CC          OPERATING SYSTEM: PC-DOS/MS-DOS
CC          SOFTWARE: patlin (Genentech)
CC          CURRENT APPLICATION DATA:
CC          APPLICATION NUMBER: PCT/US94/14277
CC          FILING DATE: 07-DEC-1994
CC          CLASSIFICATION:
CC          PRIOR APPLICATION DATA:
CC          APPLICATION NUMBER: 08/164596
CC          FILING DATE: 09-DEC-1993
CC          ATTORNEY/AGENT INFORMATION:

```

CC NAME: Love, Richard B.  
CC REGISTRATION NUMBER: 34,659  
CC REFERENCE/DOCKET NUMBER: 866PCT  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415/225-5530  
CC TELEFAX: 415/952-9881  
CC TELEX: 910/371-7168  
CC INFORMATION FOR SEQ ID NO: 3:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 202 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC SEQUENCE: 202 AA; 23375 MW; 241129 CN;

Query Match 22.2%; Score 705; DB 4; Length 202;  
Best Local Similarity 49.0%; Pred. No. 6,64e-51;  
Matches 99; Conservative 39; Mismatches 62; Indels 1; Gaps 1;

Db 2 NIKPPENIDYIIDNTYILKSSHGSGSVTFSAEYTKDERKMLKAPCOHTTTTKE 61  
Qy NIKSFOKVEVDIIDNFILKMRSDSEYGNVTFSEYQKGMNLIKSGCONITSTCN 88  
Db 62 FSLDPTNYIKTFQVRABEGNSTSMNEVDPEIPFYTAHMSPEVRLEREDKALVHS 121  
Qy FSSLALNYEEIKIRAREKEN-TSSWEVDSTPPKRAQIGPEVHLEAEKALVHS 147  
Db 122 PGQGNMALKPEPSFYIRIMOKSSSDKKTINSYYVEKIPELLPEYTCLEKXAIHP 181  
Qy 148 POKTOSYVWALDGLSTFTSLILKMKSSGYEERIENTYSHKIKLSPETTYCLAKYKALL 207  
Db 182 SLKHSNSTXOCISTYVAN 201  
Qy 208 TSMKIGVYSPVHCITVEN 227

RESULT 10  
ID PCT-US94-14277-4 STANDARD; PRT: 200 AA.  
AC xxxxxx  
XX  
XX  
XX  
XX

Sequence 4, Application PC/TUS9414277

GENERAL INFORMATION:

APPLICANT: Aguet, Michel

APPLICANT: Bonni, Ruth

APPLICANT: Hemmi, Silvio

TITLE OF INVENTION: Receptor Subunit Polypeptides

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 KB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14277

FILING DATE: 07-DEC-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/164596

FILING DATE: 09-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

CC REFERENCE/DOCKET NUMBER: 866PCT  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415/225-5530  
CC TELEFAX: 415/952-9881  
CC TELEX: 910/371-7168  
CC INFORMATION FOR SEQ ID NO: 4:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 200 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC SEQUENCE: 200 AA; 22525 MW; 227601 CN;

Query Match 20.1%; Score 640; DB 4; Length 200;  
Best Local Similarity 47.6%; Pred. No. 4.26e-45;  
Matches 99; Conservative 43; Mismatches 53; Indels 13; Gaps 11;

Db 1 MPVFNLOVDAGKSYVLMKMDYIASADYLFROMPGYSKSSGSHSDMKRIPICANYO 60  
Qy 229 LPPENIEVSQNONIVTLKMDI-TYANMTFOVMHLAKRPNGLIKMKIIPCCENYK 287  
Db 61 TTHCVFSDPTXYTGFPLVQASBGNHTSFWSSE-KFIDSQKHLPPPVITVTAMSDTL 119  
Qy 288 TTQCVFQVQVFKGIYLLRYQASDGNNTSFWSEELKF-DTEIQAFILPPVFNIRSLDSF 346  
Db 120 LVYXNC--QDS-T-C--D-GLNVEIIFEMENST-KISMEKGPFTLKNLOPLVYCYO 171  
Qy 347 HIYIAPKOSGNTPIQOYPLIYEIIFEMENSNABRKIEKR-TVTVNKLPLVYCYK 405  
Db 172 ARV-LFRALNKTNSFEKCEKTRPGS 198  
Qy 406 ARAHTMDEKLNKSVSDVACEKTRPGN 433

RESULT 11  
ID US-08-683-743-4 STANDARD; PRT: 325 AA.  
AC xxxxxx  
XX  
XX  
XX  
XX  
XX

Sequence 4, Application US/08683743

GENERAL INFORMATION:

APPLICANT: Pestka, Sidney

APPLICANT: Kotenko, Sergei

TITLE OF INVENTION: CITOKINE RECEPTOR SIGNAL TRANSDUCTION

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/683,743

FILING DATE: 17-JUL-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 601-1-050

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

CC TELEFAX: 201-343-1684  
 CC INFORMATION FOR SEQ ID NO: 4:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 325 amino acids  
 CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC HYPOTHEICAL: NO  
 CC FRAGMENT TYPE:  
 CC SEQUENCE 325 AA: 37011 MW: 589685 CN:

Query Match 8.6%; Score 274; DB 2; Length 325;  
 Best Local Similarity 30.1%; Pred. No. 3,46e-13;  
 Matches 62; Conservative 55; Mismatches 75; Indels 14; Gaps 10;

DB 23 PREVNANVSFNKNILOMSEPAFAKGNLTFTAY----LSYRIFOKCMNTITTEDFS 78  
 OY 32 SPQKVEVDIIDDNFILKMNSDSVGNVTFSPDYQKGMNWKISGCONITSTKCNFS 91  
 DB 79 LS-K-YGDHTLRVAFADSHSDVNI-TFCVPDITLIGPGQVEVLADSLHRLAPK 135  
 OY 92 LKLNVEEIKIRIRAE-KETSSMYEVDSTPRKAOIGPEVHLAEKAIYIH-ISFG 149  
 DB 136 IENEYETWTKNKNYSWTINVOYKNGTDEKFOITPOYDFEVLRLNLEPWTTCVQVRGFL 195  
 OY 150 T-KDSYMAALDGL--SFYSLILMKNSGVEERIENIYSHRIKISPEYTCIAKVAAL 206  
 DB 196 PDRNKGEMSEPV-CEQTHDETVPS 220  
 OY 207 LTSWKIGVYS-PVHCITVTENELPP 231

RESULT 12  
 ID PCT-US94-14277-2 STANDARD; PRT: 332 AA.  
 AC: xxxxxx  
 DT  
 DE

Sequence 2, Application PC/TUS9414277  
 GENERAL INFORMATION:  
 APPLICANT: Aguet, Michel  
 APPLICANT: Bohni, Ruth  
 APPLICANT: Hemml, Silvio  
 TITLE OF INVENTION: Receptor Subunit Polypeptides  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/14277  
 FILING DATE: 07-DEC-1994  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/164596  
 FILING DATE: 09-DEC-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Love, Richard B.  
 REGISTRATION NUMBER: 34,659  
 REFERENCE/DOCKET NUMBER: 866PCT  
 TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 415/225-5530  
 CC TELEFAX: 415/952-9881  
 CC TELEX: 910/371-7168  
 CC INFORMATION FOR SEQ ID NO: 2:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 332 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC SEQUENCE 332 AA: 37471 MW: 605032 CN:

Query Match 7.6%; Score 241; DB 4; Length 332;  
 Best Local Similarity 27.8%; Pred. No. 1.92e-10;  
 Matches 60; Conservative 56; Mismatches 80; Indels 20; Gaps 16;

DB 10 SILICLGA-AASSPFSQALAPLPRHLVNDQILTWESPSSNDPRPVYQVEYFS 68  
 OY 10 TLVLAVAGVWLSAAGKLNLSPOKVEVDIIDDNFILKMRNDSVGN-N-VTFSPDYK 67  
 DB 69 ID-GSHRLLEPNCIDITETKCDLGTGGRILKLPFPFTVLRVRAKGNLTSKWGLDEP 127  
 OY 68 TGMNMIKL--SGCONITSTKCNFSSL-KLNYEE-IR--LRIRAKEN-TSSWYEVDSF 120  
 DB 128 QHRENTVGPKNISVTPKGSIVYHFSPPF-D-V--FHGATFOYLHYWEKSETOQSD 182  
 OY 121 TFFRKAOIGPP-EVHLAEKAIYIHISPTKDSVMALDGLSFTYSLILMKNSGVEER 179  
 DB 183 VEGPFSNSIVGNLKPPIVYCLQTEPAOLLNKKI 218  
 OY 180 IENIYSRRI-Y-KLSPETTCIAKVAAL-LTSWKI 212

RESULT 13  
 ID US-08-943-087-20 STANDARD; PRT: 553 AA.  
 AC: xxxxxx  
 DT  
 DE

Sequence 20, Application US/08943087  
 GENERAL INFORMATION:  
 APPLICANT: Lok, SI  
 APPLICANT: Kho, Choon J.  
 APPLICANT: Jelmeberg, Anna C.  
 APPLICANT: Adams, Robyn L.  
 APPLICANT: Whitmore, Theodore E.  
 APPLICANT: Farrah, Theresa M.  
 TITLE OF INVENTION: CYTOKINE RECEPTOR  
 NUMBER OF SEQUENCES: 60  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Zymogenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/943,087  
 FILING DATE:  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/803,305  
 FILING DATE: 20-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lunn, Paul G  
 REGISTRATION NUMBER: 32,743



CC REFERENCE/DOCKET NUMBER: 96-24C1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEX:  
CC INFORMATION FOR SEQ ID NO: 20:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 553 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
CC SEQUENCE 553 AA; 62533 MW; 1648042 CN;  
SQ  
Query Match 7.6%; Yscore 243; DB 2; Length 553;  
Best Local Similarity 30.3%; Pred. No. 1,316-10;  
Matches 43; Conservative 37; Mismatches 57; Indels 5; Gaps 5;  
Db 18 LLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTQTPPEGIGVYVYTYOYFTYG 77  
11 LVLAVGFWVLSAAGGNLKSPOKVEYDIIDNFIIMNNSDESVG-NVTFSPDYQKTG 69  
Qy 78 QKKMLNSECNRINNTYCDLSAETSD-YEQYIAVKAIWGTCKSKMAESGRFYPLETQ 136  
70 MDNNIKLSGCONITSTKCNFSSLKLNVE-EIKLIRAEKENTSS-WYEVDSFTPFRAQ 127  
Qy 137 IGPEVALTTDEKISIVLTAP 158  
128 IGPEVHLEADKAI-VIHISP 148  
Qy  
RESULT 14  
ID US-08-943-087-22 STANDARD; PRT: 553 AA.  
XX xxxxxx  
DE Sequence 22, Application US/08943087  
CC Sequence 22, Application US/08943087  
CC Patent No. 5945311  
CC GENERAL INFORMATION:  
CC APPLICANT: Lok, Si  
CC APPLICANT: Kho, Choon J.  
CC APPLICANT: Jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.  
CC APPLICANT: Farrah, Theodore E.  
CC APPLICANT: Whitmore, Theresa M.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East  
CC CITY: Seattle  
CC STATE: WA  
CC COUNTRY: USA  
CC ZIP: 98102  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FASTSEQ for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/943,087  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION NUMBER: 08/803,305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lunn, Paul G

CC REGISTRATION NUMBER: 32,743  
CC REFERENCE/DOCKET NUMBER: 96-24C1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEX:  
CC INFORMATION FOR SEQ ID NO: 22:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 553 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
CC SEQUENCE 553 AA; 62533 MW; 1648042 CN;  
SQ  
Query Match 7.6%; Score 243; DB 2; Length 553;  
Best Local Similarity 30.3%; Pred. No. 1,316-10;  
Matches 43; Conservative 37; Mismatches 57; Indels 5; Gaps 5;  
Db 18 LLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLTQTPPEGIGVYVYTYOYFTYG 77  
11 LVLAVGFWVLSAAGGNLKSPOKVEYDIIDNFIIMNNSDESVG-NVTFSPDYQKTG 69  
Qy 78 QKKMLNSECNRINNTYCDLSAETSD-YEQYIAVKAIWGTCKSKMAESGRFYPLETQ 136  
70 MDNNIKLSGCONITSTKCNFSSLKLNVE-EIKLIRAEKENTSS-WYEVDSFTPFRAQ 127  
Qy 137 IGPEVALTTDEKISIVLTAP 158  
128 IGPEVHLEADKAI-VIHISP 148  
Qy  
RESULT 15  
ID US-08-943-087-30 STANDARD; PRT: 553 AA.  
XX xxxxxx  
DE Sequence 30, Application US/08943087  
CC Sequence 30, Application US/08943087  
CC Patent No. 5945311  
CC GENERAL INFORMATION:  
CC APPLICANT: Lok, Si  
CC APPLICANT: Kho, Choon J.  
CC APPLICANT: Jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.  
CC APPLICANT: Farrah, Theodore E.  
CC APPLICANT: Whitmore, Theresa M.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East  
CC CITY: Seattle  
CC STATE: WA  
CC COUNTRY: USA  
CC ZIP: 98102  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FASTSEQ for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/943,087  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION NUMBER: 08/803,305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lunn, Paul G

Tue Aug 22 08:32:01 2000

US-09-240-675-2.rai

Page 10

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CC      NAME: lunn, Paul G
CC
CC      REGISTRATION NUMBER: 32,743
CC
CC      REFERENCE/DOCKET NUMBER: 96-24C1
CC
CC      TELECOMMUNICATION INFORMATION:
CC
CC      TELEPHONE: 206-442-6627
CC
CC      TELEFAX: 206-442-6678
CC
CC      TELEX:
CC
CC      INFORMATION FOR SEQ ID NO: 30:
CC
CC      SEQUENCE CHARACTERISTICS:
CC
CC      LENGTH: 553 amino acids
CC
CC      TYPE: amino acid
CC
CC      STRANDEDNESS: single
CC
CC      TOPOLOGY: linear
CC
CC      MOLECULE TYPE: protein
CC
CC      FRAGMENT TYPE: internal
CC
CC      SEQUENCE 553 AA: 62553 MW: 1648042 CN
SQ

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Query Match	7.68;	Score 243;	DB 2;	Length 553;
Best Local Similarity	30.3%;	Pred. No. 1.31e-10;		
Matches 43; Conservative		Mismatches 57;	Indels 5;	Gaps 5;

Db 18 LLLLLAAPGCRADVCVSGGLPRANTFFLSINKNVLYQNTPPREGLOGVKTTYVQVPTIYG 77  
11 LVLVAAPGPMWLSAAGGRKNLSPKQVEYDIIIDNFIILRMRSSESVYG-NYTFSEFDYKTG 69  
OY  
Db- 78 ORKWLNSSECRNINRYTCOLSAESD-YEHQYAKVAILNGTCSKMAEGRRYPLETO 136  
70 MDNNIKLSGQNTSTSTGCSNFSLSKLNLYE-EIKLRIRAEKENTSS-WYEDSTSPFKAQ 127  
OY  
Db 137 IGPPEVALITDEKSIISVLTAAP 158  
128 IGPPEVHLAEADKAI-VIHISLP 148  
OY

Search completed: Mon Aug 21 10:27:43 2000  
Job time : 14 secs.

\*\*\*\*\*  
 W I L D T Y P E  
 (TM)  
 \*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit,  
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 Distribution Rights by Oxford Molecular Ltd

MSRCH\_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 21 10:25:11 2000; Maspar time 23.63 Seconds

Tabular output not generated. 870.350 Million cell updates/sec

Title: >US-09-240-675-2

Description: (1-436) from US09240675.pep

Perfect Score: 3178

Sequence: 1 MMYVLGATTLVAVGPNV.....KSSVSDAVCEKTRPGNTSK 436

Scoring table: PAM 150

Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 48.543; Variance 89.320; scale 0.543

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	3178	100.0	557	2 A32694	interferon alpha rece	0.00e+00
2	2949	92.8	545	2 S17112	interferon alpha/beta	0.00e+00
3	2103	66.2	560	2 S27387	interferon alpha rece	0.00e+00
4	1513	47.6	530	2 A45283	interferon alpha/beta	0.00e+00
5	285	9.0	349	2 JC6311	interferon receptor-c	6.40e-32
6	280	8.6	273	2 G01418	cytokine receptor fam	9.67e-31
7	274	8.6	325	2 A47003	cytokine receptor fam	9.67e-31
8	241	7.6	332	2 A49847	interferon gamma rece	2.35e-24
9	183	5.8	337	2 I38500	interferon gamma rece	1.15e-13
10	140	4.4	489	2 A31555	interferon gamma rece	2.01e-06
11	132	4.2	575	2 A49667	interleukin-10 recept	3.59e-05
12	128	4.0	918	2 A36337	membrane glycoprotein	1.47e-04
13	123	3.9	56	2 S41602	interferon alpha rece	8.27e-04
14	123	3.9	26926	1 I36344	interleukin-10 recept	8.27e-04
15	116	3.7	578	2 I56215	interleukin-10 recept	8.65e-03
16	118	3.7	662	2 I37892	TL12 receptor compone	4.48e-03
17	119	3.7	918	2 A44257	interleukin-6 signa	3.20e-03
18	113	3.6	6805	2 S20901	titin, rabbit (fragm	2.32e-02
19	107	3.4	817	2 A48721	titin, muscle - chick	1.57e-01
20	108	3.4	877	2 I48967	brain-specific kinase	1.15e-01
21	107	3.4	877	2 S51603	receptor-like tyrosin	1.57e-01
22	107	3.4	898	2 S47489	receptor tyrosine kin	1.57e-01
23	109	3.4	979	2 E72236	clostridium-related p	8.37e-02

24	107	3.4	981	2 S51604	receptor-like tyrosin	1.57e-01
25	107	3.4	1005	2 S49015	receptor tyrosine kin	1.57e-01
26	104	3.3	346	2 S66958	UPEI protein - yeast	3.98e-01
27	104	3.3	837	2 T03151	primase - alcelaphine	3.98e-01
28	104	3.3	917	2 I49699	glycoprotein 130 - mo	3.98e-01
29	101	3.2	132	2 S56573	hypothetical 14.6K pr	9.88e-01
30	101	3.2	215	2 I40299	variable outer membra	9.88e-01
31	103	3.2	897	1 A32555	cytokine receptor com	5.40e-01
32	101	3.2	2606	2 T03159	large tegument protei	9.88e-01
33	103	3.2	6839	2 S57242	twitclan - Caenorhabd	5.40e-01
34	100	3.1	306	2 F72287	esterase - Thermotoga	1.33e+00
35	99	3.1	356	2 S74766	hypothetical protein	1.79e+00
36	98	3.1	449	2 C69086	chotismate mutase - M	2.40e+00
37	100	3.1	466	2 S19685	dihydroliponamide dehy	1.33e+00
38	98	3.1	641	2 A71163	hypothetical protein	2.40e+00
39	98	3.1	686	2 B75061	alpha chain of format	2.40e+00
40	99	3.1	688	1 TVVPTJ	large T antigen - pol	1.79e+00
41	98	3.1	691	1 TVVPTJ	large T antigen - pol	2.40e+00
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43	97	3.1	708	1 TVVPT4	large T antigen - rbe	3.22e+00
44	98	3.1	1013	2 I50615	receptor-type protein	2.40e+00
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RESULT 1  
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 TITLE Interferon alpha receptor precursor - human  
 ORGANISM Homo sapiens #common\_name man  
 DATE 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 24-Sep-1998

ACCESSIONS A32694  
 REFERENCE A32694  
 #authors Uze, G.; Lutfalla, G.; Gresser, I.  
 #journal Cell (1990) 60:225-234  
 #title Genetic transfer of a functional human interferon alpha receptor into mouse cells: cloning and expression of its cDNA.

#cross-references MIM:90124632

#accession A32694

#status preliminary

#molecule\_type mRNA

#residues 1-557 #label UZE

#cross-references GB:J03171; NID:g184645; PID:g306914

# GENETICS

#gene GDB:16NAR1; tBNR: IFC

#cross-references GDB:120078; OMIM:107450

#map\_position 21q22.1-21q22.1

KEYWORDS cytokine, receptor, transmembrane protein, #length 557 #molecular\_weight 63525 #checksum 7035

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Query Match 100.0% Score 3178 DB 2; Length 557;

Best Local Similarity 100.0% Pred. No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	FSFDYOKTGMWIKISGONTSTKCNSSKLINYEIKIRIAEKENTSSWEVDSF	120
QY	61	FSFDYOKTGMWIKISGONTSTKCNSSKLINYEIKIRIAEKENTSSWEVDSF	120
DB	121	TFPRKAOIPPEVHLAEKKAIVHISPTKTSVMALDGLSFTSLIMKSSGVEERI	180
QY	121	TFPRKAOIPPEVHLAEKKAIVHISPTKTSVMALDGLSFTSLIMKSSGVEERI	180
DB	181	ENIYSRHKYIKLSPETTYLAKKALITSMKIGVSPVCITTYENELPPENIEVSQ	240
QY	181	ENIYSRHKYIKLSPETTYLAKKALITSMKIGVSPVCITTYENELPPENIEVSQ	240
DB	241	NONYVLKMDYTYANMTFOVMHAEFLKRNPGNHLKMKWQIPDCENKVTTCQVFPONVFC	300

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OY 241 NONTVLKMDTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENKTCQVFPQNTOK 300
DB 301 GYLLLRQASDGNNTSFMSSEIKFDTETIOAFLLPVENIRSLSDSFHLYIGAPKOSGNTP 360
OY 301 GYLLLRQASDGNNTSFMSSEIKFDTETIOAFLLPVENIRSLSDSFHLYIGAPKOSGNTP 360
DB 361 VIODPLIYEIIFEMENSNARKIIEKKTDTVTNLRPLVYCYKARAHNTDEKLNSV 420
OY 361 VIODPLIYEIIFEMENSNARKIIEKKTDTVTNLRPLVYCYKARAHNTDEKLNSV 420
DB 421 FSDAVCEKTRKPGNTSK 436
OY 421 FSDAVCEKTRKPGNTSK 436

RESULT 2
ENTRY 2
TITLE S17112 #type complete
ORGANISM Interferon alpha/beta receptor - human
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
ACCESSIONS S17112
REFERENCE S17112
#authors Lutfalla, G.; Gardiner, X.Y.Z.; Proudhon, D.; Vleth, E.;
#submission submitted to the EMBL Data Library, July 1991
#description The structure of the human interferon alpha/beta receptor
#accession S17112
#status preliminary
#molecule_type DNA
#residues 1-545 #label LOT
#cross-references EMBL:X60459
GENETICS
#introns 26/3; 67/2; 126/1; 177/3; 225/1; 263/2; 330/1; 369/3; 420/1;
468/3
KEYWORDS cytokine receptor; transmembrane protein
SUMMARY #length 545 #molecular_weight 62169 #checksum 672
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Best Local Similarity 97.0%; Pred. No. 0.00e+00;
Matches 423; Conservative 1; Mismatches 0; Indels 12; Gaps 2;

DB 1 MNTVLLCATLTVLVAAPVWLSAAGKKNLSPQKVEVDIIDDNFILRMNSDESIGNVT 60
OY 1 MNTVLLCATLTVLVAAPVWLSAAGKKNLSPQKVEVDIIDDNFILRMNSDESIGNVT 60
DB 61 FSPDYKGTGMNWKILSGCONITSTKCNFSSKLNVYEIKLRIRAKEMTSWYEDSF 120
OY 61 FSPDYKGTGMNWKILSGCONITSTKCNFSSKLNVYEIKLRIRAKEMTSWYEDSF 120
DB 121 TPEKAOIGPEVHLEADAIVHISPGKDSVMALDGLSFYSLILMNSGVEERI 180
OY 121 TPEKAOIGPEVHLEADAIVHISPGKDSVMALDGLSFYSLILMNSGVEERI 180
DB 181 ENIYSRRIKIKLSPETTYCLKVAALITSMKIGVSPVHCIKTVENELPPENIEVSQ 240
OY 181 ENIYSRRIKIKLSPETTYCLKVAALITSMKIGVSPVHCIKTVENELPPENIEVSQ 240
DB 241 NONTVLKMDTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENKTCQVFPQNTOK 300
OY 241 NONTVLKMDTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENKTCQVFPQNTOK 300
DB 301 GYLLLRQASDGNNTSFMSSEIKFDTETIOAFLLPVENIRSLSDSFHLYIGAPKOSGNTP 360
OY 301 GYLLLRQASDGNNTSFMSSEIKFDTETIOAFLLPVENIRSLSDSFHLYIGAPKOSGNTP 360
DB 349 VIODPLIYEIIFEMENSNARKIIEKKTDTVTNLRPLVYCYKARAHNTDEKLNSV 408
OY 349 VIODPLIYEIIFEMENSNARKIIEKKTDTVTNLRPLVYCYKARAHNTDEKLNSV 408
DB 409 FSDAVCEKTRKPGNTSK 424

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OY 421 FSDAVCEKTRKPGNTSK 436

RESULT 3
ENTRY 3
TITLE S27387 #type complete
ORGANISM Interferon alpha receptor type 1 precursor - bovine
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
ACCESSIONS S27387; S33770
REFERENCE S27387
#authors Mouchel-Viehl, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.
#journal FEBS Lett. (1992) 313:255-259
#title Specific antiviral activities of the human alpha interferons
#cross-references MIMD:93076908
#accession S27387
#status preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-560 #label MOU
#cross-references EMBL:X68443; NID:9431; PID:9432
#experimental_source MDBK cells
REFERENCE S33770
#authors Lim, J.K.; Langer, J.A.
#journal Biochim. Biophys. Acta (1993) 1173:314-319
#title Cloning and characterization of a bovine alpha interferon
#accession MIMD:93305725
#status preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-421, 423-560 #label LIM
#cross-references EMBL:L06320; NID:9163187; PID:9163188
#experimental_source lung
KEYWORDS antiviral; cytokine receptor; transmembrane protein
FEATURE
1-24 #domain signal sequence #status predicted #label sig\
25-560 #product interferon alpha receptor type 1 #status
SUMMARY #length 560 #molecular_weight 63818 #checksum 4991
Query Match 66.2%; Score 2103; DB 2; Length 560;
Best Local Similarity 65.2%; Pred. No. 0.00e+00;
Matches 287; Conservative 78; Mismatches 67; Indels 8; Gaps 8;

DB 1 MLLILGATTLTVA-GRWVLRASGEANLK-PENVEIHIIIDNFFILKNSSSSVYANVF 58
OY 2 MNTVLLCATLTVLVAAPVWLSAAGKKNLSPQKVEVDIIDDNFILRMNSDESIGNVT 61
DB 59 SADYOLIGTDNMKILSGCOHITSTKCNFSSVELENFETELRIAEKGNSTWYEEVP 118
OY 62 SPDYKGTGMNWKILSGCONITSTKCNFSSKLNVYEIKLRIRAKEMTSWYEDSF 119
DB 119 FVPLENIGPDPVHLEADAIVHISPGKDSVMALDGLSFYSLILMNSGVEERI 178
OY 120 TPEKAOIGPEVHLEADAIVHISPGKDSVMALDGLSFYSLILMNSGVEERI 178
DB 179 KETFTVPEKIVLSPETTYCLKVAALITSMKIGVSPVHCIKTVENELPPENIEVSQ 237
OY 179 KETFTVPEKIVLSPETTYCLKVAALITSMKIGVSPVHCIKTVENELPPENIEVSQ 237
DB 238 NADNOLVLLKMDTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENKTCQVFPQNTOK 297
OY 238 SYONONVLLKMDTYANMTFOVOMLHAFKRNPNHLYKMKQIPDCENKTCQVFPQNTOK 297
DB 298 SSGGIIVVRASNGSGISFMSSEIKFDTETIOAFLLPVENIRSLSDSFHLYIGAPKOS 357
OY 298 FKGIIILRQASDGNNTSFMSSEIKFDTETIOAFLLPVENIRSLSDSFHLYIGAPKOS 356
DB 358 ENMSVMOPLIYEIIFEMENSNARKIIEKKTDTVTNLRPLVYCYKARAHNTDEKLNSV 417
OY 357 GNTVPIODPLIYEIIFEMENSNARKIIEKKTDTVTNLRPLVYCYKARAHNTDEKLNSV 416

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Db 418 KSSFSPTVCEKTRKPGNTSK 437  
 OY 417 KSSVPSDAVCEKTRKPGNTSK 436

RESULT 4  
 ENTRY 445283 #type complete  
 TITLE Interferon alpha/beta receptor - mouse  
 ORGANISM #formal name Mus musculus #common name mouse  
 DATE 25-Mar-1993 #sequence revision 18-Nov-1994 #text change

ACCESSIONS  
 A45283; 148423; 148424; 148425; 148426; 148427; 148428;  
 148429

REFERENCE  
 #authors Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.  
 #journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:4774-4778  
 #title Behavior of a cloned murine interferon alpha/beta receptor expressed in homospesific or heterospesific background.  
 #cross-references MUID:92262522  
 #accession A45283  
 #status preliminary  
 #molecule-type mRNA  
 #residues 1-590 #label UZE  
 #cross-references GB:M89641; NID:9194111; PID:9194112  
 #note sequence extracted from NCBI backbone (NCBIN:102354, NCBIPI:102357)

REFERENCE  
 #authors Lutfalla, G.; Uze, G.  
 #journal Gene (1994) 148:343-346  
 #title Structure of the murine interferon alpha/beta receptor-encoding gene: high-frequency rearrangements in the interferon-resistant L1210 cell line.  
 #cross-references MUID:95047447  
 #accession 148423  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule-type DNA  
 #residues 118-125 #label RES  
 #cross-references EMBL:U06237; NID:9497103; PID:9755810  
 #accession 148424  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule-type DNA  
 #residues 127-224 #label RE2  
 #cross-references EMBL:U06238; NID:9497104; PID:9755811  
 #accession 148425  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule-type DNA  
 #residues 243-264 #label RE3  
 #cross-references EMBL:U06239; NID:9497106; PID:9755812  
 #accession 148426  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule-type DNA  
 #residues 265-375 #label RE4  
 #cross-references EMBL:U06240; NID:9497108; PID:9510262  
 #accession 148427  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule-type DNA  
 #residues 397-424 #label RE5  
 #cross-references EMBL:U06241; NID:9497110; PID:9755812  
 #accession 148428  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule-type DNA  
 #residues 426-445 #label RE6  
 #cross-references EMBL:U06242; NID:9497112; PID:9755813  
 #accession 148429  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule-type DNA  
 #residues 473-590 #label RE7  
 #cross-references EMBL:U06244; NID:9497114; PID:9510265

GENETICS  
 #gene IFNAR  
 #introns 177/3; 331/1

KEYWORDS  
 SUMMARY cytokine receptor; transmembrane protein  
 #length 590 #molecular weight 65776 #checksum 833

Query Match 47.6%; Score 1513; DB 2; Length 590;  
 Best Local Similarity 50.1%; Pred. No. 0.00e+00;  
 Matches 219; Conservative 93; Mismatches 109; Indels 16; Gaps 14;

Db 1 MAAVGAALVAVGAPVLPASAGGNIKRPENIDVYIIDNTLTKSSHGSGSYTF 60  
 OY 2 MVLIGATVIVVANGPVLSAAGKRLKSPQAYEVIIIDNPLRNKRDESGVNTF 61  
 Db 61 SAETRTDANMLKYPECHHTTTTKCEFLDTNWTYIKTORVRAEGNSSTSNWNEVDF 120  
 OY 62 SEDYQKGMWIKISGCONITSPKCNSSILKLVAEIKIRIRAKEN-TSSVYEDSF 120  
 Db 121 IPFYAHMSPPVRLKADKALVHISPPGQGNMALEKRSFSTIRINOKSSDKTI 180  
 OY 121 TPFRAQIGPPEVHLKADKALVHISGTDVSMALDGSIFYSLIMKNSGVBERI 180  
 Db 181 NSTYVERKIPPELTTCLEKKAHPKLSKHSNSTVQCTSTYVANKMPGNLOVDAQ 240  
 OY 181 ENIYSRHKIYKLSPEITTCLEKKAHPKLSKHSNSTVQCTSTYVANKMPGNLOVDAQ 240  
 Db 241 GKSIVLKWVYASADVLEFRAQMLPEYSSKSSGSHDKKPIPCANVOTHCVSQDTY 300  
 OY 241 NONVYLKWDY-TYANMTPYOVMALHFLKRNPNHLYKFKQIPDCENVTQCVFPON-VF 298  
 Db 301 TGTFFLAVOASGEGNHTSFNSE-KFIDSQHILPPPVITVYAMSGLLYVNC-QDS 356  
 OY 299 OKGIYLLRVQASDGNSTSFMSSEIKF-DTEIOAFLLPVFVIRISLSDSFHIGAPKOSG 357  
 Db 357 T-C-D-GLNVEITFMENTSNF-KISMEKGPETTLKNDLPVLYVQOAVH-LFRALIN 409  
 OY 358 NTPVYQDIPPLIYEITFMENTSNKRIIEK-TDVTYNALPLVYCYKAAAHMDEKLN 416  
 Db 410 KTSNFEKLCERTKPGS 426  
 OY 417 KSSVPSDAVCEKTRKPGN 433

RESULT 5  
 ENTRY JC6311 #type complete  
 TITLE Interferon receptor-class II cytokine receptor - mouse  
 ORGANISM #formal name Mus musculus #common name house mouse  
 DATE 16-Jul-1999 #sequence revision 16-Jul-1999 #text change

ACCESSIONS  
 JC6311  
 #authors Gibbs, V.C.; Pennica, D.  
 #journal Gene (1997) 186:97-101  
 #title CRF 4: Isolation of cDNA clones encoding the human and mouse proteins.  
 #accession JC6311  
 #status preliminary  
 #molecule-type mRNA  
 #residues 1-349 #label GIB  
 #cross-references GB:U53696  
 #length 349 #molecular weight 39766 #checksum 3090

SUMMARY  
 Query Match 9.0%; Score 285; DB 2; Length 349;  
 Best Local Similarity 28.5%; Pred. No. 6.60e-33;  
 Matches 59; Conservative 60; Mismatches 73; Indels 15; Gaps 14;

Db 23 PPEKVRANSVNFKNLOVEVAFPTNITFTAYEST-R-S-FO-DHCKRTASTQCFDSH 78  
 OY 32 SPOKVEVDIIDNPLRNKRDESGVNTFEDYQKGMWIKISGCONITSPKCNSS 91  
 Db 79 LS-K-YGDTYTRVRAELADESEVNV-TQPVEDTIIIGPEMGIESTASLEKRFAPQ 135  
 OY 92 LKLVYETIKIRIRK-KENSSWYEDSPFPRKAOIGPPEVHLKADKALVHIS-PG 149  
 Db 136 IENEPETWLNKIVDSNAYVQYKNGNTEKFEQVSPDSVLENLLEPWTTCIOVGFL 195

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OY 150 T-KDSVWMLDGL--SFTYSLLIMKNSGVEERENIYSHKIKLSPETTYCLAKYKAL 206
Db 196 LDNRKGESEPV-CEITG-NDEITPS 220
OY 207 LTSWKIGVYS-PVHCITKTYENELPP 232

RESULT 6
ENTRY 601418 #type complete
TITLE cytokine receptor family II, member 4 - human
ORANISM #formal_name Homo sapiens #common_name man
DATE 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change
17-Jul-1998

ACCESSIONS 601418
REFERENCE G06935
#authors Lutfalla, G.
#submission submitted to the EMBL Data Library, April 1994
#accession G01418
#status preliminary; translated from GR/EMBL/DBJ
#molecule_type DNA
#residues 1-273 ##label LUT
#cross-references EMBL:U08988; NID:9571295; PID:9571296

GENETICS
#gene GDB:CRFB4; CRF2-4
#map_position 21q22.1-21q22.2
#introns 17/1; 58/2; 111/1; 166/3; 216/1
SUMMARY #length 273 #molecular_weight 31546 #checksum 144

Query Match 8.8%; Score 280; DB 2; Length 273;
Best Local Similarity 30.6%; Pred. No. 6,40e-32;
Matches 63; Conservative 55; Mismatches 74; Indels 14; Gaps 10;

Db 23 PPNVNMNSVNFNIIQWESPAFAKGNLFTAY---LSYRIFOKCMNTLTEDFS 78
OY 32 SPQKVEVDIIDDFILRMNSDESVCNVTFSPYQKTGMNWKISGCONITSTKCNFS 91
Db 79 LS-K-YGDHTLRARAEADSHDWNI-TCFVDDITIGPGQVEVLADSLMRFLAPK 135
OY 92 LKINVEEIKLRIRAE-KENTSSMYEVDSTPPRKAQIGPEVHLAEADKAIYIH-ISP 149
Db 136 IENEYETWTKKNVNSMTYVVOYKNGTDEKFOITPOYDEVLRLNPEPTTCVQVRGL 195
OY 150 T-KDSVWMLDGL--SFTYSLLIMKNSGVEERENIYSHKIKLSPETTYCLAKYKAL 206
Db 196 LDNRKGESEPV-CEQTHDEITPS 220
OY 207 LTSWKIGVYS-PVHCITKTYENELPP 232

RESULT 7
ENTRY A47003 #type complete
TITLE cytokine receptor family class II protein CRF2-4 precursor
ORANISM human
DATE 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change
10-Sep-1997

ACCESSIONS A47003
REFERENCE A47003
#authors Lutfalla, G.; Gardiner, K.; Uze, G.
#journal Genomics (1993) 16:366-373
#title A new member of the cytokine receptor gene family maps on
#cross-references MUID:93300510
#accession A47003
#status preliminary;
#molecule_type mRNA
#residues 1-325 ##label LUT
#cross-references GB:Z1727; NID:9393378; PID:9393379

GENETICS
#map_position 21q
#transmembrane protein
KEYWORDS #length 325 #molecular_weight 37011 #checksum 9050
SUMMARY

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Query Match 8.6%; Score 274; DB 2; Length 325;
Best Local Similarity 30.1%; Pred. No. 9.67e-31;
Matches 62; Conservative 55; Mismatches 75; Indels 14; Gaps 10;

Db 23 PPNVNMNSVNFNIIQWESPAFAKGNLFTAY---LSYRIFOKCMNTLTEDFS 78
OY 32 SPQKVEVDIIDDFILRMNSDESVCNVTFSPYQKTGMNWKISGCONITSTKCNFS 91
Db 79 LS-K-YGDHTLRARAEADSHDWNI-TCFVDDITIGPGQVEVLADSLMRFLAPK 135
OY 92 LKINVEEIKLRIRAE-KENTSSMYEVDSTPPRKAQIGPEVHLAEADKAIYIH-ISP 149
Db 136 IENEYETWTKKNVNSMTYVVOYKNGTDEKFOITPOYDEVLRLNPEPTTCVQVRGL 195
OY 150 T-KDSVWMLDGL--SFTYSLLIMKNSGVEERENIYSHKIKLSPETTYCLAKYKAL 206
Db 196 LDNRKGESEPV-CEQTHDEITPS 220
OY 207 LTSWKIGVYS-PVHCITKTYENELPP 232

RESULT 8
ENTRY A49947 #type complete
TITLE interferon gamma receptor beta subunit - mouse
ALTERNATE_NAMES IFN-gamma R beta chain; IFN-gamma R species-specific
ORANISM cofactor; type I transmembrane protein
#formal_name Mus musculus #common_name house mouse
DATE 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
29-Jan-1999

ACCESSIONS A49947
REFERENCE A49947
#authors Hemmi, S.; Bohnl, R.; Stark, G.; Di Marco, F.; Agnet, M.
#journal Cell (1994) 76:803-810
#title A novel member of the interferon receptor family complements
#cross-references MUID:94170381
#accession A49947
#status preliminary
#molecule_type mRNA
#residues 1-332 ##label HEM
#cross-references GB:569336; NID:9545841; PID:9545842
#experimental_source early B-cell line Y16
#note sequence extracted from NCBI backbone (NCBIN:145654,
NCBIP:145656)
KEYWORDS cytokine receptor
SUMMARY #length 332 #molecular_weight 37471 #checksum 3196

Query Match 7.6%; Score 241; DB 2; Length 332;
Best Local Similarity 27.8%; Pred. No. 2.35e-24;
Matches 60; Conservative 56; Mismatches 80; Indels 20; Gaps 16;

Db 10 SLLDGLGA-AASSDPSQSALAPLNRLHLNDOILLTWPSPSSNDPRPVYQVVSF 68
OY 10 TLVLAAGVWVLSAAGCNILKSPQKVEVDIIDDFILRMNSDSVSG-N-VTFSPDQK 67
Db 69 ID-GSMHRLRNCNDIDETKCDLGGGRKLFPPHPTVFLAVRAKRGNTSKWGLSPF 127
OY 68 TQMDNMWIKL--SGCONITSTKCNFS--KLNYER-IR-LAIRKERN-TSSMYEVSF 120
Db 128 QHYEVNTGPPPNISIVTQKGLVHFSPPF-D-V--FHGATFOYLVHYNEKSTQOEO 182
OY 121 TPFRAAOIGRP-EVHLAEADKAIYIHISPGTDSYMAALDGLSFTYSLLIMKNSGVEER 179
Db 183 VEGPFSNSIYGNKPYRYVCLQTEAQLIKNKRI 218
OY 180 IENIYSRKRI-Y-KLSPETTYCLAKYKAL-LTSMRI 212

RESULT 9
ENTRY I38500 #type complete
TITLE interferon gamma receptor accessory factor-1 precursor

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#accession A36337
#status preliminary
#molecule_type mRNA
#residues 1-918 #label H1B
#cross-references GB:M57230; NID:g186353; PID:g186354
GENETICS
#gene GDB:1165T: GP130
#cross-references GDB:126725; OMIM:600694
#map_position 5q11-5q11
KEYWORDS
SUMMARY
glycoprotein; membrane protein
#length 918 #molecular_weight 103522 #checksum 2664

Query Match
Best Local Similarity 4.0%; Score 128; DB 2; Length 918;
Matches 19; Conservative: 25; Mismatches 36; Indels 3; Gaps 3;

Db 231 INSELSIIKLTWNPISIKVILIKYNIQRTDASTWQIIP-EDTASRSSFTYQDL 289
Oy 36 VEDDIIDNFTLR-NSDSVGVNTSFDTQKGMNWKLSGCONITSTKCFSSIKL 94
Db 290 KPTEYVRIKCKEDKGYMSD 312
Oy 95 NYEEIKIRIRAKERTSS-WYE 116

RESULT 13
ENTRY
TITLE S41602 #type fragments
ORIGIN Interferon alpha receptor 2 - human (fragments)
#formal_name Homo sapiens #common_name man
DATE 25-Dec-1994 #sequence_revision 01-Dec-1995 #text_change
30-May-1997

ACCESSIONS
REFERENCE
S41601
S41602
#authors Abramovich, C.; Ratovitski, E.; Lundgren, E.; Revel, M.
#journal FEBS Lett. (1994) 338:295-300.
#title Identification of mRNAs encoding two different soluble forms
of the human interferon alpha receptor.
#cross-references MIM:9413943
#accession S41602
#molecule_type mRNA
#residues 1-56 #label ABR
KEYWORDS
SUMMARY cytokine receptor
#length 56 #checksum 845

Query Match
Best Local Similarity 3.9%; Score 123; DB 2; Length 56;
Matches 18; Conservative: 1; Mismatches 7; Indels 0; Gaps 0;

Db 1 PLTYCVKARAHMDESDAVCEFFSE 26
Oy 398 PLTYCVKARAHMDEKLNKSSVFSD 423

RESULT 14
ENTRY
TITLE I38344 #type complete
ALTERNATE_NAMES titin, cardiac muscle - human
CONTAINS
CONNECTIN
ORGANISM serine/threonine-specific protein kinase (EC 2.7.1.1)
#formal_name Homo sapiens #common_name man
DATE 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
16-Jul-1999
I38344; I38345; S20898; S20899; S63665; S37393
#authors Labelt, S.; Kolmerer, B.
#journal Science (1995) 270:293-296
#title titin: giant proteins in charge of muscle ultrastructure and
elasticity.
#cross-references MIM:96026330
#accession I38344
#status
#nucleic acid sequence not shown; translation not shown;
#molecule_type mRNA
#residues translated from GB/EMBL/DBJ
#map_position 1-26926 #label LAB1

```

```

#cross-references EMBL:X90568; NID:g1017424; PID:g1017425
REFERENCE
I38345
#authors Musco, G.; Tziatzios, C.; Schuck, P.; Pastore, A.
#journal Biochemistry (1995) 34:553-561
#title Dissecting titin into its structural motifs: identification
of an alpha-helix motif near the titin N-terminus.
#cross-references MIM:95119041
#accession I38345
#status
#molecule_type mRNA
#residues 1977-2014 #label MUS
#cross-references EMBL:X83270; NID:g602579; PID:CAA58243.1;
PID:g602580
#note conformation and properties are reported for a synthetic
peptide corresponding to the translated fragment shown

REFERENCE
S20897
#authors Labelt, S.; Gaute, M.; Lakey, A.; Trinick, J.
#journal EMBO J. (1992) 11:1711-1716
#title Towards a molecular understanding of titin.
#cross-references MIM:92258380
#accession S20898
#status
#molecule_type mRNA
#residues 13597-14200; 'I', 14202-14696 #label LAB2
#cross-references EMBL:X64698; NID:g377192; PID:CAA45939.1; PID:g377193
#accession S20897
#status
#molecule_type mRNA
#residues 16330-16382; 'S', 16384-16756; 'F', 16758-16860 #label LAB3
#cross-references EMBL:X64699; NID:g377190; PID:CAA45940.1; PID:g377191
#accession S20899
#status
#molecule_type mRNA
#residues 'P', 22278-22431; 'R', 22433-22448; 'G', 22450-22453; 'Q',
22455-22480; 'TR', 22483-22669; 'N', 22671-22696; 'SA',
22699-23323; 'L', 23325-25376 #label LAB4
#cross-references EMBL:X64697; NID:g377190; PID:CAA45938.1; PID:g377195
#accession S63665
#authors Kolmerer, B.; Olivieri, N.; Witt, C.C.; Herrmann, B.G.;
Labelt, S.
#journal J. Mol. Biol. (1996) 256:556-563
#title Genomic organization of M line titin and its tissue-specific
expression in two distinct isoforms.
#cross-references MIM:9617761
#accession S63665
#status
#molecule_type DNA
#residues 26729-26825 #label KOL
#cross-references EMBL:X92412; NID:g1236761
#accession S37393
#authors Gaute, M.; Leonard, K.; Labelt, S.
#journal EMBO J. (1993) 12:3827-3834
#title Phosphorylation of KSP motifs in the C-terminal region of
titin in differentiating myoblasts.
#cross-references MIM:9408990
#accession S37393
#molecule_type mRNA
#residues 26831-26926 #label GAD
#accession A66736
#authors Impropa, S.; Poltjou, A.S.; Pastore, A.
#submission submitted to the Brookhaven Protein Data Bank, February 1996
#cross-references PDB:1ITR
#contents annotation; conformation by (1)H-NMR, residues 5253-5341
#authors Pihl, M.; Pastore, A.
#submission submitted to the Brookhaven Protein Data Bank, August 1996
#cross-references PDB:1NCT
#contents annotation; conformation by (1)H-NMR, residues 'S',
26059-26155

GENETICS
#gene GDB:TTN
#cross-references GDB:127867; OMIM:188840
#map_position 2q31-2q32

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0801 0000 0000 0000

URGENT 02 55 08 13:05 3000  
FM WFO  
TO WFO  
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[Illegible text follows]

[Illegible text follows]

[Illegible text follows]

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 N I P E R E H  
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 (TM)

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Mpsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 21 10:33:06 2000; Maspar time 33.14 Seconds

Tabular output not generated. 912.297 Million cell updates/sec

Title: >US-09-240-675-2  
 Description: (1-436) from US09240675.pep  
 Perfect Score: 436  
 Sequence: 1 MMVLLGATLVLVANGPMV.....KSVFSDAVCEKPKPNTSK 436

Scoring table: TABLE uniprotatable  
 Gap 60

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%  
 Listing first 1000 summaries

Database: sptrembl12  
 1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human  
 5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle  
 9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified  
 13:sp.vertebrate 14:sp.virus

Statistics: Mean 3.666; Variance 0.409; scale 8.964

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	9	2.1	569	13	INTERFERON ALPHA/BETA	1.18e-04
2	8	1.8	421	10	FEEL3.9 PROTEIN	2.34e-02
3	8	1.8	571	5	TYROSINE KINASE (FRAGM	2.34e-02
4	8	1.8	1235	5	TYROSINE KINASE (FRAGM	2.34e-02
5	7	1.6	93	2	ORF1, 5' END; NADH-PER	2.89e+00
6	7	1.6	101	14	DNA METHYLTRANSFERASE	2.89e+00
7	7	1.6	141	5	PUTATIVE MULTIFUNCTION	2.89e+00
8	7	1.6	150	14	REV. PROTEIN.	2.89e+00
9	7	1.6	153	1	METHYL-COENZYME M REDU	2.89e+00
10	7	1.6	153	1	METHYL-COENZYME M REDU	2.89e+00
11	7	1.6	163	1	METHYL-COENZYME M REDU	2.89e+00
12	7	1.6	163	1	METHYL-COENZYME M REDU	2.89e+00
13	7	1.6	163	1	METHYL-COENZYME M REDU	2.89e+00
14	7	1.6	163	1	METHYL-COENZYME M REDU	2.89e+00
15	7	1.6	163	1	METHYL-COENZYME M REDU	2.89e+00
16	7	1.6	163	1	METHYL-COENZYME M REDU	2.89e+00
17	7	1.6	163	1	METHYL-COENZYME M REDU	2.89e+00
18	7	1.6	163	1	METHYL-COENZYME M REDU	2.89e+00
19	7	1.6	239	11	TROPONIN T3, SKELETAL	2.89e+00
20	7	1.6	239	11	TROPONIN T3, SKELETAL	2.89e+00

21	7	1.6	248	11	TROPONIN T3, SKELETAL	2.89e+00
22	7	1.6	248	11	TROPONIN T3, SKELETAL	2.89e+00
23	7	1.6	248	11	TROPONIN T3, SKELETAL	2.89e+00
24	7	1.6	250	11	TROPONIN T3, SKELETAL	2.89e+00
25	7	1.6	250	11	TROPONIN T3, SKELETAL	2.89e+00
26	7	1.6	250	11	TROPONIN T3, SKELETAL	2.89e+00
27	7	1.6	255	11	TROPONIN T3, SKELETAL	2.89e+00
28	7	1.6	259	9	TROPONIN T3, SKELETAL	2.89e+00
29	7	1.6	259	9	TROPONIN T3, SKELETAL	2.89e+00
30	7	1.6	262	11	TROPONIN T3, SKELETAL	2.89e+00
31	7	1.6	268	11	TROPONIN T3, SKELETAL	2.89e+00
32	7	1.6	287	13	TROPONIN T3, SKELETAL	2.89e+00
33	7	1.6	298	2	TROPONIN T3, SKELETAL	2.89e+00
34	7	1.6	336	2	TROPONIN T3, SKELETAL	2.89e+00
35	7	1.6	344	5	TROPONIN T3, SKELETAL	2.89e+00
36	7	1.6	364	7	TROPONIN T3, SKELETAL	2.89e+00
37	7	1.6	380	13	TROPONIN T3, SKELETAL	2.89e+00
38	7	1.6	394	11	TROPONIN T3, SKELETAL	2.89e+00
39	7	1.6	403	11	TROPONIN T3, SKELETAL	2.89e+00
40	7	1.6	412	10	TROPONIN T3, SKELETAL	2.89e+00
41	7	1.6	451	1	TROPONIN T3, SKELETAL	2.89e+00
42	7	1.6	454	10	TROPONIN T3, SKELETAL	2.89e+00
43	7	1.6	563	2	TROPONIN T3, SKELETAL	2.89e+00
44	7	1.6	588	14	TROPONIN T3, SKELETAL	2.89e+00
45	7	1.6	594	2	TROPONIN T3, SKELETAL	2.89e+00
46	7	1.6	601	2	TROPONIN T3, SKELETAL	2.89e+00
47	7	1.6	628	5	TROPONIN T3, SKELETAL	2.89e+00
48	7	1.6	643	5	TROPONIN T3, SKELETAL	2.89e+00
49	7	1.6	673	4	TROPONIN T3, SKELETAL	2.89e+00
50	7	1.6	675	4	TROPONIN T3, SKELETAL	2.89e+00
51	7	1.6	686	4	TROPONIN T3, SKELETAL	2.89e+00
52	7	1.6	687	2	TROPONIN T3, SKELETAL	2.89e+00
53	7	1.6	688	2	TROPONIN T3, SKELETAL	2.89e+00
54	7	1.6	730	14	TROPONIN T3, SKELETAL	2.89e+00
55	7	1.6	746	2	TROPONIN T3, SKELETAL	2.89e+00
56	7	1.6	757	4	TROPONIN T3, SKELETAL	2.89e+00
57	7	1.6	771	5	TROPONIN T3, SKELETAL	2.89e+00
58	7	1.6	782	5	TROPONIN T3, SKELETAL	2.89e+00
59	7	1.6	879	5	TROPONIN T3, SKELETAL	2.89e+00
60	7	1.6	866	5	TROPONIN T3, SKELETAL	2.89e+00
61	7	1.6	972	11	TROPONIN T3, SKELETAL	2.89e+00
62	7	1.6	993	2	TROPONIN T3, SKELETAL	2.89e+00
63	7	1.6	1010	5	TROPONIN T3, SKELETAL	2.89e+00
64	7	1.6	1184	2	TROPONIN T3, SKELETAL	2.89e+00
65	7	1.6	1199	5	TROPONIN T3, SKELETAL	2.89e+00
66	7	1.6	1201	10	TROPONIN T3, SKELETAL	2.89e+00
67	7	1.6	1271	2	TROPONIN T3, SKELETAL	2.89e+00
68	7	1.6	1324	2	TROPONIN T3, SKELETAL	2.89e+00
69	7	1.6	1343	14	TROPONIN T3, SKELETAL	2.89e+00
70	7	1.6	1379	4	TROPONIN T3, SKELETAL	2.89e+00
71	7	1.6	2206	14	TROPONIN T3, SKELETAL	2.89e+00
72	7	1.6	2207	14	TROPONIN T3, SKELETAL	2.89e+00
73	7	1.6	4588	5	TROPONIN T3, SKELETAL	2.89e+00
74	7	1.6	40	6	TROPONIN T3, SKELETAL	2.89e+00
75	7	1.4	44	5	TROPONIN T3, SKELETAL	2.89e+00
76	7	1.4	57	14	TROPONIN T3, SKELETAL	2.89e+00
77	7	1.4	58	10	TROPONIN T3, SKELETAL	2.89e+00
78	7	1.4	63	10	TROPONIN T3, SKELETAL	2.89e+00
79	7	1.4	64	14	TROPONIN T3, SKELETAL	2.89e+00
80	7	1.4	66	14	TROPONIN T3, SKELETAL	2.89e+00
81	7	1.4	76	2	TROPONIN T3, SKELETAL	2.89e+00
82	7	1.4	79	2	TROPONIN T3, SKELETAL	2.89e+00
83	7	1.4	89	14	TROPONIN T3, SKELETAL	2.89e+00
84	7	1.4	89	14	TROPONIN T3, SKELETAL	2.89e+00
85	7	1.4	89	14	TROPONIN T3, SKELETAL	2.89e+00
86	7	1.4	93	1	TROPONIN T3, SKELETAL	2.89e+00
87	7	1.4	94	5	TROPONIN T3, SKELETAL	2.89e+00
88	7	1.4	97	2	TROPONIN T3, SKELETAL	2.89e+00
89	7	1.4	98	14	TROPONIN T3, SKELETAL	2.89e+00
90	7	1.4	101	6	TROPONIN T3, SKELETAL	2.89e+00
91	7	1.4	102	14	TROPONIN T3, SKELETAL	2.89e+00
92	7	1.4	102	14	TROPONIN T3, SKELETAL	2.89e+00
93	7	1.4	102	14	TROPONIN T3, SKELETAL	2.89e+00

94	6	1.4	102 14	036140	HEPATITIS DELTA ANTIGE	1.96e+02	167	181 14	090109	LARGE T ANTIGEN (FRAG	1.96e+02
95	6	1.4	102 14	036103	HEPATITIS DELTA ANTIGE	1.96e+02	168	181 10	090417	CYCLOC PHOSPHODIESTER	1.96e+02
96	6	1.4	102 14	036086	HEPATITIS DELTA ANTIGE	1.96e+02	169	181 6	P79389	ELAFIN FAMILY MEMBER P	1.96e+02
97	6	1.4	102 14	036062	HEPATITIS DELTA ANTIGE	1.96e+02	170	181 6	011356	SIMILAR TO VARIOLA N3L	1.96e+02
98	6	1.4	102 14	036121	HEPATITIS DELTA ANTIGE	1.96e+02	171	181 14	090124	T ANTIGEN (FRAGMENT)	1.96e+02
99	6	1.4	102 14	036128	HEPATITIS DELTA ANTIGE	1.96e+02	172	182 2	052944	GLASIMID PLUS32 DNA FOR	1.96e+02
100	6	1.4	102 14	036152	HEPATITIS DELTA ANTIGE	1.96e+02	173	182 13	09W656	GLUTAMATE DECARBOXYLASE	1.96e+02
101	6	1.4	102 14	036122	HEPATITIS DELTA ANTIGE	1.96e+02	174	182 2	053869	PURATIVE	1.96e+02
102	6	1.4	102 14	036131	HEPATITIS DELTA ANTIGE	1.96e+02	175	183 2	045054	PURATIVE LIPROTEIN	1.96e+02
103	6	1.4	102 14	036091	HEPATITIS DELTA ANTIGE	1.96e+02	176	184 1	09YCV0	HYPOHETICAL 21.3 KD P	1.96e+02
104	6	1.4	102 14	036088	HEPATITIS DELTA ANTIGE	1.96e+02	177	184 2	050894	184A LONG HYPOHETICAL	1.96e+02
105	6	1.4	102 14	036081	HEPATITIS DELTA ANTIGE	1.96e+02	178	184 4	050853	CONSERVED HYPOHETICAL	1.96e+02
106	6	1.4	102 14	036116	HEPATITIS DELTA ANTIGE	1.96e+02	179	185 2	053806	OUTER MEMBRANE PROTEIN	1.96e+02
107	6	1.4	102 14	036115	HEPATITIS DELTA ANTIGE	1.96e+02	180	185 2	018232	HYPOHETICAL 20.1 KD P	1.96e+02
108	6	1.4	102 14	036115	HEPATITIS DELTA ANTIGE	1.96e+02	181	186 5	056745	C26F1.3 PROTEIN	1.96e+02
109	6	1.4	102 14	036101	HEPATITIS DELTA ANTIGE	1.96e+02	182	186 2	056745	DNA (FRAGMENT)	1.96e+02
110	6	1.4	102 14	036109	HEPATITIS DELTA ANTIGE	1.96e+02	183	187 3	007091	REGULATOR PROTEIN	1.96e+02
111	6	1.4	102 14	036085	HEPATITIS DELTA ANTIGE	1.96e+02	184	187 1	028824	TRANSCRIPTIONAL REGULA	1.96e+02
112	6	1.4	102 14	036094	HEPATITIS DELTA ANTIGE	1.96e+02	185	189 2	0928K3	BIOPOLYMER TRANSPORT P	1.96e+02
113	6	1.4	102 14	036158	HEPATITIS DELTA ANTIGE	1.96e+02	186	190 10	023413	HYPOHETICAL PROTEIN	1.96e+02
114	6	1.4	105 1	09YFX2	105AA LONG HYPOHETICA	1.96e+02	187	191 6	029124	VIA-2 (FRAGMENT)	1.96e+02
115	6	1.4	105 5	09YXW6	F53F1.4 PROTEIN	1.96e+02	188	191 2	054192	PURATIVE TRANSCRIPTION	1.96e+02
116	6	1.4	108 1	09YGO0	108AA LONG HYPOHETICA	1.96e+02	189	192 2	095300	NIFH, GLNDA, GLNDB, AN	1.96e+02
117	6	1.4	110 4	09YXN6	HYPOHETICAL 13.0 KD P	1.96e+02	190	192 2	066677	PEPTIDYL-TRNA HYDROLAS	1.96e+02
118	6	1.4	111 9	092X37	GP41	1.96e+02	191	192 9	064334	GP20	1.96e+02
119	6	1.4	112 4	09YX3	CCL27 CHEMOKINE	1.96e+02	192	194 10	09X552	ABETA3A3 HOMOLOG RABP3	1.96e+02
120	6	1.4	114 1	09YX2	114AA LONG HYPOHETICA	1.96e+02	193	194 2	092E81	ANTHRANILATE SYNTHASE	1.96e+02
121	6	1.4	115 2	09X107	50S RIBOSOMAL PROTEIN	1.96e+02	194	194 2	066404	HYPOHETICAL 23.4 KD P	1.96e+02
122	6	1.4	115 6	092646	NONE	1.96e+02	195	195 5	027791	SUPEROXIDE DISMUTASE (	1.96e+02
123	6	1.4	116 10	029248	SODIUM/POTASSIUM ATPAS	1.96e+02	196	195 5	002616	DELTA ANTIGEN	1.96e+02
124	6	1.4	116 10	022485	LIPID TRANSFER PROTEIN	1.96e+02	197	195 14	P87885	DELTA ANTIGEN	1.96e+02
125	6	1.4	119 10	040810	S-BNASE (FRAGMENT)	1.96e+02	198	196 4	081834	DELTA ANTIGEN	1.96e+02
126	6	1.4	121 2	048721	HYPOHETICAL 14.5 KD P	1.96e+02	199	196 4	093062	WS-1/TYPER	1.96e+02
127	6	1.4	122 2	048305	DNA ORF1-ORF5	1.96e+02	200	197 14	081847	DELTA ANTIGEN (FRAGMEN	1.96e+02
128	6	1.4	122 2	092749	CTF16 HYPOHETICAL PRO	1.96e+02	201	197 11	09WVB0	HEMES	1.96e+02
129	6	1.4	123 6	095277	PROTEIN KINASE (FRAGME	1.96e+02	202	199 10	000318	22 KD GAMMA-COIXIN PRE	1.96e+02
130	6	1.4	125 2	P95271	HYPOHETICAL 13.6 KD P	1.96e+02	203	200 13	094933	40S RIBOSOMAL PROTEIN	1.96e+02
131	6	1.4	128 1	026723	HYPOHETICAL 13.1 KD P	1.96e+02	204	202 13	090675	TISSUE-TYPE PLASMINOGE	1.96e+02
132	6	1.4	131 13	057446	INSULIN-LIKE GROWTH FA	1.96e+02	205	203 10	P93450	LIGHT-HARVESTING COMPL	1.96e+02
133	6	1.4	131 2	P94342	CHEXY	1.96e+02	206	204 2	P94431	DNA FOR 25-36 DEGREE R	1.96e+02
134	6	1.4	133 2	066170	TRBC	1.96e+02	207	204 4	092516	RBP-MS/TYPER 2	1.96e+02
135	6	1.4	135 8	036742	ATPASE 8 PROTEIN (FRAG	1.96e+02	208	207 2	050259	LEUCYL/PHENILALANYL-TR	1.96e+02
136	6	1.4	140 14	P89914	16 KDA PROTEIN (FRAGME	1.96e+02	209	208 8	021530	NMDH DEHYDROGENASE SUB	1.96e+02
137	6	1.4	141 11	062237	SEX-LIMITED PROTEIN SL	1.96e+02	210	211 2	09X819	HYPOHETICAL 21.1 KD P	1.96e+02
138	6	1.4	144 2	09WV29	INNER MEMBRANE HG(II)	1.96e+02	211	213 1	09Y8C4	213AA LONG HYPOHETICA	1.96e+02
139	6	1.4	145 8	099994	RIBOSOMAL PROTEIN L16	1.96e+02	212	214 2	09XCD0	POTATIVE PARTITION PRO	1.96e+02
140	6	1.4	154 1	030100	TRANSPORASE PUTATIVE	1.96e+02	213	215 5	P92003	LARGE DELTA ANTIGEN	1.96e+02
141	6	1.4	157 6	09X783	INTERLEUKIN 2 PRECURSO	1.96e+02	214	215 10	039946	F33F1.5 PROTEIN	1.96e+02
142	6	1.4	157 1	058919	157AA LONG HYPOHETICA	1.96e+02	215	216 9	080201	ABETA3A3 HOMOLOG PAP3	1.96e+02
143	6	1.4	158 14	099097	CONSERVED PROTEIN	1.96e+02	216	216 14	084523	HYPOHETICAL 25.3 KD P	1.96e+02
144	6	1.4	162 2	050536	A2 MATING TYPE LOCUS	1.96e+02	217	216 5	017526	W02D1.5 PROTEIN	1.96e+02
145	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	218	217 1	093659	TRIMETHYLAMINE CORRIKO	1.96e+02
146	6	1.4	163 1	048922	METHYL-COENZYME M REDU	1.96e+02	219	218 2	092517	RBP-MS/TYPER 3	1.96e+02
147	6	1.4	163 1	050257	METHYL-COENZYME M REDU	1.96e+02	220	219 8	003361	ATP SYNTHASE A CHAIN (	1.96e+02
148	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	221	219 8	003361	ZINC INDUCIBLE T-LYMPHO	1.96e+02
149	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	222	220 8	003361	CYTOTOXIC T-LYMPHO	1.96e+02
150	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	223	221 10	022538	HYPOHETICAL 24.1 KD P	1.96e+02
151	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	224	222 6	062824	BETA-CASEIN	1.96e+02
152	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	225	224 2	005248	HYPOHETICAL 24.7 KD P	1.96e+02
153	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	226	225 5	001604	COSMID T10E9	1.96e+02
154	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	227	225 5	001604	NIFH CLASS-IV PROTEIN	1.96e+02
155	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	228	226 6	062824	HYPOHETICAL 25.9 KD P	1.96e+02
156	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	229	227 2	001536	REPLICATION-ASSOCIATED	1.96e+02
157	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	230	228 2	001536	W03B1.3 PROTEIN	1.96e+02
158	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	231	229 2	001536	243AA LONG HYPOHETICA	1.96e+02
159	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	232	230 2	001536	F13A7.4 PROTEIN	1.96e+02
160	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	233	231 2	001536	252AA LONG HYPOHETICA	1.96e+02
161	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	234	232 2	001536	CHROMOSOME XVI COSMID	1.96e+02
162	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	235	233 2	001536	CHROMOSOME COMPONENT	1.96e+02
163	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	236	234 2	001536	PSEUDOURIDYLATE SYNTHA	1.96e+02
164	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	237	235 2	001536		
165	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	238	236 2	001536		
166	6	1.4	163 1	050828	METHYL-COENZYME M REDU	1.96e+02	239	237 2	001536		

240	6	1.4	254	4	Q9YK2	KALLIREIN 4	1.966+02	313	316	2	P95164	HYPOHETICAL 32.7 KD P	1.966+02
241	6	1.4	254	6	Q9XSN6	ENAMEL MATRIX SERINE P	1.966+02	314	316	2	P95114	HYPOHETICAL 32.7 KD P	1.966+02
242	6	1.4	255	11	Q9Z0M1	ENAMEL MATRIX SERINE P	1.966+02	315	319	2	P96845	HYPOHETICAL 33.5 KD P	1.966+02
243	6	1.4	256	1	Q26605	POTASSIUM CHANNEL RELA	1.966+02	316	319	2	P96850	HYPOHETICAL 33.5 KD P	1.966+02
244	6	1.4	257	14	Q98624	MATRIX PROTEIN	1.966+02	317	321	2	P92820	HYPOHETICAL 33.5 KD P	1.966+02
245	6	1.4	257	13	Q13069	KN-B2 PRECURSOR	1.966+02	318	322	1	P95895	HYPOHETICAL 33.5 KD P	1.966+02
246	6	1.4	258	2	Q85382	EXTRACELLULAR ENTROTO	1.966+02	319	323	5	O15557	HYPOHETICAL 33.5 KD P	1.966+02
247	6	1.4	259	5	Q23406	SIMILARITY TO DROSOPHI	1.966+02	320	323	5	O16002	HYPOHETICAL 33.5 KD P	1.966+02
248	6	1.4	260	13	Q13057	SERINE PROTEASE PRECUR	1.966+02	321	324	2	O12222	LAMBDA CII STABILITY-G	1.966+02
249	6	1.4	260	13	Q13060	SERINE PROTEASE PRECUR	1.966+02	322	324	2	O12222	HYPOHETICAL 37.8 KD P	1.966+02
250	6	1.4	261	5	Q19431	FL39-6 PROTEIN	1.966+02	323	324	13	O90320	CANDIDAL HOMOLOG CDX1	1.966+02
251	6	1.4	261	5	Q62052	COBFI1.10 PROTEIN	1.966+02	324	324	5	O45806	3D3.7 PROTEIN	1.966+02
252	6	1.4	261	2	Q34627	HYPOHETICAL 29.2 KD P	1.966+02	325	324	5	O26911	HEAT SHOCK PROTEIN	1.966+02
253	6	1.4	262	1	Q9YF28	262AA LONG HYPOHETICA	1.966+02	326	326	5	O9XW66	X379A.2 PROTEIN	1.966+02
254	6	1.4	265	1	Q58351	265AA LONG HYPOHETICA	1.966+02	327	327	5	O17032	MULTISE PRECURSOR (FRA	1.966+02
255	6	1.4	267	6	Q02764	OX40 PRECURSOR (FRAGME	1.966+02	328	327	5	O16979	TFBP	1.966+02
256	6	1.4	268	14	Q65117	MULTIGENE FAMILY 300 P	1.966+02	329	329	5	O44829	327AA LONG HYPOHETICA	1.966+02
257	6	1.4	268	5	Q26561	NE-YA SUBUNIT	1.966+02	330	328	13	O93550	POTASSIUM CHANNEL RECP	1.966+02
258	6	1.4	269	2	Q85135	FLAGELAR PROTEIN FLIR	1.966+02	331	328	5	O17706	C54C8.1 PROTEIN	1.966+02
259	6	1.4	269	2	Q92E14	DIHYDRODIOL DEHYDROGEN	1.966+02	332	328	5	O56126	OUTER MEMBRANE PROTEIN	1.966+02
260	6	1.4	272	2	Q9XHH1	VOLTAGE-GATED POTASSIU	1.966+02	333	329	5	O92735	CYTIDINE DEAMINASE 7	1.966+02
261	6	1.4	273	6	Q9XSP9	HYPOHETICAL 28.8 KD P	1.966+02	334	330	10	O92735	NADH-UBIQUINONE OXIDOR	1.966+02
262	6	1.4	273	10	Q23571	HYPOHETICAL 28.8 KD P	1.966+02	335	330	10	O92735	COMPLEMENT COMPONENT 1	1.966+02
263	6	1.4	273	5	Q68480	ACCESSORY PROTEIN NOST	1.966+02	336	331	11	O62353	PECTATE LYASE (FRAGMENT	1.966+02
264	6	1.4	274	5	Q44071	MEROZOITE ANTIGEN 2	1.966+02	337	331	14	O98337	SPIKE PROTEIN (FRAGMENT	1.966+02
265	6	1.4	276	6	Q09078	PANTOATE--BETA-ALANINE	1.966+02	338	334	5	O25121	HYPOHETICAL 37.4 KD P	1.966+02
266	6	1.4	276	5	Q92N52	SIMILAR TO D. MELANOCA	1.966+02	339	335	2	O83811	HYPOHETICAL 37.4 KD P	1.966+02
267	6	1.4	279	14	Q84943	COAT PROTEIN (FRAGMENT	1.966+02	340	336	5	O93642	F30A10.2 PROTEIN	1.966+02
268	6	1.4	280	1	Q26743	HYPOHETICAL 31.7 KD P	1.966+02	341	337	2	O92KJ6	POTASSIUM CHANNEL RECP	1.966+02
269	6	1.4	280	1	Q26743	HYPOHETICAL 31.7 KD P	1.966+02	342	340	5	O48759	C54C8.1 PROTEIN	1.966+02
270	6	1.4	281	14	Q98601	MOVEMENT PROTEIN	1.966+02	343	340	5	P91232	CSMD F08D12	1.966+02
271	6	1.4	282	4	Q9Y390	CG1-81 PROTEIN	1.966+02	344	343	5	O01758	SIMILARITY TO INSECT-T	1.966+02
272	6	1.4	283	14	Q71132	PUTATIVE MOVEMENT PROT	1.966+02	345	344	5	O01758	TO5D4.3 PROTEIN	1.966+02
273	6	1.4	283	14	Q70914	PUTATIVE MOVEMENT PROT	1.966+02	346	345	5	O01758	NP-HEROSE 4-KETORDDUC	1.966+02
274	6	1.4	283	14	Q70916	PUTATIVE MOVEMENT PROT	1.966+02	347	347	14	O55649	AYLOLEIN	1.966+02
275	6	1.4	283	14	Q71130	MOVEMENT PROTEIN	1.966+02	348	348	10	O92KJ6	TC1-LIKE TRANSPOSASE	1.966+02
276	6	1.4	284	14	Q98599	MOVEMENT PROTEIN	1.966+02	349	349	3	P87249	HAPD PROTEIN	1.966+02
277	6	1.4	285	14	Q85205	PUTATIVE MOVEMENT PROT	1.966+02	350	351	1	O9YV98	PEROXIDASE	1.966+02
278	6	1.4	285	14	Q71142	MOVEMENT PROTEIN	1.966+02	351	352	10	O9XG26	331AA LONG HYPOHETICA	1.966+02
279	6	1.4	288	14	Q71140	MAJOR HISTOCOMPATIBILI	1.966+02	352	352	10	O9XG26	TIN24.5 PROTEIN	1.966+02
280	6	1.4	288	7	Q46707	CODED FOR BY C. ELEGAN	1.966+02	353	353	1	O9YV98	HYPOHETICAL 37.5 KD P	1.966+02
281	6	1.4	289	5	P91392	REVERSE TRANSCRIPTASE	1.966+02	354	353	14	O84642	HYDROGENASE SMALL SUBU	1.966+02
282	6	1.4	290	14	Q9YU2	TUMOR SUPPRESSING STP	1.966+02	355	354	14	O84642	PROTEIN 10	1.966+02
283	6	1.4	290	14	Q9YU2	HYPOHETICAL 31.0 KD P	1.966+02	356	355	14	O84642	GENOME PARTIAL SEQUEN	1.966+02
284	6	1.4	290	2	Q67210	HYPOHETICAL 34.5 KD P	1.966+02	357	356	14	O84642	BA74	1.966+02
285	6	1.4	291	14	Q9YU99	REVERSE TRANSCRIPTASE	1.966+02	358	357	10	O9XG26	CYSTINE SYNTHASE (EC	1.966+02
286	6	1.4	291	2	Q86678	HYPOHETICAL 31.0 KD P	1.966+02	359	357	10	O9XG26	MELANOCORTIN 2-RECEPT	1.966+02
287	6	1.4	293	2	Q53855	RECA-LIKE PROTEIN (REC	1.966+02	360	358	1	O9YK29	MHC CLASS I ALPHA CHAI	1.966+02
288	6	1.4	293	14	Q89458	POLY(A) POLYMERASE REG	1.966+02	361	359	5	O14045	358AA LONG HYPOHETICA	1.966+02
289	6	1.4	293	2	Q92M66	CONSERVED HYPOHETICAL	1.966+02	362	360	14	O9YK29	POTASSIUM CHANNEL RECP	1.966+02
290	6	1.4	293	2	Q25080	HYPOHETICAL 32.9 KD P	1.966+02	363	361	5	O14045	HYPOHETICAL 37.5 KD P	1.966+02
291	6	1.4	294	5	Q19891	F28H7.3 PROTEIN	1.966+02	364	362	14	O9YK29	MHC CLASS I ALPHA CHAI	1.966+02
292	6	1.4	295	3	Q04947	HYPOHETICAL 32.9 KD P	1.966+02	365	363	5	O14045	CINNAMYL ALCOHOL DEHYD	1.966+02
293	6	1.4	296	2	Q56953	YFEB	1.966+02	366	364	10	O9X190	HYPOHETICAL 42.2 KD P	1.966+02
294	6	1.4	299	2	Q04816	OREF PROTEIN PRECURSOR	1.966+02	367	365	10	O9X190	CHLOROPLAST CYCLOIS	1.966+02
295	6	1.4	299	2	Q9XK98	HYPOHETICAL 34.4-KDA	1.966+02	368	366	10	O9X190	GLYCULATE OXIDASE (EC	1.966+02
296	6	1.4	300	2	Q87534	FTMH	1.966+02	369	367	10	O9X190	IRON UPTAKE PROTEIN	1.966+02
297	6	1.4	300	5	Q9XK22	L291.1.3 PROTEIN	1.966+02	370	368	10	O9X190	COPEP	1.966+02
298	6	1.4	300	13	Q90262	ZE-CAD1 PROTEIN	1.966+02	371	369	10	O9X190	POLYPROTEIN (FRAGMENT	1.966+02
299	6	1.4	301	10	Q9XK24	POLLEN ALLERGEN IOL P	1.966+02	372	370	2	O51901	POLYPROTEIN (FRAGMENT	1.966+02
300	6	1.4	301	8	Q02681	HYPOHETICAL 35.3 KD P	1.966+02	373	370	2	O51901	ENVELOPE PROTEIN (FRAG	1.966+02
301	6	1.4	302	10	Q9XTH3	FL3F21.10 PROTEIN	1.966+02	374	371	14	O9XK29	373AA LONG HYPOHETICA	1.966+02
302	6	1.4	303	2	Q925H0	HYPOHETICAL 33.2 KD P	1.966+02	375	371	14	O9XK29	TESTICULAR 3-BETA HYDR	1.966+02
303	6	1.4	304	5	Q93792	ESB12.2 PROTEIN	1.966+02	376	371	14	O9XK29	INTERGASE (FRAGMENT)	1.966+02
304	6	1.4	305	1	Q26838	CONSERVED PROTEIN	1.966+02	377	372	14	O9XK29	ATP SYNTHASE BETA-SUBU	1.966+02
305	6	1.4	305	1	Q9YK95	305AA LONG HYPOHETICA	1.966+02	378	373	14	O9XK29	HYPOHETICAL 41.9 KD P	1.966+02
306	6	1.4	310	10	Q9XK24	CHLORIDE CHANNEL C1C-5	1.966+02	379	374	13	O73851	HYPOHETICAL 40.4 KD P	1.966+02
307	6	1.4	310	11	Q9XK24	CHLORIDE CHANNEL C1C-5	1.966+02	380	375	8	O98916	HYPOHETICAL 40.8 KD P	1.966+02
308	6	1.4	312	2	Q52060	ACETALDEHYDE DEHYDROGE	1.966+02	381	376	8	O98916	GLYCOPROTEIN (FRAGMENT	1.966+02
309	6	1.4	312	2	Q50821	DNA SEQUENCE COMPLETE	1.966+02	382	377	3	O04326		
310	6	1.4	312	13	Q57338	SULFOTRANSFERASE	1.966+02	383	378	3	O04326		
311	6	1.4	312	13	Q9M625	XIMPACT	1.966+02	384	380	2	O05875		
312	6	1.4	313	10	Q39089	PALE CRESS GENE	1.966+02	385	381	14	P87762		

386	6	1.4	381 14	P87763	GLYCOPROTEIN (FRAGMENT	1.96e+02	459	6	1.4	452 1	029889	DNA REPAIR PROTEIN RAD	1.96e+02
387	6	1.4	382 2	005825	DNAJ2	1.96e+02	460	6	1.4	452 2	09X019	NADH DEHYDROGENASE, PU	1.96e+02
388	6	1.4	383 11	09W4M2	DEMATTIN 48 KDA SUBUNIT	1.96e+02	461	6	1.4	458 1	026298	CONSERVED PROTEIN	1.96e+02
389	6	1.4	385 8	098475	NADH DEHYDROGENASE SUB	1.96e+02	462	6	1.4	458 2	084822	PHOSPHOLIPIDOMITASE	1.96e+02
390	6	1.4	387 2	055304	ORF GENES, COMPLETE CD	1.96e+02	463	6	1.4	459 8	035376	MTDNA FOR LARGE SUBUNIT	1.96e+02
391	6	1.4	389 2	048816	HELIC AND ORF2 PROTEIN	1.96e+02	464	6	1.4	460 14	089222	ORF1L (FRAGMENT)	1.96e+02
392	6	1.4	390 8	098481	NADH DEHYDROGENASE SUB	1.96e+02	465	6	1.4	461 5	021419	K1003.5 PROTEIN	1.96e+02
393	6	1.4	391 2	P72824	HYPOTHETICAL 42.2 KD P	1.96e+02	466	6	1.4	461 11	061706	RNA FOR TYPE IIB INTRA	1.96e+02
394	6	1.4	391 1	09Y238	HYPOTHETICAL 37.4 KD P	1.96e+02	467	6	1.4	463 3	P74294	HYPOTHETICAL 52.5 KD P	1.96e+02
395	6	1.4	391 2	P95247	SIMILAR TO DOMAINS OF	1.96e+02	468	6	1.4	463 5	09X109	TNF-RECEPTOR-ASSOCIATE	1.96e+02
396	6	1.4	392 5	019858	CONSERVED HYPOTHETICAL	1.96e+02	469	6	1.4	464 5	002068	METHYLASPARTATE MUTASE	1.96e+02
397	6	1.4	392 2	09X145	RUBREDOXIN OXIDOREDUCT	1.96e+02	470	6	1.4	466 5	046125	SIMILARITY TO XENOPUS	1.96e+02
398	6	1.4	393 2	005099	393AA LONG HYPOTHETICA	1.96e+02	471	6	1.4	470 2	092887	HGM1 PROTEIN PRECURSOR	1.96e+02
399	6	1.4	393 11	09W920	ACID CERAMIDASE (EC 3	1.96e+02	472	6	1.4	473 3	P78719	DICARBOXYLASE TRANSLOC	1.96e+02
400	6	1.4	394 8	098473	NADH DEHYDROGENASE SUB	1.96e+02	473	6	1.4	477 5	001597	CELSUAD T05E8	1.96e+02
401	6	1.4	395 8	069639	SERINE PROTEINASE	1.96e+02	474	6	1.4	479 1	029072	ACTIVATOR 1, REPLICATI	1.96e+02
402	6	1.4	397 2	006670	POTATIVE SERINE PROTEA	1.96e+02	475	6	1.4	480 2	056817	FATTY ACID REDUCTASE	1.96e+02
403	6	1.4	398 2	084701	HYPOTHETICAL 44.3 KD P	1.96e+02	476	6	1.4	482 5	096267	CHROMATIN-BINDING PROT	1.96e+02
404	6	1.4	398 8	098478	NADH DEHYDROGENASE SUB	1.96e+02	477	6	1.4	484 2	053466	ORF2 PROTEIN (FRAGMENT	1.96e+02
405	6	1.4	399 2	056257	CODED FOR BY C. ELEGAN	1.96e+02	478	6	1.4	485 2	P77811	RIBULOSE BIPHOSPHATE	1.96e+02
406	6	1.4	399 2	056257	DOCB.	1.96e+02	479	6	1.4	485 11	0921M4	S6 KINASE 2	1.96e+02
407	6	1.4	400 4	014183	ORF401.	1.96e+02	480	6	1.4	485 5	09X177	Y54E2A.8 PROTEIN.	1.96e+02
408	6	1.4	401 2	047476	NADH DEHYDROGENASE SUB	1.96e+02	481	6	1.4	487 5	09X186	Y51A2D.13 PROTEIN.	1.96e+02
409	6	1.4	403 8	098479	DOCB.	1.96e+02	482	6	1.4	489 13	091781	POTASSIUM CHANNEL.	1.96e+02
410	6	1.4	403 11	P70611	DEMATTIN 52 KDA SUBUNIT	1.96e+02	483	6	1.4	490 3	060028	ALPHA-GALACTOSIDASE.	1.96e+02
411	6	1.4	405 4	013215	AP-ENONUCLEASE	1.96e+02	484	6	1.4	491 2	04465	AGSPL1 PROTEIN.	1.96e+02
412	6	1.4	405 5	015921	HYPOTHETICAL 45.9 KD P	1.96e+02	485	6	1.4	493 14	083449	DINITROGENASE ALPHA SU	1.96e+02
413	6	1.4	405 11	05527	DOUBLE C2, ALPHA (DOCB	1.96e+02	486	6	1.4	493 14	083444	NSP1	1.96e+02
414	6	1.4	405 11	05527	CYTOCHROME P450 LIN (E	1.96e+02	487	6	1.4	493 14	093184	HYPOTHETICAL 54.5 KD P	1.96e+02
415	6	1.4	406 2	09W4V6	ORF407.	1.96e+02	488	6	1.4	494 11	092188	CYTOCHROME P-450 2A14.	1.96e+02
416	6	1.4	407 10	022028	407AA LONG HYPOTHETICA	1.96e+02	489	6	1.4	495 4	094809	P70 RIBOSOMAL S6 KINAS	1.96e+02
417	6	1.4	408 2	048658	LMRP INTEGRAL MEMBRANE	1.96e+02	490	6	1.4	495 13	093187	RIBOSE ABC TRANSPORTER	1.96e+02
418	6	1.4	408 14	041629	ENVELOPE GLYCOPROTEIN	1.96e+02	491	6	1.4	497 13	09Y1A7	ZIC-RELATED-2.	1.96e+02
419	6	1.4	409 1	09YACT	409AA LONG HYPOTHETICA	1.96e+02	492	6	1.4	499 5	045364	FLAH3.10-PROTEIN.	1.96e+02
420	6	1.4	411 2	P95146	HYPOTHETICAL 43.6 KD P	1.96e+02	493	6	1.4	499 5	09Y1A7	ZINC FINGER PROTEIN ZI	1.96e+02
421	6	1.4	412 11	070450	HMG BOX TRANSCRIPTION	1.96e+02	494	6	1.4	501 13	093487	ZINC TRANSPORTER 1 (ZN	1.96e+02
422	6	1.4	412 8	098476	NADH DEHYDROGENASE SUB	1.96e+02	495	6	1.4	501 13	093487	RIBOSOMAL MATURASE (FR	1.96e+02
423	6	1.4	413 8	098476	NADH DEHYDROGENASE SUB	1.96e+02	496	6	1.4	507 8	047119	KIAA0020 PROTEIN.	1.96e+02
424	6	1.4	413 8	098476	NADH DEHYDROGENASE SUB	1.96e+02	497	6	1.4	508 4	015397	HYPOTHETICAL 56.7 KD P	1.96e+02
425	6	1.4	413 8	098476	NADH DEHYDROGENASE SUB	1.96e+02	498	6	1.4	509 2	P74537	HYPOHETICAL 54.6 KD P	1.96e+02
426	6	1.4	415 4	095906	Y102A5D.1-PROTEIN.	1.96e+02	499	6	1.4	510 5	024425	TROPOMIOSIN 1 (ISOFORM	1.96e+02
427	6	1.4	415 14	041523	PROTEIN THAT INTERACTS	1.96e+02	500	6	1.4	510 5	075926	PUTATIVE SUGAR TRANSPO	1.96e+02
428	6	1.4	416 5	09X64	NADH DEHYDROGENASE SUB	1.96e+02	501	6	1.4	511 10	09X1H7	POTASSIUM CHANNEL.	1.96e+02
429	6	1.4	416 11	062083	NADH DEHYDROGENASE SUB	1.96e+02	502	6	1.4	515 5	016968	FISH HOMOLOG.	1.96e+02
430	6	1.4	417 8	095683	LIPASE (EC 3.1.1.3) (T	1.96e+02	503	6	1.4	517 4	09Y202	SIGMA-LIKE FACTOR PREC	1.96e+02
431	6	1.4	417 2	059260	ATAXIN-2 (FRAGMENT)	1.96e+02	504	6	1.4	519 10	0928X9	VENTRAL NEURAL CADHERI	1.96e+02
432	6	1.4	417 2	059260	PUTATIVE MEMBRANE PROT	1.96e+02	505	6	1.4	520 8	032477	HYPOTHETICAL PROTEIN.	1.96e+02
433	6	1.4	417 8	095683	SIMILAR TO ACETYLCHOLIN	1.96e+02	506	6	1.4	521 10	082507	NADH DEHYDROGENASE SUB	1.96e+02
434	6	1.4	419 11	P97421	SNF1 RELATED PROTEIN K	1.96e+02	507	6	1.4	524 5	09XUT4	F2P5.14 PROTEIN.	1.96e+02
435	6	1.4	425 2	020569	COSMID M03A8	1.96e+02	508	6	1.4	525 5	044079	Y49E10.17 PROTEIN.	1.96e+02
436	6	1.4	425 2	P74524	HOMOSERINE DEHYDROGENA	1.96e+02	509	6	1.4	527 2	051259	CHITINASE	1.96e+02
437	6	1.4	426 2	P71006	ALDEHYDE DEHYDROGENASE	1.96e+02	510	6	1.4	527 6	097492	GLUCINOL-3-PHOSPHATE D	1.96e+02
438	6	1.4	426 2	P71006	DNA FOR TYPE IIB INTRA	1.96e+02	511	6	1.4	527 2	068018	CAVALASE (EC 1.11.1.6)	1.96e+02
439	6	1.4	434 4	060647	EYES ABSENT HOMOLOG (F	1.96e+02	512	6	1.4	529 4	015680	HYPOTHETICAL 56.2 KD P	1.96e+02
440	6	1.4	434 11	061709	MAL3P8.11 PROTEIN.	1.96e+02	513	6	1.4	529 4	034355	TYROSINASE PRECURSOR (	1.96e+02
441	6	1.4	433 10	065516	SIMILAR TO ESTERASE AN	1.96e+02	514	6	1.4	530 10	023732	GLUTATHIONE SYNTHETASE	1.96e+02
442	6	1.4	433 10	065516	VP2 PROTEIN (FRAGMENT)	1.96e+02	515	6	1.4	531 4	024426	TROPOMIOSIN ISOFORM 33	1.96e+02
443	6	1.4	441 14	065744	MG-PROTOPORPHIRIN IX M	1.96e+02	516	6	1.4	531 5	015676	PUTATIVE TYROSINASE PR	1.96e+02
444	6	1.4	442 3	014131	HYPOTHETICAL 49.8 KD P	1.96e+02	517	6	1.4	533 2	0929M5	SIMILAR TO UDP-GLUCURO	1.96e+02
445	6	1.4	444 5	051926	NADH DEHYDROGENASE 1 C	1.96e+02	518	6	1.4	534 4	015675	TNNB3PROTEIN.	1.96e+02
446	6	1.4	445 5	019296	SIMILAR TO REPEAT OF C	1.96e+02	519	6	1.4	534 10	080853	TYROSINASE	1.96e+02
447	6	1.4	446 8	058175	CORBI ORF.	1.96e+02	520	6	1.4	535 3	001165	TRANSPOSASE	1.96e+02
448	6	1.4	448 8	058175	449AA LONG HYPOTHETICA	1.96e+02	521	6	1.4	536 1	09YBMS	536AA LONG HYPOTHETICA	1.96e+02
449	6	1.4	450 1	09YBMS	450AA LONG HYPOTHETICA	1.96e+02	522	6	1.4	536 2	074506	HYPOTHETICAL 58.7 KD P	1.96e+02
450	6	1.4	451 2	058588	PUTATIVE LIPROTEIN.	1.96e+02	523	6	1.4	538 2	085801	REPLICATION PROTEIN A.	1.96e+02
451	6	1.4	451 2	058588	HYPOTHETICAL 45.8 KD P	1.96e+02	524	6	1.4	538 5	09YX00	T26C5.3B PROTEIN.	1.96e+02

532	6	1.4	541 10	092796	1.96e+02	605	6	1.4	635 2	045820	1.96e+02	CSPB GENE
533	6	1.4	547 2	052981	1.96e+02	606	6	1.4	636 8	099479	1.96e+02	REVERSE TRANSCRIPTASE
534	6	1.4	547 2	092981	1.96e+02	607	6	1.4	643 5	061904	1.96e+02	72704.2 PROTEIN
535	6	1.4	547 14	098269	1.96e+02	608	6	1.4	646 2	092693	1.96e+02	PENICILLIN BINDING PRO
536	6	1.4	548 4	015371	1.96e+02	609	6	1.4	647 2	092693	1.96e+02	PURIFIED GAMMA-GLOBULIN
537	6	1.4	549 13	092639	1.96e+02	610	6	1.4	648 8	032073	1.96e+02	NADH DEHYDROGENASE SUB
538	6	1.4	549 3	014030	1.96e+02	611	6	1.4	653 5	021209	1.96e+02	HYPOHETICAL 73.3 K D P
539	6	1.4	551 11	097471	1.96e+02	612	6	1.4	655 4	015311	1.96e+02	FLI76.7 PROTEIN
540	6	1.4	552 4	013485	1.96e+02	613	6	1.4	656 2	092101	1.96e+02	DNA LIGASE (POLYOMYX
541	6	1.4	552 11	070437	1.96e+02	614	6	1.4	658 2	025252	1.96e+02	HYPOHETICAL 78.2 K D P
542	6	1.4	552 11	092437	1.96e+02	615	6	1.4	661 5	022249	1.96e+02	10698.2 PROTEIN
543	6	1.4	553 2	092924	1.96e+02	616	6	1.4	664 1	058354	1.96e+02	664A LONG HYPOHETICAL
544	6	1.4	555 4	092924	1.96e+02	617	6	1.4	669 2	066983	1.96e+02	ATP-DEPENDENT DNA HELI
545	6	1.4	555 4	092924	1.96e+02	618	6	1.4	671 2	092489	1.96e+02	HYPOHETICAL 77.2 K D P
546	6	1.4	557 11	092131	1.96e+02	619	6	1.4	675 2	057071	1.96e+02	PTS SYSTEM, GLUCOSE-SP
547	6	1.4	557 14	036392	1.96e+02	620	6	1.4	676 2	007365	1.96e+02	PURIFIED PROTEIN INITI
548	6	1.4	558 13	092666	1.96e+02	621	6	1.4	677 5	045619	1.96e+02	H12119.5C PROTEIN
549	6	1.4	559 5	092666	1.96e+02	622	6	1.4	680 10	023225	1.96e+02	HYPOHETICAL 75.3 K D P
550	6	1.4	559 5	026645	1.96e+02	623	6	1.4	682 10	092485	1.96e+02	MICROTUBULE-ASSOCIATED
551	6	1.4	559 10	004582	1.96e+02	624	6	1.4	682 8	047007	1.96e+02	NADH DEHYDROGENASE (FR
552	6	1.4	563 2	092419	1.96e+02	625	6	1.4	682 8	032035	1.96e+02	NADH DEHYDROGENASE SUB
553	6	1.4	564 5	023118	1.96e+02	626	6	1.4	683 8	046936	1.96e+02	NADH DEHYDROGENASE (FR
554	6	1.4	564 2	034830	1.96e+02	627	6	1.4	683 8	047008	1.96e+02	NADH DEHYDROGENASE (FR
555	6	1.4	566 3	012433	1.96e+02	628	6	1.4	684 8	019831	1.96e+02	NADH DEHYDROGENASE (FR
556	6	1.4	567 9	092433	1.96e+02	629	6	1.4	684 8	022319	1.96e+02	NADH DEHYDROGENASE (FR
557	6	1.4	568 14	068954	1.96e+02	630	6	1.4	686 8	095641	1.96e+02	NADH DEHYDROGENASE (FR
558	6	1.4	570 2	094544	1.96e+02	631	6	1.4	686 8	095641	1.96e+02	NADH DEHYDROGENASE (FR
559	6	1.4	572 11	092177	1.96e+02	632	6	1.4	686 8	095641	1.96e+02	NADH DEHYDROGENASE (FR
560	6	1.4	572 12	092407	1.96e+02	633	6	1.4	686 8	095641	1.96e+02	NADH DEHYDROGENASE (FR
561	6	1.4	572 10	092407	1.96e+02	634	6	1.4	686 8	095641	1.96e+02	NADH DEHYDROGENASE (FR
562	6	1.4	572 14	075927	1.96e+02	635	6	1.4	687 5	092418	1.96e+02	NADH DEHYDROGENASE (FR
563	6	1.4	573 14	069067	1.96e+02	636	6	1.4	687 5	092418	1.96e+02	NADH DEHYDROGENASE (FR
564	6	1.4	574 5	000708	1.96e+02	637	6	1.4	688 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
565	6	1.4	574 10	065653	1.96e+02	638	6	1.4	688 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
566	6	1.4	575 5	024062	1.96e+02	639	6	1.4	688 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
567	6	1.4	576 2	031903	1.96e+02	640	6	1.4	688 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
568	6	1.4	576 13	092761	1.96e+02	641	6	1.4	688 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
569	6	1.4	576 9	064145	1.96e+02	642	6	1.4	688 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
570	6	1.4	580 2	087278	1.96e+02	643	6	1.4	688 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
571	6	1.4	581 10	065478	1.96e+02	644	6	1.4	688 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
572	6	1.4	582 10	092060	1.96e+02	645	6	1.4	688 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
573	6	1.4	583 5	044468	1.96e+02	646	6	1.4	688 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
574	6	1.4	584 11	070573	1.96e+02	647	6	1.4	688 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
575	6	1.4	584 3	059736	1.96e+02	648	6	1.4	689 8	095642	1.96e+02	NADH DEHYDROGENASE (FR
576	6	1.4	585 13	092665	1.96e+02	649	6	1.4	689 8	033090	1.96e+02	NADH DEHYDROGENASE SUB
577	6	1.4	587 10	023241	1.96e+02	650	6	1.4	689 8	033090	1.96e+02	NADH DEHYDROGENASE SUB
578	6	1.4	588 14	066043	1.96e+02	651	6	1.4	691 8	047006	1.96e+02	HYPOHETICAL PROTEIN C
579	6	1.4	591 14	085379	1.96e+02	652	6	1.4	691 8	047006	1.96e+02	NADH DEHYDROGENASE (FR
580	6	1.4	591 8	092293	1.96e+02	653	6	1.4	692 11	035804	1.96e+02	JANUS PROTEIN TYROSINE
581	6	1.4	591 14	089209	1.96e+02	654	6	1.4	693 11	092666	1.96e+02	NADH DEHYDROGENASE SUB
582	6	1.4	593 2	024873	1.96e+02	655	6	1.4	693 11	092666	1.96e+02	AXOTROPHIN
583	6	1.4	593 13	092666	1.96e+02	656	6	1.4	694 8	092666	1.96e+02	GLYCE-ACTIVATING PROT
584	6	1.4	597 5	092666	1.96e+02	657	6	1.4	694 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
585	6	1.4	603 2	033406	1.96e+02	658	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
586	6	1.4	604 8	031919	1.96e+02	659	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
587	6	1.4	605 5	016190	1.96e+02	660	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
588	6	1.4	605 10	023568	1.96e+02	661	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
589	6	1.4	606 2	031566	1.96e+02	662	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
590	6	1.4	609 4	012886	1.96e+02	663	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
591	6	1.4	610 2	052961	1.96e+02	664	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
592	6	1.4	611 5	092264	1.96e+02	665	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
593	6	1.4	612 10	092264	1.96e+02	666	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
594	6	1.4	613 5	092264	1.96e+02	667	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
595	6	1.4	615 5	020845	1.96e+02	668	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
596	6	1.4	619 2	092935	1.96e+02	669	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
597	6	1.4	620 5	021651	1.96e+02	670	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
598	6	1.4	621 4	075928	1.96e+02	671	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
599	6	1.4	629 6	029426	1.96e+02	672	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
600	6	1.4	632 8	023142	1.96e+02	673	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
601	6	1.4	632 5	022816	1.96e+02	674	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
602	6	1.4	632 4	060293	1.96e+02	675	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
603	6	1.4	632 4	060293	1.96e+02	676	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB
604	6	1.4	633 2	066895	1.96e+02	677	6	1.4	695 8	092666	1.96e+02	NADH DEHYDROGENASE SUB

678	6	1.4	695	8	032700	NADH DEHYDROGENASE SUB	1.96e+02	751	736	10	023362	HYPOPHOSPHATE 80.8 KD P	1.96e+02	
679	6	1.4	695	8	032339	NADH DEHYDROGENASE SUB	1.96e+02	752	737	8	019932	NADH DEHYDROGENASE (FR	1.96e+02	
680	6	1.4	695	8	P92308	NADH DEHYDROGENASE SUB	1.96e+02	753	738	8	098709	NADH DEHYDROGENASE (FR	1.96e+02	
681	6	1.4	695	8	095679	NADH DEHYDROGENASE SUB	1.96e+02	754	739	8	019931	NADH DEHYDROGENASE (FR	1.96e+02	
682	6	1.4	695	8	095687	NADH DEHYDROGENASE SUB	1.96e+02	755	740	8	095118	NADH DEHYDROGENASE (FR	1.96e+02	
683	6	1.4	695	8	095686	NADH DEHYDROGENASE SUB	1.96e+02	756	741	8	032055	NADH DEHYDROGENASE (FR	1.96e+02	
684	6	1.4	695	8	095682	NADH DEHYDROGENASE SUB	1.96e+02	757	742	8	019944	NADH DEHYDROGENASE (FR	1.96e+02	
685	6	1.4	696	8	032058	NADH DEHYDROGENASE SUB	1.96e+02	758	743	8	098703	NADH DEHYDROGENASE (FR	1.96e+02	
686	6	1.4	697	8	031877	NADH DEHYDROGENASE SUB	1.96e+02	759	744	8	089713	NADH DEHYDROGENASE (FR	1.96e+02	
687	6	1.4	697	8	003659	NADH DEHYDROGENASE (FR	1.96e+02	760	745	8	069156	NADH DEHYDROGENASE (FR	1.96e+02	
688	6	1.4	698	8	031860	NADH DEHYDROGENASE SUB	1.96e+02	761	746	8	069157	NADH DEHYDROGENASE (FR	1.96e+02	
689	6	1.4	698	8	032447	NADH DEHYDROGENASE SUB	1.96e+02	762	747	8	069158	NADH DEHYDROGENASE (FR	1.96e+02	
690	6	1.4	698	8	098653	NADH DEHYDROGENASE SUB	1.96e+02	763	748	8	069159	NADH DEHYDROGENASE (FR	1.96e+02	
691	6	1.4	698	8	098647	NADH DEHYDROGENASE SUB	1.96e+02	764	749	8	069160	NADH DEHYDROGENASE (FR	1.96e+02	
692	6	1.4	698	8	098644	NADH DEHYDROGENASE SUB	1.96e+02	765	750	8	069161	NADH DEHYDROGENASE (FR	1.96e+02	
693	6	1.4	698	8	098645	NADH DEHYDROGENASE SUB	1.96e+02	766	751	8	069162	NADH DEHYDROGENASE (FR	1.96e+02	
694	6	1.4	698	8	098641	NADH DEHYDROGENASE SUB	1.96e+02	767	752	8	069163	NADH DEHYDROGENASE (FR	1.96e+02	
695	6	1.4	698	8	098648	NADH DEHYDROGENASE SUB	1.96e+02	768	753	8	069164	NADH DEHYDROGENASE (FR	1.96e+02	
696	6	1.4	698	8	098642	NADH DEHYDROGENASE SUB	1.96e+02	769	754	8	069165	NADH DEHYDROGENASE (FR	1.96e+02	
697	6	1.4	698	8	098651	NADH DEHYDROGENASE SUB	1.96e+02	770	755	8	069166	NADH DEHYDROGENASE (FR	1.96e+02	
698	6	1.4	698	8	032665	NADH DEHYDROGENASE SUB	1.96e+02	771	756	8	069167	NADH DEHYDROGENASE (FR	1.96e+02	
699	6	1.4	698	8	098646	NADH DEHYDROGENASE SUB	1.96e+02	772	757	8	069168	NADH DEHYDROGENASE (FR	1.96e+02	
700	6	1.4	699	8	051319	NADH DEHYDROGENASE SUB	1.96e+02	773	758	8	069169	NADH DEHYDROGENASE (FR	1.96e+02	
701	6	1.4	699	8	033257	NADH DEHYDROGENASE SUB	1.96e+02	774	759	8	069170	NADH DEHYDROGENASE (FR	1.96e+02	
702	6	1.4	700	8	033281	NADH DEHYDROGENASE SUB	1.96e+02	775	760	8	069171	NADH DEHYDROGENASE (FR	1.96e+02	
703	6	1.4	700	8	033181	NADH DEHYDROGENASE SUB	1.96e+02	776	761	8	069172	NADH DEHYDROGENASE (FR	1.96e+02	
704	6	1.4	700	8	031815	NADH DEHYDROGENASE SUB	1.96e+02	777	762	8	069173	NADH DEHYDROGENASE (FR	1.96e+02	
705	6	1.4	700	8	032598	NADH DEHYDROGENASE SUB	1.96e+02	778	763	8	069174	NADH DEHYDROGENASE (FR	1.96e+02	
706	6	1.4	700	8	033046	NADH DEHYDROGENASE SUB	1.96e+02	779	764	8	069175	NADH DEHYDROGENASE (FR	1.96e+02	
707	6	1.4	700	8	033143	NADH DEHYDROGENASE SUB	1.96e+02	780	765	8	069176	NADH DEHYDROGENASE (FR	1.96e+02	
708	6	1.4	700	8	032922	NADH DEHYDROGENASE SUB	1.96e+02	781	766	8	069177	NADH DEHYDROGENASE (FR	1.96e+02	
709	6	1.4	700	8	095662	NADH DEHYDROGENASE SUB	1.96e+02	782	767	8	069178	NADH DEHYDROGENASE (FR	1.96e+02	
710	6	1.4	702	5	095662	NADH DEHYDROGENASE SUB	1.96e+02	783	768	8	069179	NADH DEHYDROGENASE (FR	1.96e+02	
711	6	1.4	702	5	014796	MO15.6 PROTEIN.	1.96e+02	784	769	8	069180	NADH DEHYDROGENASE (FR	1.96e+02	
712	6	1.4	704	5	033150	NADH DEHYDROGENASE SUB	1.96e+02	785	770	8	069181	NADH DEHYDROGENASE (FR	1.96e+02	
713	6	1.4	704	5	094856	EG.23E12.5 PROTEIN.	1.96e+02	786	771	8	069182	NADH DEHYDROGENASE (FR	1.96e+02	
714	6	1.4	704	5	032852	NADH DEHYDROGENASE SUB	1.96e+02	787	772	8	069183	NADH DEHYDROGENASE (FR	1.96e+02	
715	6	1.4	705	8	033170	NADH DEHYDROGENASE SUB	1.96e+02	788	773	8	069184	NADH DEHYDROGENASE (FR	1.96e+02	
716	6	1.4	705	8	019832	NADH DEHYDROGENASE SUB	1.96e+02	789	774	8	069185	NADH DEHYDROGENASE (FR	1.96e+02	
717	6	1.4	705	8	032675	NADH DEHYDROGENASE (FR	1.96e+02	790	775	8	069186	NADH DEHYDROGENASE (FR	1.96e+02	
718	6	1.4	706	8	095690	NADH DEHYDROGENASE SUB	1.96e+02	791	776	8	069187	NADH DEHYDROGENASE (FR	1.96e+02	
719	6	1.4	706	2	092524	POTATIVE.	1.96e+02	792	777	8	069188	NADH DEHYDROGENASE (FR	1.96e+02	
720	6	1.4	712	4	000531	TENASCIN-R (RESTRICTIN	1.96e+02	793	778	8	069189	NADH DEHYDROGENASE (FR	1.96e+02	
721	6	1.4	712	13	042443	TAP2.	1.96e+02	794	779	8	069190	NADH DEHYDROGENASE (FR	1.96e+02	
722	6	1.4	715	11	088967	ATP-DEPENDENT METALLOP	1.96e+02	795	780	8	069191	NADH DEHYDROGENASE (FR	1.96e+02	
723	6	1.4	719	2	045751	INSECTICIDAL PROTEIN.	1.96e+02	796	781	8	069192	NADH DEHYDROGENASE (FR	1.96e+02	
724	6	1.4	719	2	045756	CCGRV.	1.96e+02	797	782	8	069193	NADH DEHYDROGENASE (FR	1.96e+02	
725	6	1.4	719	2	085796	INSECTICIDAL PROTEIN.	1.96e+02	798	783	8	069194	NADH DEHYDROGENASE (FR	1.96e+02	
726	6	1.4	719	2	094811	INSECTICIDAL CRYSTAL P	1.96e+02	799	784	8	069195	NADH DEHYDROGENASE (FR	1.96e+02	
727	6	1.4	719	2	045709	CRYV465. PROTEIN.	1.96e+02	800	785	8	069196	NADH DEHYDROGENASE (FR	1.96e+02	
728	6	1.4	719	2	087404	CRYSTAL. PROTEIN TOXIN.	1.96e+02	801	786	8	069197	NADH DEHYDROGENASE (FR	1.96e+02	
729	6	1.4	719	8	098699	NADH DEHYDROGENASE (FR	1.96e+02	802	787	8	069198	NADH DEHYDROGENASE (FR	1.96e+02	
730	6	1.4	719	2	045752	INSECTICIDAL PROTEIN.	1.96e+02	803	788	8	069199	NADH DEHYDROGENASE (FR	1.96e+02	
731	6	1.4	721	8	019934	NADH DEHYDROGENASE (FR	1.96e+02	804	789	8	069200	NADH DEHYDROGENASE (FR	1.96e+02	
732	6	1.4	722	10	004514	HYPOPHOSPHATE 81.3 KD P	1.96e+02	805	790	8	069201	NADH DEHYDROGENASE (FR	1.96e+02	
733	6	1.4	724	5	017856	C31A11.1 PROTEIN.	1.96e+02	806	791	8	069202	NADH DEHYDROGENASE (FR	1.96e+02	
734	6	1.4	724	2	005748	PTBR.	1.96e+02	807	792	8	069203	NADH DEHYDROGENASE (FR	1.96e+02	
735	6	1.4	726	8	019938	NADH DEHYDROGENASE (FR	1.96e+02	808	793	8	069204	NADH DEHYDROGENASE (FR	1.96e+02	
736	6	1.4	726	8	019937	NADH DEHYDROGENASE (FR	1.96e+02	809	794	8	069205	NADH DEHYDROGENASE (FR	1.96e+02	
737	6	1.4	727	8	019942	NADH DEHYDROGENASE (FR	1.96e+02	810	795	8	069206	NADH DEHYDROGENASE (FR	1.96e+02	
738	6	1.4	728	8	098702	NADH DEHYDROGENASE (FR	1.96e+02	811	796	8	069207	NADH DEHYDROGENASE (FR	1.96e+02	
739	6	1.4	729	8	019948	NADH DEHYDROGENASE (FR	1.96e+02	812	797	8	069208	NADH DEHYDROGENASE (FR	1.96e+02	
740	6	1.4	730	8	019945	NADH DEHYDROGENASE (FR	1.96e+02	813	798	8	069209	NADH DEHYDROGENASE (FR	1.96e+02	
741	6	1.4	731	8	019947	NADH DEHYDROGENASE (FR	1.96e+02	814	799	8	069210	NADH DEHYDROGENASE (FR	1.96e+02	
742	6	1.4	731	8	098700	NADH DEHYDROGENASE (FR	1.96e+02	815	800	8	069211	NADH DEHYDROGENASE (FR	1.96e+02	
743	6	1.4	732	8	019933	NADH DEHYDROGENASE (FR	1.96e+02	816	801	8	069212	NADH DEHYDROGENASE (FR	1.96e+02	
744	6	1.4	732	8	098711	NADH DEHYDROGENASE (FR	1.96e+02	817	802	8	069213	NADH DEHYDROGENASE (FR	1.96e+02	
745	6	1.4	732	8	098710	NADH DEHYDROGENASE (FR	1.96e+02	818	803	8	069214	NADH DEHYDROGENASE (FR	1.96e+02	
746	6	1.4	733	8	098707	NADH DEHYDROGENASE (FR	1.96e+02	819	804	8	069215	NADH DEHYDROGENASE (FR	1.96e+02	
747	6	1.4	734	8	098706	NADH DEHYDROGENASE (FR	1.96e+02	820	805	8	069216	NADH DEHYDROGENASE (FR	1.96e+02	
748	6	1.4	735	1	026409	HYPOPHOSPHATE 83.5 KD P	1.96e+02	821	806	8	069217	NADH DEHYDROGENASE (FR	1.96e+02	
749	6	1.4	736	8	019936	NADH DEHYDROGENASE (FR	1.96e+02	822	807	8	069218	NADH DEHYDROGENASE (FR	1.96e+02	
750	6	1.4	736	8	019946	NADH DEHYDROGENASE (FR	1.96e+02	823	808	8	069219	NADH DEHYDROGENASE (FR	1.96e+02	
	6	1.4	736	8	019939	NADH DEHYDROGENASE (FR	1.96e+02		824	809	8	069220	NADH DEHYDROGENASE (FR	1.96e+02

678	6	1.4	695	8	032700	NADH DEHYDROGENASE SUB	1.96e+02	751	736	10	023362	HYPOPHOSPHATE 80.8 KD P	1.96e+02
679	6	1.4	695	8	032339	NADH DEHYDROGENASE SUB	1.96e+02	752	737	8	019932	NADH DEHYDROGENASE (FR	1.96e+02
680	6	1.4	695	8	P92308	NADH DEHYDROGENASE SUB	1.96e+02	753	738	8	098709	NADH DEHYDROGENASE (FR	1.96e+02
681	6	1.4	695	8	095679	NADH DEHYDROGENASE SUB	1.96e+02	754	739	8	019931	NADH DEHYDROGENASE (FR	1.96e+02
682	6	1.4	695	8	095687	NADH DEHYDROGENASE SUB	1.96e+02	755	740	8	095118	NADH DEHYDROGENASE (FR	1.96e+02
683	6	1.4	695	8	095686	NADH DEHYDROGENASE SUB	1.96e+02	756	741	8	032055	NADH DEHYDROGENASE (FR	1.96e+02
684	6	1.4	695	8	095682	NADH DEHYDROGENASE SUB	1.96e+02	757	742	8	019944	NADH DEHYDROGENASE (FR	1.96e+02
685	6	1.4	696	8	032058	NADH DEHYDROGENASE SUB	1.96e+02	758	743	8	098703	NADH DEHYDROGENASE (FR	1.96e+02
686	6	1.4	697	8	031877	NADH DEHYDROGENASE SUB	1.96e+02	759	744	8	089713	NADH DEHYDROGENASE (FR	1.96e+02
687	6	1.4	697	8	003659	NADH DEHYDROGENASE (FR	1.96e+02	760	745	8	069156	NADH DEHYDROGENASE (FR	1.96e+02
688	6	1.4	698	8									

1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02	1.96e+02
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824	6	1.4	973	2	092836	POLYMORPHIC OUTER MEMB	1.96e+02	897	6	1.4	1304	5	015765	CYTOPLASMIC DYNEIN HEA	1.96e+02
825	6	1.4	986	10	064429	ALDEHYDE OXIDASE (FRAG	1.96e+02	898	6	1.4	1323	3	013686	HYDROTHERMAL 149.1 KD	1.96e+02
826	6	1.4	987	8	003684	PROBABLY DNA POLYMERAS	1.96e+02	899	6	1.4	1324	3	059328	ENO-1.3(14)-BETA-GLUCA	1.96e+02
827	6	1.4	988	14	087041	SPVCPZ, COMPLETE GENOM	1.96e+02	900	6	1.4	1348	2	060043	ENDOXILANASE PRECURSOR	1.96e+02
828	6	1.4	992	14	069119	NUCLEAR ANTIGEN PRECUR	1.96e+02	901	6	1.4	1358	4	092752	TEANASCIN-R.	1.96e+02
829	6	1.4	1002	2	000037	TRANSPOSON GAMMA-DELTA	1.96e+02	902	6	1.4	1375	4	099461	ASR1	1.96e+02
830	6	1.4	1002	3	074674	VARIANT REGION OF MAJO	1.96e+02	903	6	1.4	1379	11	035099	MER KINASE 5 (APOPTOSI	1.96e+02
831	6	1.4	1005	13	013075	NUCLEAR FACTOR NF-KB1.	1.96e+02	904	6	1.4	1385	5	091389	SIMILARITY TO SEVERAL	1.96e+02
832	6	1.4	1009	3	074378	2-OXOGUTARATE DEHYDRO	1.96e+02	905	6	1.4	1388	3	014139	HYDROTHERMAL 159.4 KD	1.96e+02
833	6	1.4	1018	3	094068	CONSERVED HYDROTHERMAL	1.96e+02	906	6	1.4	1394	4	000512	BC19 PROTEIN.	1.96e+02
834	6	1.4	1019	3	094267	PUTATIVE YEAST CELL DI	1.96e+02	907	6	1.4	1398	1	092186	BI22 PROTEIN.	1.96e+02
835	6	1.4	1020	5	025415	GLUTAMATE DEHYDROGENAS	1.96e+02	908	6	1.4	1408	10	092438	RETROFIT.	1.96e+02
836	6	1.4	1026	5	094071	PUTATIVE LIPRIN BETA (	1.96e+02	909	6	1.4	1445	5	010463	T24H7.5 PROTEIN.	1.96e+02
837	6	1.4	1035	10	093812	F19P19.7	1.96e+02	910	6	1.4	1454	5	010463	T24H7.5 PROTEIN.	1.96e+02
838	6	1.4	1039	10	022792	F499.18 PROTEIN.	1.96e+02	911	6	1.4	1477	5	076931	TUMOR-SUPPRESSOR PROTEI	1.96e+02
839	6	1.4	1039	2	074552	HELICASE OF THE SNE2/R	1.96e+02	912	6	1.4	1477	5	076931	LAMININ A (FRAGMENT)	1.96e+02
840	6	1.4	1045	3	093796	TRANSLATION ELONGATION	1.96e+02	913	6	1.4	1518	5	021442	USHER SYNDROME TYPE II	1.96e+02
841	6	1.4	1049	14	088099	(CLONE 2) (ENV).	1.96e+02	914	6	1.4	1551	4	075445	SIMILAR TO S.-CEREVISI	1.96e+02
842	6	1.4	1051	14	066108	CITRUS-LEAF RUGOSE ILA	1.96e+02	915	6	1.4	1556	10	092438	T22H22.1 PROTEIN.	1.96e+02
843	6	1.4	1054	5	096077	EPFDE3	1.96e+02	916	6	1.4	1575	4	013576	RASAP-RELATED PROTEIN	1.96e+02
844	6	1.4	1054	4	094887	KIA00793 PROTEIN.	1.96e+02	917	6	1.4	1590	5	091152	SIMILAR TO DROSOPHILA	1.96e+02
845	6	1.4	1055	14	065146	HELICASE.	1.96e+02	918	6	1.4	1602	2	065933	HYDROTHERMAL 167.1 KD	1.96e+02
846	6	1.4	1055	2	053348	F25E5.1 PROTEIN.	1.96e+02	919	6	1.4	1611	10	049311	PUTATIVE MYOSIN HEAVY	1.96e+02
847	6	1.4	1062	5	076657	F23H11.20 PROTEIN.	1.96e+02	920	6	1.4	1640	13	092438	COMPLEMENT C3-H2.	1.96e+02
848	6	1.4	1064	2	073770	P-TYPE TRANSPORTING AT	1.96e+02	921	6	1.4	1663	5	001510	SIMILARITY TO THW P13/	1.96e+02
849	6	1.4	1080	3	043134	HYDROTHERMAL 123.6 KD	1.96e+02	922	6	1.4	1696	11	092438	SCOP.	1.96e+02
850	6	1.4	1083	5	019336	FLA10.3 PROTEIN.	1.96e+02	923	6	1.4	1701	5	061164	ERYTHROCYTE BINDING PR	1.96e+02
851	6	1.4	1102	2	095684	SUBTILISIN-LIKE PROTEA	1.96e+02	924	6	1.4	1721	4	095216	INTERSCITIN LONG FORM.	1.96e+02
852	6	1.4	1108	2	092568	PUTATIVE MEMBRANE ASSO	1.96e+02	925	6	1.4	1738	11	070346	COMPLEMENT C4.	1.96e+02
853	6	1.4	1108	10	092568	F23H11.20 PROTEIN.	1.96e+02	926	6	1.4	1740	5	097019	ASC3 PROTEIN.	1.96e+02
854	6	1.4	1113	4	024515	CALCIUM DEPENDENT POTA	1.96e+02	927	6	1.4	1751	5	017143	TRANSCRIPTIONAL CO-REP	1.96e+02
855	6	1.4	1120	10	024515	UNCONVENTIONAL MYOSIN	1.96e+02	928	6	1.4	1762	2	030480	PKS MODULE 2.	1.96e+02
856	6	1.4	1132	4	014636	RECEPTOR-ASSOCIATED TY	1.96e+02	929	6	1.4	1763	14	066914	POLYPROTEIN.	1.96e+02
857	6	1.4	1132	4	075297	JAK2 KINASE.	1.96e+02	930	6	1.4	1763	14	066914	NON-STRUCTURAL PROTEIN	1.96e+02
858	6	1.4	1134	6	028204	LARGE CONDUCTANCE CALC	1.96e+02	931	6	1.4	1773	5	066913	TRANSCRIPTIONAL CO-REP	1.96e+02
859	6	1.4	1146	5	092099	BCDNA.LD24702.	1.96e+02	932	6	1.4	1774	11	071442	PROCOLLAGEN, TYPE XVII	1.96e+02
860	6	1.4	1148	11	061372	C4 COMPLEMENT PROTEIN	1.96e+02	933	6	1.4	1795	4	014674	KIA00165 PROTEIN.	1.96e+02
861	6	1.4	1151	6	018867	CALCIUM-ACTIVATED POTA	1.96e+02	934	6	1.4	1807	2	030480	HYDROTHERMAL 229.9KD P	1.96e+02
862	6	1.4	1152	6	018866	CALCIUM-ACTIVATED POTA	1.96e+02	935	6	1.4	1847	2	030480	POLYKETIDE SYNTHASE	1.96e+02
863	6	1.4	1153	5	091398	F29D11.2 PROTEIN.	1.96e+02	936	6	1.4	1860	3	092438	GLUCAN SYNTHASE (FRAGM	1.96e+02
864	6	1.4	1154	4	012921	CALCIUM-ACTIVATED POTA	1.96e+02	937	6	1.4	1894	11	072026	PLEKXIN 1.	1.96e+02
865	6	1.4	1156	6	028265	CALCIUM-ACTIVATED POTA	1.96e+02	938	6	1.4	1903	3	092438	FKBP PROTEIN INVOLVED	1.96e+02
866	6	1.4	1156	6	046371	LARGE CONDUCTANCE CALC	1.96e+02	939	6	1.4	1905	3	092225	1,3-BETA-D-GLUCAN SYNT	1.96e+02
867	6	1.4	1156	14	093209	POL. PROTEIN.	1.96e+02	940	6	1.4	1919	3	064298	HYDROTHERMAL 217.7 KD	1.96e+02
868	6	1.4	1162	5	093139	ORF2.	1.96e+02	941	6	1.4	1928	4	092438	HSCGN1 (FRAGMENT).	1.96e+02
869	6	1.4	1163	11	008626	CALCIUM-ACTIVATED POTA	1.96e+02	942	6	1.4	1976	2	092438	ALPHA-1,2-MANNOSIDASE	1.96e+02
870	6	1.4	1167	4	075578	INTEGRIN SUBUNIT ALPHA	1.96e+02	943	6	1.4	2061	5	077025	PUTATIVE FATTY ACID SY	1.96e+02
871	6	1.4	1172	14	006526	STRUCTURAL PROTEIN.	1.96e+02	944	6	1.4	2080	3	092215	SIMILAR TO MYOSIN.	1.96e+02
872	6	1.4	1176	14	098587	HYDROTHERMAL 119.0 KD	1.96e+02	945	6	1.4	2098	5	091443	PKS MODULE 3.	1.96e+02
873	6	1.4	1178	4	031350	CALCIUM-ACTIVATED POTA	1.96e+02	946	6	1.4	2100	2	030480	HOS009.1 PROTEIN (FRAG	1.96e+02
874	6	1.4	1178	4	012960	LARGE-CONDUCTANCE CALC	1.96e+02	947	6	1.4	2109	5	076416	HYDROTHERMAL 221.0 KD	1.96e+02
875	6	1.4	1178	11	062976	CALCIUM-ACTIVATED POTA	1.96e+02	948	6	1.4	2126	2	094996	RAD9.	1.96e+02
876	6	1.4	1179	2	092618	DNA POLYMERASE III ALP	1.96e+02	949	6	1.4	2157	3	000333	TRANS-GLUTAMINASE	1.96e+02
877	6	1.4	1183	5	094447	TRP PROTEIN.	1.96e+02	950	6	1.4	2161	14	091724	COMPLETE VIRAL PROTEIN	1.96e+02
878	6	1.4	1194	2	053645	PUTATIVE ABC TRANSPORT	1.96e+02	951	6	1.4	2218	14	009705	TOXIN B.	1.96e+02
879	6	1.4	1196	11	008460	SLOWMOLOG, POTA	1.96e+02	952	6	1.4	2230	4	013439	ZONDAHSIN (FRAGMENT).	1.96e+02
880	6	1.4	1198	2	053730	POLYKETIDE SYNTHASE (F	1.96e+02	953	6	1.4	2232	14	092438	MUSC-1.267D11.3 PROTE	1.96e+02
881	6	1.4	1203	4	093704	HYPERPOLARIZATION-ACTI	1.96e+02	954	6	1.4	2357	2	046034	MYELOBLAST KIA0219 (F	1.96e+02
882	6	1.4	1208	14	039273	COUNTERPART OF HSV-1 G	1.96e+02	955	6	1.4	2379	4	092438	PKS MODULE 1.	1.96e+02
883	6	1.4	1210	11	092438	LARGE-CONDUCTANCE CALC	1.96e+02	956	6	1.4	2392	4	092438	PUTATIVE VACUOLATING C	1.96e+02
884	6	1.4	1219	4	015242	NRD CONVERTASE (EC 3.	1.96e+02	957	6	1.4	2412	4	092438	TRANSCRIPTIONAL ACTIVA	1.96e+02
885	6	1.4	1221	5	045796	TI9C9.7 PROTEIN.	1.96e+02	958	6	1.4	2589	14	066776	GIANTIN (GOLGI COMPLEX	1.96e+02
886	6	1.4	1221	4	092438	KIA1006 PROTEIN (FRAG	1.96e+02	959	6	1.4	2723	2	092438	DB035.1P (UBIQUITIN LI	1.96e+02
887	6	1.4	1229	11	035836	NRD2 CONVERTASE (EC 3.	1.96e+02	960	6	1.4	2902	2	092438	PKS MODULE 2.	1.96e+02
888	6	1.4	1230	5	060046	F49E2.5A PROTEIN.	1.96e+02	961	6	1.4	2971	4	092438	TRANSCRIPTIONAL ACTIVA	1.96e+02
889	6	1.4	1234	2	060046	XYNA PRECURSOR (EC 3.2	1.96e+02	962	6	1.4	3187	11	063714	GIANTIN (GOLGI COMPLEX	1.96e+02
890	6	1.4	1264	5	091767	NEUROGLAN.	1.96e+02	963	6	1.4	3228	5	093593	DB035.1P (UBIQUITIN LI	1.96e+02
891	6	1.4	1265	1	035604	F52G2.2 PROTEIN.	1.96e+02	964	6	1.4	3268	5	093593	DB035.1P (UBIQUITIN LI	1.96e+02
892	6	1.4	1278	11	070305	NPC1.	1.96e+02	965	6	1.4	3410	14	089278	POLYPROTEIN.	1.96e+02
893	6	1.4	1285	11	070305	NIEMANN-PICK C DISEASE	1.96e+02	966	6	1.4	3410	14	089278	POLYPROTEIN.	1.96e+02
894	6	1.4	1285	11	070305	SPINOCORREIN, TYPE XVII	1.96e+02	967	6	1.4	3410	14	089278	POLYPROTEIN.	1.96e+02
895	6	1.4	1286	10	092438	P-GALACTOSE, TYPE XVII	1.96e+02	968	6	1.4	3410	14	089278	POLYPROTEIN.	1.96e+02
896	6	1.4	1288	11	061437	PROCOLLAGEN, TYPE XVII	1.96e+02	969	6	1.4	3411	14	092438	POLYPROTEIN.	1.96e+02

970 6 1.4 3411 14 09YRN3 POLYPROTEIN. 1.96e+02  
 971 6 1.4 3411 14 09YRN2 POLYPROTEIN. 1.96e+02  
 972 6 1.4 3411 14 09YRN0 POLYPROTEIN. 1.96e+02  
 973 6 1.4 3411 14 09YRN0 POLYPROTEIN. 1.96e+02  
 974 6 1.4 3411 14 09YRN1 POLYPROTEIN. 1.96e+02  
 975 6 1.4 3411 14 09YRN1 POLYPROTEIN. 1.96e+02  
 976 6 1.4 3472 1 074056 HYPOTHETICAL 367.1 KD 1.96e+02  
 977 6 1.4 3503 5 024292 ADHERIN. 1.96e+02  
 978 6 1.4 3704 5 P91904 LAMININ ALPHA. 1.96e+02  
 979 6 1.4 3898 14 09YRN0 POLYPROTEIN. 1.96e+02  
 980 6 1.4 3898 14 09YRN1 POLYPROTEIN. 1.96e+02  
 981 6 1.4 3898 14 09YRN1 POLYPROTEIN. 1.96e+02  
 982 6 1.4 3898 14 09YRN1 POLYPROTEIN. 1.96e+02  
 983 6 1.4 3898 14 09YRN1 POLYPROTEIN. 1.96e+02  
 984 6 1.4 3898 14 09YRN1 POLYPROTEIN. 1.96e+02  
 985 6 1.4 3898 14 09YRN1 POLYPROTEIN. 1.96e+02  
 986 6 1.4 3898 14 09YRN1 POLYPROTEIN. 1.96e+02  
 987 6 1.4 3898 14 09YRN1 POLYPROTEIN. 1.96e+02  
 988 6 1.4 3898 14 09YRN1 POLYPROTEIN. 1.96e+02  
 989 6 1.4 3898 14 09YRN1 POLYPROTEIN. 1.96e+02  
 990 6 1.4 4290 2 09YRN0 POLYPROTEIN. 1.96e+02  
 991 6 1.4 4351 11 088277 MEGF1. 1.96e+02  
 992 6 1.4 4613 2 09YRN1 TYPE 1 POLYKETIDE SYNT 1.96e+02  
 993 6 1.4 4613 2 09YRN1 TYPE 1 POLYKETIDE SYNT 1.96e+02  
 994 6 1.4 4613 2 09YRN1 TYPE 1 POLYKETIDE SYNT 1.96e+02  
 995 6 1.4 4613 2 09YRN1 TYPE 1 POLYKETIDE SYNT 1.96e+02  
 996 6 1.4 4613 2 09YRN1 TYPE 1 POLYKETIDE SYNT 1.96e+02  
 997 6 1.4 4613 2 09YRN1 TYPE 1 POLYKETIDE SYNT 1.96e+02  
 998 6 1.4 4613 2 09YRN1 TYPE 1 POLYKETIDE SYNT 1.96e+02  
 999 6 1.4 4613 2 09YRN1 TYPE 1 POLYKETIDE SYNT 1.96e+02  
 1000 6 1.4 4613 2 09YRN1 TYPE 1 POLYKETIDE SYNT 1.96e+02

## ALIGNMENTS

RESULT 1  
 ID 09YRN0 PRELIMINARY; PRT: 569 AA.

AC 09YRN0  
 DT 01-MAY-1998 (TREMELREL. 10, Created)  
 DT 01-MAY-1998 (TREMELREL. 10, Last sequence update)  
 DT 01-MAY-1998 (TREMELREL. 10, Last annotation update)

DE INTERFERON ALPHA/BETA RECEPTOR 1.  
 GN IFNARI.

OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RP [1]  
 RC SEQUENCE FROM N.A.

RA TISSUE-LIVER;  
 RA REBOUT J., GARDINER K., MONNERON D., UZE G., LUTFALLA G.;  
 RA "Comparative genomic analysis of the interferon/interleukin-10  
 RA receptor gene cluster.";  
 RA Genome Res. 0:0-0(1999).

RL EMBL: AF082664; AAD1369.1;  
 DR EMBL: AF082664; AAD1369.1;  
 RT RECEPTOR.

SO SEQUENCE 569 AA; 64055 MW; F99BC099 CRC32;

Query Match 2.1%; Score 9; DB 13; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 1.18e-04;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 201 PRTYCLAY 209  
 OY 194 PRTYCLAY 202

RESULT 2  
 ID 080566 PRELIMINARY; PRT: 421 AA.

AC 080566  
 DT 01-NOV-1998 (TREMELREL. 08, Created)  
 DT 01-NOV-1998 (TREMELREL. 08, Last sequence update)  
 DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)  
 DE F6E13.9 PROTEIN.

GN F6E13.9  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; T  
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicot  
 OC core eudicots; Rosidae; eustosids II; Brassicales; Bras  
 OC Arabidopsis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA ROUNSLEY S.D., KADL S., LIN X., KETCHUM K.A., CROSBY M.L.,  
 RA BRADON R.C., SYKES S.M., MASON T.M., KERLAUGE A.R., ADAMS M.D.,  
 RA SOMERVILLE C.R., VENTER J.C.;  
 RT "Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence."  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC004005; AAC23404.1;  
 SO SEQUENCE 421 AA; 48397 MW; AERD8401 CRC32;

Query Match 1.8%; Score 8; DB 10; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 2.34e-02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 300 F6E13 307  
 OY 265 F6E13 272

RESULT 3  
 ID 018233 PRELIMINARY; PRT: 571 AA.

AC 018233  
 DT 01-JAN-1998 (TREMELREL. 05, Created)  
 DT 01-JAN-1998 (TREMELREL. 05, Last sequence update)  
 DT 01-JAN-1998 (TREMELREL. 05, Last annotation update)

DE Y57G11C.7 PROTEIN.  
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditia;  
 OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

RP [1]  
 RC SEQUENCE FROM N.A.

RA MCWURRAY A.;  
 RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

RL [2]  
 RP SEQUENCE FROM N.A.

RA MEDLINE: 94150718.  
 RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERRS M.,  
 RA BOWFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., COULSON A.,  
 RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARSONS J., PERCY C., RIFKIN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;  
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RA elegans.";  
 RL Nature 368:32-38(1994).

SO SEQUENCE 571 AA; 66883 MW; 2A34A731 CRC32;

Query Match 1.8%; Score 8; DB 5; Length 571;  
 Best Local Similarity 100.0%; Pred. No. 2.34e-02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 164 YVEIKLR 171  
 OY 96 YVEIKLR 103

RESULT 4  
 ID 024315 PRELIMINARY; PRT: 1235 AA.

AC 024315  
 DT 01-NOV-1996 (TREMELREL. 01, Created)

DT 01-NOV-1996 (TREMBLER. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLER. 12, Last annotation update)  
 DE TYROSINE KINASE (FRAGMENT)  
 OS Drosophila melanogaster (Fruit fly)  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA ITO M., MATSUI T., TANIGUCHI T., CHIHARA K.;  
 RT "Alternative splicing generates two distinct transcripts for the  
 RT Drosophila melanogaster fibroblast growth factor receptor homolog."  
 RL Gene 0:0-0(1994).  
 DR EMBL: D17550; BAA04488.1;  
 DR HSSP: P08631; 2HCK.  
 DR FLYBASE: FBgn0014073; Tle.  
 DR PFW: PF00069; pkinase.2.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 1235 AA; 135257 MW; 86277084 CRC32;

Query Match 1.6%; Score 7; DB 5; Length 1235;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 731 TLVLVAVG 738  
 QY 10 TLVLVAVG 17

RESULT 5  
 ID 054100; PRELIMINARY; PRT; 93 AA.  
 AC 054100;  
 DT 01-NOV-1996 (TREMBLER. 01, Created)  
 DT 01-NOV-1999 (TREMBLER. 01, Last sequence update)  
 DE ORF1\_5 END; NADH-FERREDOXIN OXIDOREDUCTASE (FOXA) (FRAGMENT).  
 OS Saccharopolyspora erythraea (Streptomyces erythraeus).  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;  
 OC Actinomycetales; Pseudonocardiales; Pseudonocardaceae;  
 OC Saccharopolyspora.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-MNH22;  
 RC MEDLINE: 95255650.  
 RA ZOTCHEV S.B., HUTCHINSON C.R.;  
 RT "Cloning and heterologous expression of the genes encoding nonspecific  
 RT electron transport components for a cytochrome P450 system of  
 RT Saccharopolyspora erythraea involved in erythromycin production."  
 RL Gene 156:101-106(1995).  
 DR EMBL: L38646; AAA74472.1;  
 FT NON\_TER 93 93  
 SQ SEQUENCE 93 AA; 10784 MW; E8184524 CRC32;

Query Match 1.6%; Score 7; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 48 TLVLVAVG 54  
 QY 9 TLVLVAVG 15

RESULT 6  
 ID 09YRD2; PRELIMINARY; PRT; 101 AA.  
 AC 09YRD2;  
 DT 01-MAY-1999 (TREMBLER. 10, Created)  
 DT 01-MAY-1999 (TREMBLER. 10, Last sequence update)  
 DE DNA METHYLTRANSFERASE (FRAGMENT).  
 OS European catfish virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Ranavirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA MAO J., WANG J., CHINCHAR G.D., CHINCHAR V.G.;  
 RT "Molecular characterization of a Ranavirus isolated from largemouth  
 RT bass (Micropterus salmoides)."  
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF100201; AAC79866.1;  
 KW Transferase; Methyltransferase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 101 AA; 11970 MW; 1642573D CRC32;

Query Match 1.6%; Score 7; DB 14; Length 101;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 VLKWDYT 8  
 QY 245 VLKWDYT 251

RESULT 7  
 ID 061696; PRELIMINARY; PRT; 141 AA.  
 AC 061696;  
 DT 01-AUG-1998 (TREMBLER. 07, Created)  
 DT 01-AUG-1998 (TREMBLER. 07, Last sequence update)  
 DE PUTATIVE MULTIFUNCTIONAL PROTEIN ADE2 (FRAGMENT).  
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Sphingioidea; Sphingidae; Sphinginae; Manduca.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA SCHOLZ F.R., TRENCEK T., KANOST M.R.;  
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF060796; AAC15763.1;  
 DR PFW: PF01259; SAICAR synt. 1.  
 FT NON\_TER 141 141  
 SQ SEQUENCE 141 AA; 15515 MW; 97657734 CRC32;

Query Match 1.6%; Score 7; DB 5; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 111 FLKRNPG 117  
 QY 265 FLKRNPG 271

RESULT 8  
 ID 076631; PRELIMINARY; PRT; 150 AA.  
 AC 076631;  
 DT 01-NOV-1996 (TREMBLER. 01, Created)  
 DT 01-NOV-1999 (TREMBLER. 01, Last sequence update)  
 DE REV PROTEIN.  
 GN REV.  
 OS Human immunodeficiency virus type 2.  
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA BARNETT S.W., QUIROGA M., WERNER A., DINA D., LEVY J.A.;  
 RT "Distinctive features of an infectious molecular clone of the  
 RT highly divergent and noncytopathic human immunodeficiency virus type 2  
 RT ucl strain."  
 RL J. Virol. 67:1006-1014(1993).  
 DR EMBL: L07625; AAA33939.1;  
 DR PFW: PF00424; REV. 1.  
 SQ SEQUENCE 150 AA; 17186 MW; 2825384E CRC32;

Query Match 1.6%; Score 7; DB 14; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 55 IRSIDS 61  
OY 339 IRSIDS 345

## RESULT 9

ID 050273 PRELIMINARY; PRT: 163 AA.  
AC 050273; 050272;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).

GN MCR1

OS Methanohalophilus portuacensis.

OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;

OC Methanohalophilus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-VARIOUS STRAINS;

RX MEDLINE; 96174929.

RA SPRINGER E., SACHS M.S., WOESE C.R., BOONE D.R.;

RT "Partial gene sequences for the A subunit of methyl-coenzyme M

reductase (mcrI) as a phylogenetic tool for the family

Methanosarcinaceae."

RL Int. J. Syst. Bacteriol. 45:554-559(1995).

DR EMBL; U22239; AAC43416.1;

DR HSSP; P11558; IMRO.

FT NON\_TER 1

FT SEQUENCE 163 AA; 17603 MW; BA95C61C CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;  
Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 VLSAAG 97  
OY 20 VLSAAG 26

## RESULT 10

ID 050908 PRELIMINARY; PRT: 163 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).

GN MCR1

OS Methanohalophilus zhilinae.

OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;

OC Methanohalophilus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WENS, OREGON COLLECTION OF METHANOGENS ACCESSION #OCM 62;

RX MEDLINE; 96174929.

RA SPRINGER E., SACHS M.S., WOESE C.R., BOONE D.R.;

RT "Partial gene sequences for the A subunit of methyl-coenzyme M

reductase (mcrI) as a phylogenetic tool for the family

Methanosarcinaceae."

RL Int. J. Syst. Bacteriol. 45:554-559(1995).

DR EMBL; U22252; AAC43429.1;

DR HSSP; P11558; IMRO.

FT NON\_TER 1

FT SEQUENCE 163 AA; 17573 MW; 5EBF170F CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;  
Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 VLSAAG 97  
OY 20 VLSAAG 26

RESULT 11  
ID 048921 PRELIMINARY; PRT: 163 AA.

AC 048921;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).

GN MCR1

OS Methanococcus burtonii.

OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;

OC Methanococoides.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-DSM 6242, OREGON COLLECTION OF METHANOGENS ACCESSION #OCM 468;

RX MEDLINE; 96174929.

RA SPRINGER E., SACHS M.S., WOESE C.R., BOONE D.R.;

RT "Partial gene sequences for the A subunit of methyl-coenzyme M

reductase (mcrI) as a phylogenetic tool for the family

Methanosarcinaceae."

RL Int. J. Syst. Bacteriol. 45:554-559(1995).

DR EMBL; U22234; AAC43406.1;

DR HSSP; P11558; IMRO.

FT NON\_TER 1

FT SEQUENCE 163 AA; 17494 MW; 5826284D CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;  
Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 VLSAAG 97  
OY 20 VLSAAG 26

## RESULT 12

ID 057067 PRELIMINARY; PRT: 163 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).

GN MCR1

OS Methanohalophilus sp. (strain Cas-1),

OS Methanohalophilus sp. (strain Ref-1), and

OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CAS-1 / OCM 135, REF-1 / OCM 57, SF-1 / OCM 13;

RX MEDLINE; 96174929.

RA SPRINGER E., SACHS M.S., WOESE C.R., BOONE D.R.;

RT "Partial gene sequences for the A subunit of methyl-coenzyme M

reductase (mcrI) as a phylogenetic tool for the family

Methanosarcinaceae."

RL Int. J. Syst. Bacteriol. 45:554-559(1995).

DR EMBL; U22240; AAC43417.1;

DR HSSP; P11558; IMRO.

FT NON\_TER 1

FT SEQUENCE 163 AA; 17565 MW; 1DCCF1D5 CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;  
Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 VLSAAG 97  
 OY 20 VLSAAG 26

RESULT 13  
 ID 049114 PRELIMINARY; PRT; 163 AA.

AC 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT)  
 GN MCRI  
 OS Methanohalobium evestigatum  
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;  
 CC Methanohalobium  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX SPRINGER E.; SACHS M.S.; WOESE C.R.; BOONE D.R.;  
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M  
 RT reductase (mcrI) as a phylogenetic tool for the family  
 RT Methanosarcinaceae."  
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).  
 DR EMBL; U22336; AAC43408.1;  
 DR HSSP; P11558; IMRO.  
 FT NON\_TER 1 1  
 FT NON\_TER 163 163  
 SQ SEQUENCE 163 AA; 17559 MW; 56692275 CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 VLSAAG 97  
 OY 20 VLSAAG 26

RESULT 14  
 ID 050215 PRELIMINARY; PRT; 163 AA.

AC 050215;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT)  
 GN MCRI  
 OS Methanohalophilus mahli  
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;  
 CC Methanohalophilus  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX SPRINGER E.; SACHS M.S.; WOESE C.R.; BOONE D.R.;  
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M  
 RT reductase (mcrI) as a phylogenetic tool for the family  
 RT Methanosarcinaceae."  
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).  
 DR EMBL; U22337; AAC43411.1;  
 DR HSSP; P11558; IMRO.  
 FT NON\_TER 1 1  
 FT NON\_TER 163 163  
 SQ SEQUENCE 163 AA; 17617 MW; 56673AD4 CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 VLSAAG 97  
 OY 20 VLSAAG 26

RESULT 15  
 ID 050387 PRELIMINARY; PRT; 163 AA.

AC 050387;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT)  
 GN MCRI  
 OS Methanohalobium sp. (strain SD-1)  
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;  
 CC [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-SD-1 / OCM 134;  
 RX SPRINGER E.; SACHS M.S.; WOESE C.R.; BOONE D.R.;  
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M  
 RT reductase (mcrI) as a phylogenetic tool for the family  
 RT Methanosarcinaceae."  
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).  
 DR EMBL; U22356; AAC43423.1;  
 DR HSSP; P11558; IMRO.  
 FT NON\_TER 1 1  
 FT NON\_TER 163 163  
 SQ SEQUENCE 163 AA; 17606 MW; 90801B67 CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 VLSAAG 97  
 OY 20 VLSAAG 26

RESULT 16  
 ID 050214 PRELIMINARY; PRT; 163 AA.

AC 050214;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT)  
 GN MCRI  
 OS Methanococcus methyluans  
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;  
 CC Methanococcus  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX SPRINGER E.; SACHS M.S.; WOESE C.R.; BOONE D.R.;  
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M  
 RT reductase (mcrI) as a phylogenetic tool for the family  
 RT Methanosarcinaceae."  
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).  
 DR EMBL; U22335; AAC43410.1;  
 DR HSSP; P11558; IMRO.  
 FT NON\_TER 1 1  
 FT NON\_TER 163 163  
 SQ SEQUENCE 163 AA; 17548 MW; 1F36B74 CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 91 VLSAAG 97  
 OY 20 VLSAAG 26

RESULT 17  
 ID 049535 PRELIMINARY; PRT; 163 AA.  
 AC 049535;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DE 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).  
 GN MCRI.  
 OS Methanohalophilus halophilus.  
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;  
 OC Methanohalophilus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-2-7982, OREGON COLLECTION OF METHANOGENS ACCESSION #OCM 160;  
 RX MEDLINE; 96174929.  
 RA SPRINGER E.; SACHS M.S.; MOESE C.R.; BOONE D.R.;  
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M  
 reductase (mcrl) as a phylogenetic tool for the family  
 Methanosarcinaceae."  
 RT Methanosarcinaceae.  
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).  
 DR EMBL; U22259; AAC3409.1;  
 DR HSSP; P11558; IMRO.  
 FT NON\_TER 1 1  
 FT 163 163  
 SQ SEQUENCE 163 AA; 17603 MW; BA95C61C CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 VLSAAG 97  
 |||||  
 QY 20 VLSAAG 26

RESULT 18  
 ID 050386 PRELIMINARY; PRT; 163 AA.  
 AC 050386;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
 DE METHYL-COENZYME M REDUCTASE SUBUNIT A (FRAGMENT).  
 GN MCRI.  
 OS Methanohalophilus sp. (strain HCM6).  
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-HCM6, OREGON COLLECTION OF METHANOGENS ACCESSION #OCM 152;  
 RX MEDLINE; 96174929.  
 RA SPRINGER E.; SACHS M.S.; MOESE C.R.; BOONE D.R.;  
 RT "Partial gene sequences for the A subunit of methyl-coenzyme M  
 reductase (mcrl) as a phylogenetic tool for the family  
 Methanosarcinaceae."  
 RT Methanosarcinaceae.  
 RL Int. J. Syst. Bacteriol. 45:554-559(1995).  
 DR EMBL; U22255; AAC3442.1;  
 DR HSSP; P11558; IMRO.  
 FT NON\_TER 1 1  
 FT 163 163  
 SQ SEQUENCE 163 AA; 17595 MW; 4C706148 CRC32;

Query Match 1.6%; Score 7; DB 1; Length 163;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 91 VLSAAG 97  
 |||||  
 QY 20 VLSAAG 26

RESULT 19  
 ID 035576 PRELIMINARY; PRT; 239 AA.  
 AC 035576;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
 DE TROPONIN T3, SKELETAL, FAST.  
 GN TNN3.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RX MEDLINE; 97390134.  
 RA WANG J.; JIN J.P.;  
 RT "Primary structure and developmental acidic to basic transition of 13  
 alternatively spliced mouse fast skeletal muscle troponin T  
 isoforms."  
 RT Gene 193:105-114(1997).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RA GSDB;  
 RL Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; I48989; AAB67284.1;  
 DR MGI; MGI:109550; Tnn3.  
 DR PFAM; PF00992; Troponin; 1.  
 SQ SEQUENCE 239 AA; 28337 MW; D29A2E63 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 89 RIRAKE 95  
 |||||  
 QY 103 RIRAKE 109

RESULT 20  
 ID 035575 PRELIMINARY; PRT; 239 AA.  
 AC 035575;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
 DE TROPONIN T3, SKELETAL, FAST.  
 GN TNN3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RX MEDLINE; 97390134.  
 RA WANG J.; JIN J.P.;  
 RT "Primary structure and developmental acidic to basic transition of 13  
 alternatively spliced mouse fast skeletal muscle troponin T  
 isoforms."  
 RT Gene 193:105-114(1997).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RA GSDB;  
 RL Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; I48988; AAB67283.1;  
 DR MGI; MGI:109550; Tnn3.  
 DR PFAM; PF00992; Troponin; 1.  
 SQ SEQUENCE 239 AA; 28335 MW; 16C16AE3 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 89 RIRAKE 95  
 |||||  
 QY 103 RIRAKE 109

RESULT 21  
 ID 035581 PRELIMINARY; PRT; 248 AA.  
 AC 035581;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE TROPONIN T3, SKELETAL, FAST  
 GN TNN3  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129; TISSUE-FAST SKELETAL MUSCLE;  
 RX MEDLINE; 97390134.  
 RA WANG J., JIN J.P.;  
 RT "Primary structure and developmental acidic to basic transition of 13  
 RT alternatively spliced mouse fast skeletal muscle troponin T  
 RT isoforms."  
 RL Gene 193:105-114(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129; TISSUE-FAST SKELETAL MUSCLE;  
 RA GSDB;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; L48918; AAB67289.1;  
 DR MGD; MGI:109550; Tnn3.  
 DR PFAM; PF00992; Troponin T.  
 SO SEQUENCE 248 AA; 29346 MW; 740C8991 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 98 RIRAKE 104  
 OY 103 RIRAKE 109

RESULT 22 PRELIMINARY; PRT; 248 AA.  
 AC P97456;  
 DT 01-MAY-1997 (TREMblrel. 03, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE TROPONIN T3, SKELETAL, FAST  
 DE (FAST SKELETAL MUSCLE TROPONIN T ISOFORM PTHOPT).  
 GN TNN3  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129; TISSUE-FAST SKELETAL MUSCLE;  
 RA KOCH A., JUAN T.S.C., JENKINS N.A., GILBERT D.J., COPELAND N.G.,  
 RA MCNEICE I.K., FLETCHER F.A.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U77779; AAB39743.1;  
 DR MGD; MGI:109550; Tnn3.  
 DR PFAM; PF00992; Troponin T.  
 SO SEQUENCE 248 AA; 29376 MW; B2CB1C58 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 98 RIRAKE 104  
 OY 103 RIRAKE 109

RESULT 23 PRELIMINARY; PRT; 248 AA.  
 AC O35578;  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE TROPONIN T3, SKELETAL, FAST

GN TNN3  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ma  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RX MEDLINE; 97390134.  
 RA WANG J., JIN J.P.;  
 RT "Primary structure and developmental acidic to basic transition of 13  
 RT alternatively spliced mouse fast skeletal muscle troponin T  
 RT isoforms."  
 RL Gene 193:105-114(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RA GSDB;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; L48991; AAB67286.1;  
 DR MGD; MGI:109550; Tnn3.  
 DR PFAM; PF00992; Troponin T.  
 SO SEQUENCE 248 AA; 29344 MW; B057CD11 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 248;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 98 RIRAKE 104  
 OY 103 RIRAKE 109

RESULT 24 PRELIMINARY; PRT; 250 AA.  
 AC O35579;  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE TROPONIN T3, SKELETAL, FAST  
 GN TNN3  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RX MEDLINE; 97390134.  
 RA WANG J., JIN J.P.;  
 RT "Primary structure and developmental acidic to basic transition of 13  
 RT alternatively spliced mouse fast skeletal muscle troponin T  
 RT isoforms."  
 RL Gene 193:105-114(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RA GSDB;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; L48992; AAB67287.1;  
 DR MGD; MGI:109550; Tnn3.  
 DR PFAM; PF00992; Troponin T.  
 SO SEQUENCE 250 AA; 29757 MW; DCD2DBE7 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 100 RIRAKE 106  
 OY 103 RIRAKE 109

RESULT 25 PRELIMINARY; PRT; 250 AA.  
 AC O35580;  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
 DE TROPONIN T3, SKELETAL, FAST

AC 035580;  
 DT 01-JAN-1998 (TRENBLREL. 05, Created)  
 DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)  
 DT 01-NOV-1999 (TRENBLREL. 12, Last annotation update)  
 DE TROPONIN T3, SKELETAL, FAST.  
 GN TNN3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RX MEDLINE: 97390134.  
 RA WANG J., JIN J.P.;  
 RT "Primary structure and developmental acidic to basic transition of 13  
 RT alternatively spliced mouse fast skeletal muscle tropoin T  
 RT isoforms".  
 RT Gene 193:105-114(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RX GSDS;  
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: L48993; AAB67288.1;  
 DR MGD: MGI:109550; Tnn3.  
 DR PFM: PF00992; Troponin T.  
 SQ SEQUENCE 250 AA; 29759 MW; 18899C67 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 100 RIRAKE 106  
 OY 103 RIRAKE 109

RESULT 26  
 ID 035577; PRELIMINARY; PRT: 254 AA.  
 AC 035577;  
 DT 01-JAN-1998 (TRENBLREL. 05, Created)  
 DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)  
 DT 01-NOV-1999 (TRENBLREL. 12, Last annotation update)  
 DE TROPONIN T3, SKELETAL, FAST.  
 GN TNN3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RX MEDLINE: 97390134.  
 RA WANG J., JIN J.P.;  
 RT "Primary structure and developmental acidic to basic transition of 13  
 RT alternatively spliced mouse fast skeletal muscle tropoin T  
 RT isoforms".  
 RT Gene 193:105-114(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RX GSDS;  
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: L48990; AAB67285.1;  
 DR MGD: MGI:109550; Tnn3.  
 DR PFM: PF00992; Troponin T.  
 SQ SEQUENCE 254 AA; 30152 MW; E05CC749 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 254;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 104 RIRAKE 110  
 OY 103 RIRAKE 109

OY 103 RIRAKE 109  
 RESULT 27  
 ID 035585; PRELIMINARY; PRT: 255 AA.  
 AC 035585;  
 DT 01-JAN-1998 (TRENBLREL. 05, Created)  
 DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)  
 DT 01-NOV-1999 (TRENBLREL. 12, Last annotation update)  
 DE TROPONIN T3, SKELETAL, FAST  
 GN TNN3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RX MEDLINE: 97390134.  
 RA WANG J., JIN J.P.;  
 RT "Primary structure and developmental acidic to basic transition of 13  
 RT alternatively spliced mouse fast skeletal muscle tropoin T  
 RT isoforms".  
 RT Gene 193:105-114(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SV129;  
 RX GSDS;  
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: L48472; AAB67293.1;  
 DR MGD: MGI:109550; Tnn3.  
 DR PFM: PF00992; Troponin T.  
 SQ SEQUENCE 255 AA; 30315 MW; 9C8834F3 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 105 RIRAKE 111  
 OY 103 RIRAKE 109

RESULT 28  
 ID 092WZ8; PRELIMINARY; PRT: 259 AA.  
 AC 092WZ8;  
 DT 01-MAY-1999 (TRENBLREL. 10, Created)  
 DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)  
 DT 01-MAY-1999 (TRENBLREL. 10, Last annotation update)  
 DE GP82.  
 OS Mycobacteriophage TM4.  
 OC Viruses.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA FORD M.E., STENSTROM C., HENDRIX R.W., HATFULL G.F.;  
 RT "Mycobacteriophage TM4: Genome structure and gene expression".  
 RT Tuber. Lung Dis. 79:63-73(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA FORD M.E., STENSTROM C., HENDRIX R.W., HATFULL G.F.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF068845; AAD17647.1;  
 SQ SEQUENCE 259 AA; 26662 MW; 4B4C5D92 CRC32;

Query Match 1.6%; Score 7; DB 9; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 59 VILGAT 65  
 OY 3 VILGAT 9



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RESULT: 29 PRELIMINARY; PRT; 259 AA.
ID 035583
DTG:01-JAN-1998 (TREMblrel_05, Created)
DTG:01-JAN-1998 (TREMblrel_05, Last sequence update)
DT 01-NOV-1999 (TREMblrel_12, Last annotation update)
DE TROPONIN T3, SKELETAL, FAST
DE (TROPONIN T FAST SKELETAL MUSCLE ISOFORM).
CN TNNT3
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SV129;
RX MEDLINE; 97390134.
RA WANG J., JIN J.P.;
RT "Primary structure and developmental acidic to basic transition of 13
RT alternatively spliced mouse fast skeletal muscle troponin T
isoforms."
RL Gene 193:105-114 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SV129;
RX MEDLINE; 97390134.
RA GSDB;
RP Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; L49470; AAB67291.1; -.
DR MGD; MGI:109550; Tnnt3.
DR PFAM; PF00992; Troponin; 1.
SQ SEQUENCE 259 AA; 30709 MW; 4631F971 CRC32;

Query Match 1.6%; Score 7; DB 11; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.89e+00; Mismatches 0; Indels 0; Gaps 0.
Matches 7; Conservative 0;

Db 109 RIRAKE 115
Cy 103 RIRAKE 109

RESULT: 30 PRELIMINARY; PRT; 262 AA.
ID 035584
DTG:01-JAN-1998 (TREMblrel_05, Created)
DT 01-JAN-1998 (TREMblrel_05, Last sequence update)
DT 01-NOV-1999 (TREMblrel_12, Last annotation update)
DE TROPONIN T3, SKELETAL, FAST
DE (TROPONIN T FAST SKELETAL MUSCLE ISOFORM).
CN TNNT3
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SV129;
RX MEDLINE; 97390134.
RA WANG J., JIN J.P.;
RT "Primary structure and developmental acidic to basic transition of 13
RT alternatively spliced mouse fast skeletal muscle troponin T
isoforms."
RL Gene 193:105-114 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SV129;
RX MEDLINE; 97390134.
RA GSDB;
RP Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; L49471; AAB67292.1; -.
DR MGD; MGI:109550; Tnnt3.
DR PFAM; PF00992; Troponin; 1.
SQ SEQUENCE 262 AA; 31038 MW; 0D965DEF CRC32;

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Query Match	1.68;	Score 7;	DB 11;	Length 262;
Best Local Similarity	100.08;	Pred. No.	2.89e+00;	

Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
DB	112	RIRAEK	118						
QY	103	RIRAEK	109						

ID	RESULT	31	PRELIMINARY;	PRT;	268 AA.
AC	035582;				
AD	01-JAN-1998	(TREMBLrel. 05, Created)			
DT	01-JAN-1998	(TREMBLrel. 05, last sequence update)			
DT	01-NOV-1999	(TREMBLrel. 12, last annotation update)			
DE	TROPONIN T3, SKELETAL, FAST				
DE	TROPONIN T FAST SKELETAL MUSCLE ISOFORM.				
GN	TNNI3.				
OS	Mus. musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Mammalia;				
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-SV129;				
RX	MEDLINE; 97390134.				
RA	WANG J., JIN J.P.;				
KT	Primary structure and developmental acidic to basic transition of 13				
KT	alternatively spliced mouse fast skeletal muscle troponin T				
RT	isoforms.				
RL	Gene 193:105-114(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-SV129;				
RA	GSDS;				
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; L49466; AAB67290.1; -				
DR	MGD; MGI:109550; Tnni3.				
DR	PFAM; PF000992; Troponin1; 1				
SO	SEQUENCE 268 AA; 31846 MW; 2AB79748 CRC32;				

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Query Match          1.6%; Score 7; DB 11; Length 268;
Best Local Similarity 100.0%; Pred. No. 2,89e+00;
Matches              7; Conservative          0; Mismatches          0; Indels          0; Gaps          0;

Dd      118 RIRAEKE 124
        |||||
QY      103 RIRAEKE 109

RESULT      32
ID 057559    PRELIMINARY;      PRT;      287 AA.
AC 057559;

DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE TROPONIN T VARIANT TINTX-El6.
   Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.
OC (1)
RN RP SEQUENCE FROM N.A.
RC STRAIN-LEGHORN.
RA JIN J.-P., HUANG Q.O., WANG J., OGUT O.;
  Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044922; AAC70917.1;
  PFM; PF00992; Troponin; 1.
SQ SEQUENCE 287 AA; 33799 MW; 05C1E0A1 CRC32;

Query Match          1.6%; Score 7; DB 13; Length 287;
Best Local Similarity 100.0%; Pred. No. 2,89e+00;
Matches              7; Conservative          0; Mismatches          0; Indels          0; Gaps          0;

Dd      139 RIRAEKE 145
        |||||
QY      103 RIRAEKE 109

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RESULT 33  
ID P73049 PRELIMINARY; PRT: 298 AA.  
AC P73049.  
DT 01-FEB-1997 (Tremblrel. 02, Created)  
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)  
DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)  
DE HYPOTHEICAL 32.8 KD PROTEIN  
OS Synchocystis sp. (strain PCC 6803)  
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PCC6803;  
RA TABATA S.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PCC6803;  
RX MEDLINE; 97061201.  
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,  
RA MIYAJIMA N., HIROKAWA M., SUGIURA M., SASAKOTO S., KITMURA T.,  
RA SHIMOTO T., MATSUO A., MORI A., NAKAZAKI N., NARO R., OKUMURA S.,  
RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,  
RA TABATA S.;  
RT \*Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.\*;  
RL DNA Res. 3:109-136(1996).  
DR EMBL; D90903; BAA17070.1; -  
DR PFM; PF01145; Baa17070.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 298 AA; 32828 MW; 0BBBC7E0 CRC32;

Query Match 1.6%; Score 7; DB 2; Length 298;  
Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 AERTIE 242  
|||  
QY 380 AERTIE 386

RESULT 34  
ID 069606 PRELIMINARY; PRT: 336 AA.  
AC 069606.  
DT 01-AUG-1998 (Tremblrel. 07, Created)  
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)  
DT 01-AUG-1998 (Tremblrel. 07, Last annotation update)  
DE TAI44 PLASMID PTA144 UP, COMPLETE SEQUENCE.  
GN REPC.  
OS Moraxella sp.  
OC Plasmid PTA144 UP.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;  
OC Moraxellaceae; Moraxella.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-TAI44;  
RA MORETTI M.A., TUTINO L., DUTILLO A., SANNA G., MARINO G.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ224743; CA12111.1; -  
KW Plasmid.  
SQ SEQUENCE 336 AA; 38277 MW; 48794102 CRC32;

Query Match 1.6%; Score 7; DB 2; Length 336;  
Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 51 IRSLSDS 57  
|||  
QY 339 IRSLSDS 345

RESULT 35  
ID 020382 PRELIMINARY; PRT: 344 AA.  
AC 020382.  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-NOV-1996 (Tremblrel. 01, Last annotation update)  
DE COSMID F44A2.  
GN F44A2.7.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
OC Rhabditina; Rhabditidae; Rhabditidae; Pelodietinae; Caenorhabditis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 94150718.  
RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERKS M.,  
RA BONFIELD J., BURTON J., CONNELL M., COPELY T., COOPER J., COULSON A.,  
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
RA GARDNER A., GREEN P., HARKINS T., HILLER L., JIER M., JOHNSTON L.,  
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATEILLE P.,  
RA LIGHTING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
RA WATSON A., WINTSTOCK L., WILKINSON-SPROUT J., WOHLMAN P.,  
RT \*2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.\*;  
RL Nature 368:32-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA DU Z., LE T.;  
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA WATERSTON R.;  
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U41993; AAA83448.1; -  
SQ SEQUENCE 344 AA; 39963 MW; 3CFDDFD8 CRC32;

Query Match 1.6%; Score 7; DB 5; Length 344;  
Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 EVDIIDD 9  
|||  
QY 37 EVDIIDD 43

RESULT 36  
ID 09XS14 PRELIMINARY; PRT: 364 AA.  
AC 09XS14.  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)  
DE MHC CLASS I ANTIGEN (FRAGMENT).  
OS Aulonocara hansbaenschli.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
OC Perciformes; Labridae; Cichlidae; Aulonocara.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 97293242.  
RA SATO A., KLEIN D., SUTTMANN H., FIGUEROA F., O'HUIGIN C., KLEIN J.;  
RT \*Class I mhc genes of cichlid fishes: Identification, expression, and  
RT polymorphism.\*;  
RL Immunogenetics 46:63-72(1997).  
DR EMBL; AF038551; AAD37814.1; -  
FT NON\_TER  
SQ SEQUENCE 364 AA; 41428 MW; 0A580653 CRC32;

Query Match 1.6%; Score 7; DB 7; Length 364;  
Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-240-675-2.rsp

[illegible]

DE T13P21.9 PROTEIN.  
 GN T13P21.9  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC eudicotyledons; Spermatophyta; Magnoliophyta; eudicotyledons;  
 CC core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae;  
 CC Arabidopsis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA.  
 RA LIN X., KAUL S., SHEA T.P., FUJII C.T., SHEN M., VANAKEN S.E.,  
 RA BANSHEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,  
 RA CARREIRA A.J., CRESAY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,  
 RA FRASER C.M., VENTER J.C.;  
 RT "Arabidopsis thaliana chromosome II BAC T13P21 genomic sequence."  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AC006067; AAD15463.1;  
 SQ SEQUENCE 412 AA; 46462 MW; D27623A2 CRC32;

Query Match 1.6%; Score 7; DB 10; Length 412;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 376 AAAGKN 382  
 QY 23 AAAGKN 29

RESULT 41  
 ID 029121 PRELIMINARY; PRT; 451 AA.  
 AC 029121;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE MULTIDRUG RESISTANCE PROTEIN.  
 GN AF1144.  
 OS Archaeoglobus fulgidus.  
 CC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;  
 CC Archaeoglobus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;  
 RX MEDLINE; 98049343.  
 RA KLENN H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,  
 RA KETCHUM K.A., DODSON R.J., GRINN M., HICKER E.K., PETERSON J.D.,  
 RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KRYPTIDES N.C.,  
 RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,  
 RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,  
 RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,  
 RA OVERBERG R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,  
 RA COTTON M.D., SPRIGGS T., ARTACH P., KAINE B.P., STRES S.M.,  
 RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,  
 RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOBSE C.R.,  
 RA VENTER J.C.;  
 RT "The complete genome sequence of the hyperthermophilic, sulfate-  
 reducing archaeon Archaeoglobus fulgidus."  
 RL Nature 390:364-370(1997).  
 DR EMBL; AEO01025; AAB90102.1;  
 DR TIGR; AF1144;  
 DR PFAM; PF00083; sugar\_tr; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 451 AA; 47918 MW; D803BD5B CRC32;

Query Match 1.6%; Score 7; DB 1; Length 451;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 5 KAAITTS 11  
 QY 203 KAAITTS 209

RESULT 42

ID 080668 PRELIMINARY; PRT; 454 AA.  
 AC 080668;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE T3K9.4 PROTEIN.  
 GN T3K9.4  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC eudicotyledons; Spermatophyta; Magnoliophyta; eudicotyledons;  
 CC core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae;  
 CC Arabidopsis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA.  
 RA BRANDON R.C., SYKES S.M., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,  
 RA SOWERVILLE C.R., VENTER J.C.;  
 RT "Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence."  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AC004261; AAD11993.1;  
 SQ SEQUENCE 454 AA; 50448 MW; 57898FF5 CRC32;

Query Match 1.6%; Score 7; DB 10; Length 454;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 9 EKKTDVT 15  
 QY 386 EKKTDVT 392

RESULT 43  
 ID P11753 PRELIMINARY; PRT; 563 AA.  
 AC P11753;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE HYPOHETICAL 63.0 KD PROTEIN.  
 GN MTCY253.30C.  
 OS Mycobacterium tuberculosis.  
 CC Bacteria; Firmicutes; Actinobacteriia; Actinobacteridae;  
 CC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RA DEVLIN K., CHURCHER C.M.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RA BARRELL B.G., RAJANDREAM M.A.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RX MEDLINE; 96181548.  
 RA PHILLIP W.J., POULET S., EIGLMEIER K., PASCOBELLA L.,  
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,  
 RA COLE S.T.;  
 RT "An integrated map of the genome of the tubercle bacillus,  
 Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium  
 leprae."  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).  
 DR EMBL; Z81368; CAB03734.1;  
 DR PFAM; PF01077; NIR\_STR; 1.  
 DR PRINTS; PR00397; SROHAEM.  
 KW Hypothetical protein.  
 SQ SEQUENCE 563 AA; 62997 MW; 688877C5 CRC32;

Query Match 1.6%; Score 7; DB 2; Length 563;  
 Best Local Similarity 100.0%; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: Mon Aug 21 10:34:20 2000  
 Job time : 74 secs.

Db 48 ERIENIT 54  
 |||||  
 OY 178 ERIENIT 184

RESULT 44  
 ID 070681 PRELIMINARY; PRT; 588 AA.  
 AC 070681;  
 DT 01-AUG-1998 (TREMblrel. 07, Created)  
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)  
 DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)  
 DE COAT PROTEIN (FRAGMENT).  
 OS Sugarcane streak mosaic virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA HALL J.S., ADAMS B., PARSONS T.J., FRENCH R., LANE L., JENSEN S.C.;  
 RL Mol. Phylogenet. Evol. 0:0-0(1998).  
 DR EMBL; U75456; AAC16271.1;  
 DR PFAM; PF00767; Poly-coat; 1.  
 KW Coat protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 588 AA; 66336 MW; 529F3579 CRC32;

Query Match 1.68; Score 7; DB 14; Length 588;  
 Best Local Similarity 100.08; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

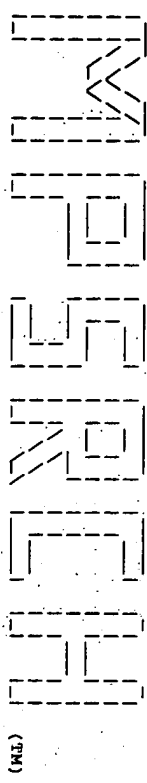
Db 214 ILMNRS 220  
 |||||  
 OY 46 ILMNRS 52

RESULT 45  
 ID 092CY6 PRELIMINARY; PRT; 594 AA.  
 AC 092CY6;  
 DT 01-MAY-1999 (TREMblrel. 10, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)  
 DE PENICILLIN-BINDING PROTEIN (PBP1).  
 GN RP565.  
 OS Rickettsia prowazekii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MADRID E;  
 RX MEDLINE; 99039499.  
 RA ANDERSSON S.G.E., ZONORODIPOUR A., ANDERSSON J.O.,  
 RA SICHERITZ-PONTEN T., ALSMARK U.C.M., PODOMSKI R.M., NÄSLUND A.K.,  
 RA ERIKSSON A.S., WINKLER H.H., KURLAND C.G.;  
 RT "The genome sequence of Rickettsia prowazekii and the origin of  
 RT mitochondria."  
 RL Nature 396:133-140(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MADRID E;  
 RA ANDERSSON S.G.E.;  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ235272; CAAL5013.1;  
 SQ SEQUENCE 594 AA; 67195 MW; C492617E CRC32;

Query Match 1.68; Score 7; DB 2; Length 594;  
 Best Local Similarity 100.08; Pred. No. 2.89e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 186 NIRSLS 192  
 |||||  
 OY 338 NIRSLS 344

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 21 10:30:38 2000; Maspar time 21.79 Seconds  
944.075 Million cell updates/sec

Tabular output not generated.

Title: >US-09-240-675-2  
Description: (1-436) from US09240675.pep  
Perfect Score: 436  
Sequence: 1 MAAVLLGATTLVAVGPMV.....KSSVPSDACEKTPGNTSK 436

Scoring table: TABLE uniprottable  
Gap 60

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%  
Listing first 1000 summaries

Database: plr64  
1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 3.711; Variance 0.436; scale 8.515

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description	Pred. No.
1	436	100.0	557	A32694	Interferon alpha rece	0.00e+00
2	312	71.6	545	S17112	Interferon alpha/beta	0.00e+00
3	16	3.7	56	S41602	Interferon alpha rece	1.22e-22
4	13	3.0	560	S27387	Interferon alpha rece	2.82e-14
5	11	2.5	590	A45283	Interferon alpha/beta	4.53e-09
6	8	1.8	421	T00676	hypothetical protein	3.98e-02
7	8	1.8	1235	T13710	protein-tyrosine kina	3.98e-02
8	7	1.6	11	B26744	megascollaklinin - gar	3.73e+00
9	7	1.6	93	PC4027	hypothetical protein	3.73e+00
10	7	1.6	195	S44459	delta large antigen -	3.73e+00
11	7	1.6	234	B44459	troponin T, fast skel	3.73e+00
12	7	1.6	249	A44459	troponin T, fast skel	3.73e+00
13	7	1.6	249	A44327	troponin T, fast skel	3.73e+00
14	7	1.6	251	D31957	troponin T, skeletal	3.73e+00
15	7	1.6	257	B34327	troponin T, fast skel	3.73e+00
16	7	1.6	257	B31957	troponin T, skeletal	3.73e+00
17	7	1.6	258	C13021	troponin T, human	3.73e+00
18	7	1.6	263	C13957	troponin T, skeletal	3.73e+00
19	7	1.6	266	TPR875	troponin T, fast skel	3.73e+00
20	7	1.6	272	A44824	troponin T, fast skel	3.73e+00
21	7	1.6	274	A31957	troponin T, skeletal	3.73e+00
22	7	1.6	298	S75156	hypothetical protein	3.73e+00
23	7	1.6	337	I38500	Interferon gamma rece	3.73e+00

24	7	1.6	353	1	B26952	electron transfer fla	3.73e+00
25	7	1.6	369	1	S14071	electron transfer fla	3.73e+00
26	7	1.6	394	2	B32495	Rep-1 protein B - mou	3.73e+00
27	7	1.6	403	2	I52590	m3-B isoform - mouse	3.73e+00
28	7	1.6	423	2	T15309	hypothetical protein	3.73e+00
29	7	1.6	425	2	S14147	multifunctional purin	3.73e+00
30	7	1.6	425	2	S55684	aminimidazole ribonu	3.73e+00
31	7	1.6	426	2	A35641	5-aminimidazole ribo	3.73e+00
32	7	1.6	442	2	S74801	ammonium transport pr	3.73e+00
33	7	1.6	450	1	W2B8A1	49.2K membrane protei	3.73e+00
34	7	1.6	451	1	G69392	multidrug resistance	3.73e+00
35	7	1.6	454	2	T02100	hypothetical protein	3.73e+00
36	7	1.6	530	2	B75080	hypothetical protein	3.73e+00
37	7	1.6	563	2	B70682	probable nitrite redu	3.73e+00
38	7	1.6	594	2	C71661	penicillin-binding pr	3.73e+00
39	7	1.6	681	2	F64889	membrane protein maco	3.73e+00
40	7	1.6	698	2	G70559	probable uvir protein	3.73e+00
41	7	1.6	929	2	A32495	rep-1 protein, form A	3.73e+00
42	7	1.6	1051	2	A40021	Integrin VLA-3 alpha-	3.73e+00
43	7	1.6	1053	2	I55534	VLA-3 alpha subunit -	3.73e+00
44	7	1.6	1126	2	UC4019	DNA mismatch repair p	3.73e+00
45	7	1.6	1184	2	G70600	hypothetical protein	3.73e+00
46	7	1.6	1201	2	T00444	hypothetical protein	3.73e+00
47	7	1.6	1205	1	GNNY2W	genome polypotein -	3.73e+00
48	7	1.6	2205	1	GNNY27	genome polypotein -	3.73e+00
49	7	1.6	2206	2	S03822	genome polypotein -	3.73e+00
50	7	1.6	2206	2	GNNY4P	genome polypotein -	3.73e+00
51	7	1.6	2207	1	S09553	genome polypotein -	3.73e+00
52	7	1.6	2207	1	GNNY5P	genome polypotein -	3.73e+00
53	7	1.6	2214	1	A48548	genome polypotein -	3.73e+00
54	7	1.6	3744	1	S46715	hypothetical protein	3.73e+00
55	7	1.4	16	2	C49655	T-cell-receptor beta	1.97e+02
56	6	1.4	28	2	A60359	pollen allergen DG3 -	1.97e+02
57	6	1.4	30	2	S55674	cearastoxin - horn v	1.97e+02
58	6	1.4	53	2	E75136	rubredoxin (rd) PAB2	1.97e+02
59	6	1.4	53	1	RUPF	rubredoxin - Pyrococc	1.97e+02
60	6	1.4	75	2	S73297	hypothetical protein	1.97e+02
61	6	1.4	79	2	H64643	hypothetical protein	1.97e+02
62	6	1.4	80	2	T10326	lef-10 protein - Orgy	1.97e+02
63	6	1.4	84	2	S44989	dmp protein - phage T	1.97e+02
64	6	1.4	85	1	CCPB6	cytochrome c6 - Plect	1.97e+02
65	6	1.4	88	1	CCPB6	cytochrome c6 - Anaba	1.97e+02
66	6	1.4	89	2	T13546	hypothetical protein	1.97e+02
67	6	1.4	93	2	A71207	hypothetical protein	1.97e+02
68	6	1.4	93	2	B27590	T-cell receptor beta	1.97e+02
69	6	1.4	103	2	E72767	hypothetical protein	1.97e+02
70	6	1.4	105	2	B30554	Ig lambda chain C reg	1.97e+02
71	6	1.4	106	2	S28239	NADH dehydrogenase (u	1.97e+02
72	6	1.4	106	2	S25416	T-cell receptor beta	1.97e+02
73	6	1.4	108	2	A72764	hypothetical protein	1.97e+02
74	6	1.4	110	2	T12499	hypothetical protein	1.97e+02
75	6	1.4	110	2	A24444	hypothetical protein	1.97e+02
76	6	1.4	111	1	CCA153	Cytochrome c6 - precus	1.97e+02
77	6	1.4	111	1	I39601	Cytochrome c6 - Anaba	1.97e+02
78	6	1.4	112	2	S10918	hypothetical 12K prot	1.97e+02
79	6	1.4	114	2	C72566	hypothetical protein	1.97e+02
80	6	1.4	114	2	I38313	T-cell receptor beta	1.97e+02
81	6	1.4	114	2	S17379	T-cell receptor beta	1.97e+02
82	6	1.4	115	2	D72237	lipid transfer protei	1.97e+02
83	6	1.4	116	2	T02044	hypothetical protein	1.97e+02
84	6	1.4	121	2	C71480	hypothetical protein	1.97e+02
85	6	1.4	122	2	A72025	ctf16, hypothetical pr	1.97e+02
86	6	1.4	125	2	C70637	hypothetical protein	1.97e+02
87	6	1.4	128	2	C69183	hypothetical protein	1.97e+02
88	6	1.4	129	1	G22845	hypothetical protein	1.97e+02
89	6	1.4	129	1	CCRF6P	Cytochrome c556 - Rio	1.97e+02
90	6	1.4	133	2	I51914	glutaryl aminopeptida	1.97e+02
91	6	1.4	134	2	D69015	fumarate hydratase, c	1.97e+02
92	6	1.4	134	2	G43868	lactate dehydrogenase	1.97e+02
93	6	1.4	136	2	I49013	thymic shared antigen	1.97e+02
94	6	1.4	137	2	B64208	hypothetical protein	1.97e+02
95	6	1.4	140	2	S36942	T-cell receptor beta	1.97e+02
96	6	1.4	141	2	I48769	Slp(wv) alpha-chain -	1.97e+02

97	1.4	141	2	B41543	Integrin alpha-3A cha	1.97e+02	170	6	1.4	220	2	E34012	H+-transporting ATP s	1.97e+02
98	1.4	142	2	D69891	Integrin alpha-3B cha	1.97e+02	171	6	1.4	220	2	B34012	H+-transporting ATP s	1.97e+02
99	1.4	143	2	T11243	Integrin alpha-3B cha	1.97e+02	172	6	1.4	220	2	C34012	H+-transporting ATP s	1.97e+02
100	1.4	144	2	C41543	Integrin alpha-3B cha	1.97e+02	173	6	1.4	220	2	F34012	H+-transporting ATP s	1.97e+02
101	1.4	145	2	A69267	Integrin alpha-3B cha	1.97e+02	174	6	1.4	221	2	JC1250	ependymin - Om-1-precu	1.97e+02
102	1.4	146	2	A42437	Integrin alpha-3B cha	1.97e+02	175	6	1.4	221	2	I50538	ependymin - northern	1.97e+02
103	1.4	147	2	T10140	Integrin alpha-3B cha	1.97e+02	176	6	1.4	221	2	T02086	zinc inducible protel	1.97e+02
104	1.4	148	2	T10140	Integrin alpha-3B cha	1.97e+02	177	6	1.4	221	2	H02986	GTP, cyclohydrolase I	1.97e+02
105	1.4	149	2	B69221	Integrin alpha-3B cha	1.97e+02	178	6	1.4	222	2	JC1384	GTP, cyclohydrolase I	1.97e+02
106	1.4	150	2	G02355	Integrin alpha-3B cha	1.97e+02	179	6	1.4	222	2	A32979	beta-casein precursor	1.97e+02
107	1.4	151	2	S64691	Integrin alpha-3B cha	1.97e+02	180	6	1.4	223	2	T09862	H+-transporting ATP s	1.97e+02
108	1.4	152	2	CYP279	Integrin alpha-3B cha	1.97e+02	181	6	1.4	223	2	B64396	H+-transporting ATP s	1.97e+02
109	1.4	153	2	CYP279	Integrin alpha-3B cha	1.97e+02	182	6	1.4	223	2	I46696	H+-transporting ATP s	1.97e+02
110	1.4	154	2	CYP279	Integrin alpha-3B cha	1.97e+02	183	6	1.4	223	2	S29895	H+-transporting ATP s	1.97e+02
111	1.4	155	2	CYP279	Integrin alpha-3B cha	1.97e+02	184	6	1.4	224	2	KBBOA2	GTP, cyclohydrolase I	1.97e+02
112	1.4	156	2	T02833	Integrin alpha-3B cha	1.97e+02	185	6	1.4	225	2	F70011	beta-casein precursor	1.97e+02
113	1.4	157	2	S69527	Integrin alpha-3B cha	1.97e+02	186	6	1.4	229	2	BVECTJ	hypothetical protein	1.97e+02
114	1.4	158	2	RMSHD3	Integrin alpha-3B cha	1.97e+02	187	6	1.4	231	2	A75103	hypothetical protein	1.97e+02
115	1.4	159	2	S64830	Integrin alpha-3B cha	1.97e+02	188	6	1.4	231	2	B64920	phosphoglycolate phos	1.97e+02
116	1.4	160	2	G72692	Integrin alpha-3B cha	1.97e+02	189	6	1.4	231	2	S37108	cuticlin 2 - Caenorha	1.97e+02
117	1.4	161	2	C70602	Integrin alpha-3B cha	1.97e+02	190	6	1.4	232	2	DXCH	ovalbumin-related x p	1.97e+02
118	1.4	162	2	S67150	Integrin alpha-3B cha	1.97e+02	191	6	1.4	234	2	S76694	hypothetical protein	1.97e+02
119	1.4	163	2	B55517	Integrin alpha-3B cha	1.97e+02	192	6	1.4	237	2	J01754	H+-transporting ATP s	1.97e+02
120	1.4	164	2	S73447	Integrin alpha-3B cha	1.97e+02	193	6	1.4	238	2	S28758	H+-transporting ATP s	1.97e+02
121	1.4	165	2	S74360	Integrin alpha-3B cha	1.97e+02	194	6	1.4	239	2	R33P6E	ribosomal protein S6	1.97e+02
122	1.4	166	2	C71869	Integrin alpha-3B cha	1.97e+02	195	6	1.4	243	2	A72669	probable glutaredoxin	1.97e+02
123	1.4	167	2	J60253	Integrin alpha-3B cha	1.97e+02	196	6	1.4	246	2	DBHU	complement factor D	1.97e+02
124	1.4	168	2	T05030	Integrin alpha-3B cha	1.97e+02	197	6	1.4	246	2	J01472	trypsin (EC 3.4.21.4)	1.97e+02
125	1.4	169	2	A70804	Integrin alpha-3B cha	1.97e+02	198	6	1.4	246	2	B69311	trypsin (EC 3.4.21.4)	1.97e+02
126	1.4	170	2	A71861	Integrin alpha-3B cha	1.97e+02	199	6	1.4	246	2	J01471	trypsin (EC 3.4.21.4)	1.97e+02
127	1.4	171	2	E72586	Integrin alpha-3B cha	1.97e+02	200	6	1.4	247	2	S05494	trypsin (EC 3.4.21.4)	1.97e+02
128	1.4	172	2	A70245	Integrin alpha-3B cha	1.97e+02	201	6	1.4	247	2	BVECTJ	trypsin (EC 3.4.21.4)	1.97e+02
129	1.4	173	2	D70257	Integrin alpha-3B cha	1.97e+02	202	6	1.4	248	2	S55065	trypsin (EC 3.4.21.4)	1.97e+02
130	1.4	174	2	S39318	Integrin alpha-3B cha	1.97e+02	203	6	1.4	248	2	S55067	trypsin (EC 3.4.21.4)	1.97e+02
131	1.4	175	2	S39317	Integrin alpha-3B cha	1.97e+02	204	6	1.4	249	2	S55066	trypsin (EC 3.4.21.4)	1.97e+02
132	1.4	176	2	B70824	Integrin alpha-3B cha	1.97e+02	205	6	1.4	249	2	H64368	trypsin (EC 3.4.21.4)	1.97e+02
133	1.4	177	2	T15643	Integrin alpha-3B cha	1.97e+02	206	6	1.4	251	2	A64363	trypsin (EC 3.4.21.4)	1.97e+02
134	1.4	178	2	T15643	Integrin alpha-3B cha	1.97e+02	207	6	1.4	252	2	F72560	trypsin (EC 3.4.21.4)	1.97e+02
135	1.4	179	2	T15643	Integrin alpha-3B cha	1.97e+02	208	6	1.4	252	2	S61142	trypsin (EC 3.4.21.4)	1.97e+02
136	1.4	180	2	G69430	Integrin alpha-3B cha	1.97e+02	209	6	1.4	253	2	A71648	trypsin (EC 3.4.21.4)	1.97e+02
137	1.4	181	2	A70153	Integrin alpha-3B cha	1.97e+02	210	6	1.4	255	2	A35340	trypsin (EC 3.4.21.4)	1.97e+02
138	1.4	182	2	S08418	Integrin alpha-3B cha	1.97e+02	211	6	1.4	256	2	J01144	trypsin (EC 3.4.21.4)	1.97e+02
139	1.4	183	2	B71855	Integrin alpha-3B cha	1.97e+02	212	6	1.4	256	2	E69166	trypsin (EC 3.4.21.4)	1.97e+02
140	1.4	184	2	B64661	Integrin alpha-3B cha	1.97e+02	213	6	1.4	256	2	B26720	trypsin (EC 3.4.21.4)	1.97e+02
141	1.4	185	2	B71421	Integrin alpha-3B cha	1.97e+02	214	6	1.4	259	2	S73911	trypsin (EC 3.4.21.4)	1.97e+02
142	1.4	186	2	A72306	Integrin alpha-3B cha	1.97e+02	215	6	1.4	259	2	MMMS28	trypsin (EC 3.4.21.4)	1.97e+02
143	1.4	187	2	T13106	Integrin alpha-3B cha	1.97e+02	216	6	1.4	261	2	A70002	trypsin (EC 3.4.21.4)	1.97e+02
144	1.4	188	2	A70331	Integrin alpha-3B cha	1.97e+02	217	6	1.4	262	2	C72764	trypsin (EC 3.4.21.4)	1.97e+02
145	1.4	189	2	D69486	Integrin alpha-3B cha	1.97e+02	218	6	1.4	262	2	T06600	trypsin (EC 3.4.21.4)	1.97e+02
146	1.4	190	2	T04161	Integrin alpha-3B cha	1.97e+02	219	6	1.4	263	2	I55608	trypsin (EC 3.4.21.4)	1.97e+02
147	1.4	191	2	R30C7	Integrin alpha-3B cha	1.97e+02	220	6	1.4	264	2	B72462	trypsin (EC 3.4.21.4)	1.97e+02
148	1.4	192	2	J61271	Integrin alpha-3B cha	1.97e+02	221	6	1.4	265	2	H71105	trypsin (EC 3.4.21.4)	1.97e+02
149	1.4	193	2	S23381	Integrin alpha-3B cha	1.97e+02	222	6	1.4	266	2	E64314	trypsin (EC 3.4.21.4)	1.97e+02
150	1.4	194	2	S23381	Integrin alpha-3B cha	1.97e+02	223	6	1.4	266	2	HPG41	trypsin (EC 3.4.21.4)	1.97e+02
151	1.4	195	2	S23381	Integrin alpha-3B cha	1.97e+02	224	6	1.4	269	2	S22781	trypsin (EC 3.4.21.4)	1.97e+02
152	1.4	196	2	S23381	Integrin alpha-3B cha	1.97e+02	225	6	1.4	270	2	S16579	trypsin (EC 3.4.21.4)	1.97e+02
153	1.4	197	2	S23381	Integrin alpha-3B cha	1.97e+02	226	6	1.4	270	2	S77191	trypsin (EC 3.4.21.4)	1.97e+02
154	1.4	198	2	S67618	Integrin alpha-3B cha	1.97e+02	227	6	1.4	273	2	H71441	trypsin (EC 3.4.21.4)	1.97e+02
155	1.4	199	2	A41899	Integrin alpha-3B cha	1.97e+02	228	6	1.4	276	2	B25345	trypsin (EC 3.4.21.4)	1.97e+02
156	1.4	200	2	E69764	Integrin alpha-3B cha	1.97e+02	229	6	1.4	276	2	H25345	trypsin (EC 3.4.21.4)	1.97e+02
157	1.4	201	2	SAVIMC	Integrin alpha-3B cha	1.97e+02	230	6	1.4	276	2	H71985	trypsin (EC 3.4.21.4)	1.97e+02
158	1.4	202	2	J02167	Integrin alpha-3B cha	1.97e+02	231	6	1.4	277	2	T16020	trypsin (EC 3.4.21.4)	1.97e+02
159	1.4	203	2	A59068	Integrin alpha-3B cha	1.97e+02	232	6	1.4	280	2	A69186	trypsin (EC 3.4.21.4)	1.97e+02
160	1.4	204	2	E72548	Integrin alpha-3B cha	1.97e+02	233	6	1.4	283	2	D64448	trypsin (EC 3.4.21.4)	1.97e+02
161	1.4	205	2	JC4928	Integrin alpha-3B cha	1.97e+02	234	6	1.4	285	2	A25561	trypsin (EC 3.4.21.4)	1.97e+02
162	1.4	206	2	SAVIDN	Integrin alpha-3B cha	1.97e+02	235	6	1.4	285	2	C25242	trypsin (EC 3.4.21.4)	1.97e+02
163	1.4	207	2	T12727	Integrin alpha-3B cha	1.97e+02	236	6	1.4	286	2	B25242	trypsin (EC 3.4.21.4)	1.97e+02
164	1.4	208	2	G71722	Integrin alpha-3B cha	1.97e+02	237	6	1.4	286	2	A25242	trypsin (EC 3.4.21.4)	1.97e+02
165	1.4	209	2	A43522	Integrin alpha-3B cha	1.97e+02	238	6	1.4	290	2	G70397	trypsin (EC 3.4.21.4)	1.97e+02
166	1.4	210	2	A43522	Integrin alpha-3B cha	1.97e+02	239	6	1.4	292	2	C65070	trypsin (EC 3.4.21.4)	1.97e+02
167	1.4	211	2	A40181	Integrin alpha-3B cha	1.97e+02	240	6	1.4	293	2	H71949	trypsin (EC 3.4.21.4)	1.97e+02
168	1.4	212	2	B70645	Integrin alpha-3B cha	1.97e+02	241	6	1.4	293	2	F64558	trypsin (EC 3.4.21.4)	1.97e+02
169	1.4	213	2	D34012	Integrin alpha-3B cha	1.97e+02	242	6	1.4	295	2	S59439	trypsin (EC 3.4.21.4)	1.97e+02



243	6	1.4	298	2	S75972	hypothetical protein	1.97e+02	316	6	1.4	379	2	S14885	hypothetical protein	1.97e+02
244	6	1.4	299	1	G64143	hypothetical protein	1.97e+02	317	6	1.4	380	2	H70590	hypothetical protein	1.97e+02
245	6	1.4	299	1	S32896	hypothetical protein	1.97e+02	318	6	1.4	382	2	D70587	probable dna2 protei	1.97e+02
246	6	1.4	300	2	S56545	filament protein flm	1.97e+02	319	6	1.4	383	1	A48222	denatn 48k chain - h	1.97e+02
247	6	1.4	300	2	S25706	zf-cadl protein - zab	1.97e+02	320	6	1.4	384	1	S17957	neurokinin A receptor	1.97e+02
248	6	1.4	301	2	D48326	cyt b intron 2 protein	1.97e+02	321	6	1.4	384	1	S00516	substance K receptor	1.97e+02
249	6	1.4	302	1	S60777	cltc protein - Riebsl	1.97e+02	322	6	1.4	384	2	S20303	substance K receptor	1.97e+02
250	6	1.4	302	1	ORBP15	replication protein 1	1.97e+02	323	6	1.4	384	2	S51671	methionine adenosyltr	1.97e+02
251	6	1.4	303	2	JC2410	ADP-ribosyl cyclase/c	1.97e+02	324	6	1.4	390	2	S18202	leuplin precursor - hu	1.97e+02
252	6	1.4	304	2	S02284	potassium channel, pro	1.97e+02	325	6	1.4	390	2	A36737	substance K receptor	1.97e+02
253	6	1.4	304	2	I49586	lymphocyte, different	1.97e+02	326	6	1.4	390	2	S18201	squamous cell carcino	1.97e+02
254	6	1.4	305	2	F72574	probable cytochrome C	1.97e+02	327	6	1.4	391	2	D72663	hypothetical protein	1.97e+02
255	6	1.4	305	2	D69199	conserved cytochrome C	1.97e+02	328	6	1.4	391	2	S74688	hypothetical protein	1.97e+02
256	6	1.4	306	2	I46903	tropomyosin T cardiac is	1.97e+02	329	6	1.4	391	2	A70663	probable ppe protein	1.97e+02
257	6	1.4	307	2	T09923	cytidine deaminase (E	1.97e+02	330	6	1.4	392	2	I39521	rubredoxin - NAD+ reu	1.97e+02
258	6	1.4	308	2	E64340	hypothetical protein	1.97e+02	331	6	1.4	392	2	E72219	conserved hypothetical	1.97e+02
259	6	1.4	308	2	S11151	amid protein - Strept	1.97e+02	332	6	1.4	393	2	T08203	polylacturonase (EC	1.97e+02
260	6	1.4	312	2	S24419	hypothetical protein	1.97e+02	333	6	1.4	393	2	C71240	hypothetical protein	1.97e+02
261	6	1.4	313	2	S59448	gene 41 protein - hum	1.97e+02	334	6	1.4	394	2	S48522	cell division control	1.97e+02
262	6	1.4	316	2	WZBE41	L-lactate dehydrogena	1.97e+02	335	6	1.4	396	2	P00813	glycoprotein, B1 - hog	1.97e+02
263	6	1.4	316	2	G70110	magnesium transport p	1.97e+02	336	6	1.4	397	2	H70789	probable serine prote	1.97e+02
264	6	1.4	316	2	B47157	hypothetical protein	1.97e+02	337	6	1.4	398	2	A71482	hypothetical protein	1.97e+02
265	6	1.4	316	2	E70664	magnesium transport p	1.97e+02	338	6	1.4	398	2	T15846	hypothetical protein	1.97e+02
266	6	1.4	316	2	A47157	probable cdc2-like pr	1.97e+02	339	6	1.4	398	2	J01059	neurokinin A receptor	1.97e+02
267	6	1.4	317	2	T09591	methionyl-tRNA formyl	1.97e+02	340	6	1.4	399	1	A26916	ribonucleoside-diphos	1.97e+02
268	6	1.4	317	2	A69626	probable acyl-coadeny	1.97e+02	341	6	1.4	400	2	JC2473	doc2 protein - human	1.97e+02
269	6	1.4	319	2	A70605	reps protein - Rhlzob	1.97e+02	342	6	1.4	401	1	B35177	chromate resistance p	1.97e+02
270	6	1.4	319	2	S75969	hypothetical protein	1.97e+02	343	6	1.4	401	2	A48423	engrailed homeodoma	1.97e+02
271	6	1.4	322	2	E71137	hypothetical protein	1.97e+02	344	6	1.4	402	2	S16595	neurokinin 2 receptor	1.97e+02
272	6	1.4	322	2	S38091	hypothetical protein	1.97e+02	345	6	1.4	403	2	B69589	argininosuccinate syn	1.97e+02
273	6	1.4	323	2	D70125	Lambda CII stability-d	1.97e+02	346	6	1.4	405	2	I39062	denatn 52k chain - h	1.97e+02
274	6	1.4	323	2	A57733	succinate-semialdehyd	1.97e+02	347	6	1.4	406	1	A48495	linalool 8-monooxygen	1.97e+02
275	6	1.4	324	2	D44423	homeotic protein engr	1.97e+02	348	6	1.4	407	2	H72573	integral acetyl CoA s	1.97e+02
276	6	1.4	324	2	I50125	cdx1 protein - common	1.97e+02	349	6	1.4	408	2	S58131	integral membrane pro	1.97e+02
277	6	1.4	325	2	E64998	hypothetical protein	1.97e+02	350	6	1.4	409	2	F72504	processing proteinase	1.97e+02
278	6	1.4	327	2	C71146	hypothetical protein	1.97e+02	351	6	1.4	411	2	B69886	hypothetical protein	1.97e+02
279	6	1.4	327	2	B65180	acetylhydroxy acid syn	1.97e+02	352	6	1.4	409	2	E70667	cathepsin D (EC 3.4.2	1.97e+02
280	6	1.4	330	2	C56931	NADH dehydrogenase (u	1.97e+02	353	6	1.4	412	1	K4HND	haptNP complex protein	1.97e+02
281	6	1.4	333	2	B64085	g1px protein - Haemop	1.97e+02	354	6	1.4	413	2	S46109	penicillin binding p	1.97e+02
282	6	1.4	335	2	E75183	ATP-binding protein P	1.97e+02	355	6	1.4	416	2	A56486	NADH dehydrogenase - su	1.97e+02
283	6	1.4	335	2	D71275	hypothetical protein	1.97e+02	356	6	1.4	417	2	T12385	triacylglycerol lipas	1.97e+02
284	6	1.4	336	1	QOBE40	BGLF2 protein - human	1.97e+02	357	6	1.4	417	2	JM0068	ylbu protein - Escher	1.97e+02
285	6	1.4	337	2	G71869	hypothetical protein	1.97e+02	358	6	1.4	421	2	B64819	hypothetical protein	1.97e+02
286	6	1.4	339	2	S20880	homeotic protein Hox	1.97e+02	359	6	1.4	425	2	S6504	hypothetical protein	1.97e+02
287	6	1.4	343	1	A57014	prostasin (EC 3.4.21.	1.97e+02	360	6	1.4	425	2	S76717	hypothetical protein	1.97e+02
288	6	1.4	344	2	T15192	hypothetical protein	1.97e+02	361	6	1.4	426	2	T16406	ubiquitinol-cyclohome	1.97e+02
289	6	1.4	344	2	C69453	transposase homolog -	1.97e+02	362	6	1.4	426	2	E70058	hypothetical protein	1.97e+02
290	6	1.4	344	2	S30706	Mg-transport system I	1.97e+02	363	6	1.4	426	2	F64419	hypothetical protein	1.97e+02
291	6	1.4	346	2	C65066	hypothetical protein	1.97e+02	364	6	1.4	428	2	S61623	hypothetical protein	1.97e+02
292	6	1.4	346	2	S42423	aspartate-semialdehyd	1.97e+02	365	6	1.4	431	2	G75017	histiyl-tRNA synthet	1.97e+02
293	6	1.4	346	2	A03308	dnak-type molecular c	1.97e+02	366	6	1.4	431	2	B51203	hypothetical protein	1.97e+02
294	6	1.4	348	2	S77104	anthranilate phosphor	1.97e+02	367	6	1.4	432	2	B65190	tyrkH protein - Escher	1.97e+02
295	6	1.4	349	2	B49412	ribonucleoside-diphos	1.97e+02	368	6	1.4	432	2	T16639	hypothetical protein	1.97e+02
296	6	1.4	349	2	B35114	anthranilate phosphor	1.97e+02	369	6	1.4	433	2	T04594	Aldehyde dehydrogenas	1.97e+02
297	6	1.4	349	2	R02506	potassium channel, pro	1.97e+02	370	6	1.4	433	1	DEBCHS	homoserine dehydrogen	1.97e+02
298	6	1.4	349	2	T02506	peforinase (EC 1.11.1	1.97e+02	371	6	1.4	437	2	S70546	3-deoxy-manno-octulos	1.97e+02
299	6	1.4	350	2	I73338	macrophage scavenger	1.97e+02	372	6	1.4	437	1	A45569	adenosylhomocysteinas	1.97e+02
300	6	1.4	351	2	C72508	hypothetical protein	1.97e+02	373	6	1.4	438	2	S30769	probable C-14 sterol	1.97e+02
301	6	1.4	352	2	E70797	hypothetical protein	1.97e+02	374	6	1.4	439	2	T15748	hypothetical protein	1.97e+02
302	6	1.4	353	2	B70358	hydrogenase (EC 1.18.	1.97e+02	375	6	1.4	441	2	T82242	Mg-protoporphyrin IX	1.97e+02
303	6	1.4	355	2	A41314	hypothetical 40k prot	1.97e+02	376	6	1.4	443	2	I38603	heine A farnesyltransf	1.97e+02
304	6	1.4	358	2	C72643	probable 3-dehydroqui	1.97e+02	377	6	1.4	444	2	T12297	NADH dehydrogenase-1	1.97e+02
305	6	1.4	359	2	A47159	potassium channel pro	1.97e+02	378	6	1.4	445	2	T16025	hypothetical protein	1.97e+02
306	6	1.4	360	1	S49188	electron transfer fla	1.97e+02	379	6	1.4	448	2	S03127	gene cob intron prote	1.97e+02
307	6	1.4	363	1	WZBE44	gene 44 protein - hum	1.97e+02	380	6	1.4	449	2	JC5391	presenilin-beta - Afr	1.97e+02
308	6	1.4	363	2	T05624	cinamyl-alcohol dehy	1.97e+02	381	6	1.4	449	2	C71156	probable helicase, pro	1.97e+02
309	6	1.4	368	2	C72260	hypothetical protein	1.97e+02	382	6	1.4	450	2	E72615	probable hlyuc APE1382	1.97e+02
310	6	1.4	369	2	S37314	cyto protein - Bradyr	1.97e+02	383	6	1.4	450	1	I0YMC	replication, initiatio	1.97e+02
311	6	1.4	370	2	S70157	cpst protein, 40, 6k	1.97e+02	384	6	1.4	451	2	S33816	kinesin light chain 1	1.97e+02
312	6	1.4	373	2	H72756	probable phosphatase-bi	1.97e+02	385	6	1.4	451	2	F66671	hypothetical protein	1.97e+02
313	6	1.4	374	1	S7FURP	trichodine synthase	1.97e+02	386	6	1.4	452	2	F69294	DNA repair protein RA	1.97e+02
314	6	1.4	378	2	D70515	hypothetical protein	1.97e+02	387	6	1.4	452	2	C72295	hypothetical protein	1.97e+02
315	6	1.4	378	2	S00842	leukostatin precursor	1.97e+02	388	6	1.4	458	2	G69123	conserved hypothetica	1.97e+02

389	6	1.4	458	2	T11526	NADH dehydrogenase (u	1.97e+02
390	6	1.4	458	2	A71467	probable phosphogluco	1.97e+02
391	6	1.4	458	2	B44407	macrophage scavenger	1.97e+02
392	6	1.4	459	2	S47879	NADH dehydrogenase (u	1.97e+02
393	6	1.4	459	2	T11866	NADH dehydrogenase	1.97e+02
394	6	1.4	459	2	S06607	23S rRNA intron 2 pro	1.97e+02
395	6	1.4	459	1	DEPSP	dihydropolypamide dehy	1.97e+02
396	6	1.4	459	2	T11372	NADH dehydrogenase su	1.97e+02
397	6	1.4	459	2	T11411	NADH dehydrogenase su	1.97e+02
398	6	1.4	462	2	S29503	mult. protein - Clostr	1.97e+02
399	6	1.4	462	2	T08199	hypothetical protein	1.97e+02
400	6	1.4	463	2	I40661	methylaspartate mutas	1.97e+02
401	6	1.4	464	2	S75889	hypothetical protein	1.97e+02
402	6	1.4	464	2	T15161	hypothetical protein	1.97e+02
403	6	1.4	470	2	H72105	dicarboxylase transio	1.97e+02
404	6	1.4	473	2	S40507	endoglucanase - rumen	1.97e+02
405	6	1.4	473	2	S64014	probable transport pr	1.97e+02
406	6	1.4	475	1	A56824	dihydropolypamide dehy	1.97e+02
407	6	1.4	478	2	H70474	ATP synthase F1, beta	1.97e+02
408	6	1.4	479	2	B69399	activator 1, replicat	1.97e+02
409	6	1.4	480	2	D75050	hypothetical protein	1.97e+02
410	6	1.4	481	2	S69808	lincomycin resistance	1.97e+02
411	6	1.4	481	2	JEO377	P70 S6 Kinase (EC 2.7	1.97e+02
412	6	1.4	482	2	G71603	chromatin-binding pro	1.97e+02
413	6	1.4	483	2	JHO532	catalase (EC 1.11.1.6	1.97e+02
414	6	1.4	484	2	S58868	G protein-coupled rec	1.97e+02
415	6	1.4	484	2	S58868	G protein-coupled rec	1.97e+02
416	6	1.4	485	2	E75015	IMP dehydrogenase (EC	1.97e+02
417	6	1.4	485	2	I39557	ribulose-bisphosphate	1.97e+02
418	6	1.4	486	1	RKRRL	ribulose-bisphosphate	1.97e+02
419	6	1.4	486	1	I39559	ribulose-bisphosphate	1.97e+02
420	6	1.4	487	1	RKALE	ribulose-bisphosphate	1.97e+02
421	6	1.4	487	2	F70765	hypothetical protein	1.97e+02
422	6	1.4	488	1	RKQXIX	ribulose-bisphosphate	1.97e+02
423	6	1.4	489	1	NIBCAT	nitrogenase (EC 1.18	1.97e+02
424	6	1.4	489	2	I51532	potassium channel - A	1.97e+02
425	6	1.4	492	2	A64498	hypothetical protein	1.97e+02
426	6	1.4	492	2	S49147	ERF-2 protein - human	1.97e+02
427	6	1.4	492	2	A34272	testosterone /alpha-h	1.97e+02
428	6	1.4	494	2	A27442	triacylglycerol lipas	1.97e+02
429	6	1.4	494	2	S10483	lipase, hepatic - rat	1.97e+02
430	6	1.4	495	2	I57680	potassium channel KCN	1.97e+02
431	6	1.4	495	2	B39113	potassium channel KVI	1.97e+02
432	6	1.4	495	2	A40090	potassium channel KVI	1.97e+02
433	6	1.4	495	2	G69360	probable ribose ABC t	1.97e+02
434	6	1.4	505	1	S54302	zinc transporter znt-	1.97e+02
435	6	1.4	505	1	S54302	lysine-tRNA ligase (	1.97e+02
436	6	1.4	507	2	S54303	zinc transport protei	1.97e+02
437	6	1.4	508	2	A70125	UDP-N-acetylmutamyla	1.97e+02
438	6	1.4	509	2	S76731	hypothetical protein	1.97e+02
439	6	1.4	509	2	C70624	probable two componen	1.97e+02
440	6	1.4	521	2	T01923	hypothetical protein	1.97e+02
441	6	1.4	521	2	T05684	hypothetical protein	1.97e+02
442	6	1.4	527	2	T03427	hypothetical protein	1.97e+02
443	6	1.4	527	2	C70130	glycerol-3-phosphate	1.97e+02
444	6	1.4	527	2	S64060	probable membrane pro	1.97e+02
445	6	1.4	528	2	A70915	conserved hypothetical	1.97e+02
446	6	1.4	529	2	F69989	conserved hypothetical	1.97e+02
447	6	1.4	529	1	YRHQ1	monophenol monooxygen	1.97e+02
448	6	1.4	530	1	NMBE2T	anthranilate synthase	1.97e+02
449	6	1.4	530	2	C38497	GI protein - vacuola	1.97e+02
450	6	1.4	531	1	NNEC2	anthranilate synthase	1.97e+02
451	6	1.4	533	2	I49736	monophenol monooxygen	1.97e+02
452	6	1.4	533	1	YRMSCS	transposase - rice bl	1.97e+02
453	6	1.4	535	2	S51577	hypothetical protein	1.97e+02
454	6	1.4	536	2	H72535	hypothetical protein	1.97e+02
455	6	1.4	536	2	A36395	spore wall maturation	1.97e+02
456	6	1.4	536	2	T04234	calmodulin-binding pr	1.97e+02
457	6	1.4	537	2	A46611	myosin-binding protei	1.97e+02
458	6	1.4	538	2	S76481	hypothetical protein	1.97e+02
459	6	1.4	540	2	B64829	membrane protein b089	1.97e+02
460	6	1.4	541	2	T01394	hypothetical protein	1.97e+02
461	6	1.4	542	1	S25276	D-alanine/glycine tra	1.97e+02
462	6	1.4	545	2	JU0341	intercellular adhesio	1.97e+02
463	6	1.4	548	1	YCEC	acetoacetate synthase	1.97e+02
464	6	1.4	551	1	QVCV25	N3L protein - vaccini	1.97e+02
465	6	1.4	551	2	A36848	N3L protein - variola	1.97e+02
466	6	1.4	552	2	S71811	probable transcrip	1.97e+02
467	6	1.4	552	1	OREBDT	aspartate chemorecept	1.97e+02
468	6	1.4	552	2	C45710	R transactivator homo	1.97e+02
469	6	1.4	554	2	G72361	hypothetical protein	1.97e+02
470	6	1.4	554	2	S59235	hypothetical protein	1.97e+02
471	6	1.4	555	2	F72555	probable molybdenum t	1.97e+02
472	6	1.4	555	2	F72111	fructose-6-phosphot	1.97e+02
473	6	1.4	557	2	T03137	minor capsid protein	1.97e+02
474	6	1.4	557	2	B28182	hemolysin B - Serrat	1.97e+02
475	6	1.4	559	1	A35029	t-plasminogen activat	1.97e+02
476	6	1.4	559	1	A29941	t-plasminogen activat	1.97e+02
477	6	1.4	564	2	S01110	potassium channel pro	1.97e+02
478	6	1.4	564	2	B69860	hypothetical protein	1.97e+02
479	6	1.4	566	2	S54629	hypothetical protein	1.97e+02
480	6	1.4	568	2	S42225	major envelope glycop	1.97e+02
481	6	1.4	568	2	T16024	hypothetical protein	1.97e+02
482	6	1.4	570	1	C69985	probable DNA-dependen	1.97e+02
483	6	1.4	572	1	S28762	gene DBP730 protein -	1.97e+02
484	6	1.4	572	1	B43675	64k protein - infecti	1.97e+02
485	6	1.4	573	2	S12838	Ig mu chain precursor	1.97e+02
486	6	1.4	574	2	S37762	225k protein - Babesi	1.97e+02
487	6	1.4	574	2	B29677	complement C9 precurs	1.97e+02
488	6	1.4	574	2	T05002	probable gamma-glutam	1.97e+02
489	6	1.4	575	1	JH0827	glutamate decarboxyla	1.97e+02
490	6	1.4	576	2	T12896	probable single-stran	1.97e+02
491	6	1.4	581	2	T04844	probable serine/threo	1.97e+02
492	6	1.4	581	2	S60159	serine/threonine-spec	1.97e+02
493	6	1.4	589	2	S33078	GIL protein - variola	1.97e+02
494	6	1.4	591	2	F42511	GIL protein - vaccini	1.97e+02
495	6	1.4	593	2	F64523	hypothetical protein	1.97e+02
496	6	1.4	594	2	E71441	LI protein (alternat	1.97e+02
497	6	1.4	599	2	S64136	methylene tetrahydrof	1.97e+02
498	6	1.4	601	2	G70983	probable glycosyl hyd	1.97e+02
499	6	1.4	602	2	A44409	gamma-aminobutyric ac	1.97e+02
500	6	1.4	602	2	A45078	gamma-aminobutyric ac	1.97e+02
501	6	1.4	604	2	T12651	NADH dehydrogenase su	1.97e+02
502	6	1.4	605	2	E71441	hypothetical protein	1.97e+02
503	6	1.4	606	2	S14942	RNA helicase SPB - y	1.97e+02
504	6	1.4	606	2	B69805	conserved hypothetical	1.97e+02
505	6	1.4	609	2	I38596	calcium-activated pot	1.97e+02
506	6	1.4	616	2	S00479	potassium channel pro	1.97e+02
507	6	1.4	619	2	A72114	s/t protein kinase -	1.97e+02
508	6	1.4	620	2	T16657	hypothetical protein	1.97e+02
509	6	1.4	626	2	S53871	pmei 17 protein - mou	1.97e+02
510	6	1.4	627	2	E70122	flagellar hook-associ	1.97e+02
511	6	1.4	627	2	S50583	hypothetical protein	1.97e+02
512	6	1.4	629	2	A46500	ly 9.2 antigen - mous	1.97e+02
513	6	1.4	629	2	S42629	keratin K3 - rabbit	1.97e+02
514	6	1.4	632	2	T00325	hypothetical protein	1.97e+02
515	6	1.4	632	2	A25784	hypothetical 70k prot	1.97e+02
516	6	1.4	633	2	C70358	hydrogenase (EC 1.18	1.97e+02
517	6	1.4	633	2	S57714	csbp protein - Clostr	1.97e+02
518	6	1.4	638	1	KORPL	plasma kallikrein (EC	1.97e+02
519	6	1.4	638	1	KOHUP	plasma kallikrein (EC	1.97e+02
520	6	1.4	638	2	S36546	El protein - human pa	1.97e+02
521	6	1.4	639	2	S48959	mitochondrial outer m	1.97e+02
522	6	1.4	642	2	I39839	beta-hexosaminidase h	1.97e+02
523	6	1.4	643	2	B75055	hypothetical protein	1.97e+02
524	6	1.4	643	2	S00480	potassium channel pro	1.97e+02
525	6	1.4	647	1	ESRCPC	2',3'-cyclic-nucleot	1.97e+02
526	6	1.4	649	2	S33813	kinesin light chain -	1.97e+02
527	6	1.4	651	2	S35708	NADH oxidase - Thermo	1.97e+02
528	6	1.4	651	2	S25102	NADH oxidase - Thermo	1.97e+02
529	6	1.4	652	1	S52695	2',3'-cyclic-nucleot	1.97e+02
530	6	1.4	653	2	C70742	probable rsbu protein	1.97e+02
531	6	1.4	653	2	T16553	hypothetical protein	1.97e+02
532	6	1.4	656	2	JH0193	potassium channel sha	1.97e+02
533	6	1.4	656	2	A64208	exonuclease ABC chal	1.97e+02
534	6	1.4	656	2	A71916	DNA ligase - Helicoba	1.97e+02

535	6	1.4	657	2	S73946	excinuclease ABC chai	1.97e+02	608	6	1.4	700	2	T13661	NADH dehydrogenase su	1.97e+02
536	6	1.4	657	2	S25184	cspl1 protein - Coryne	1.97e+02	609	6	1.4	701	2	T12296	NADH dehydrogenase su	1.97e+02
537	6	1.4	658	2	A64584	hypothetical protein	1.97e+02	610	6	1.4	702	2	T13708	NADH dehydrogenase su	1.97e+02
538	6	1.4	660	2	S16159	dark-type molecular c	1.97e+02	611	6	1.4	702	2	A34434	atylporin alpha chai	1.97e+02
539	6	1.4	661	2	A23398	dark-type molecular c	1.97e+02	612	6	1.4	704	2	T13729	NADH dehydrogenase su	1.97e+02
540	6	1.4	664	2	C71106	hypothetical protein	1.97e+02	613	6	1.4	704	2	T13581	NADH dehydrogenase su	1.97e+02
541	6	1.4	664	2	OKHOAP	alcohol oxidase (EC 1	1.97e+02	614	6	1.4	705	2	T12152	NADH dehydrogenase su	1.97e+02
542	6	1.4	667	2	S74254	homeotic protein stx5	1.97e+02	615	6	1.4	705	2	T13494	NADH dehydrogenase su	1.97e+02
543	6	1.4	667	2	T13566	tail protein - phage	1.97e+02	616	6	1.4	706	2	C71929	hypothetical protein	1.97e+02
544	6	1.4	669	2	D70369	ATP-dependent DNA hel	1.97e+02	617	6	1.4	711	2	B64169	phosphate acetyltrans	1.97e+02
545	6	1.4	670	2	T02092	beta-fructofuranosida	1.97e+02	618	6	1.4	716	2	E63672	penicillin-binding pr	1.97e+02
546	6	1.4	675	2	S46952	phosphotransferase su	1.97e+02	619	6	1.4	718	2	T05840	subtilisin-like prote	1.97e+02
547	6	1.4	677	2	S33814	kinesin light chain -	1.97e+02	620	6	1.4	719	2	T13793	NADH dehydrogenase su	1.97e+02
548	6	1.4	681	2	T13566	NADH dehydrogenase	1.97e+02	621	6	1.4	719	2	T139815	NADH dehydrogenase su	1.97e+02
549	6	1.4	681	2	S73550	DNA polymerase III ga	1.97e+02	622	6	1.4	719	2	T10590	insecticidal protein	1.97e+02
550	6	1.4	682	2	T12715	NADH dehydrogenase su	1.97e+02	623	6	1.4	719	2	T10590	insecticidal protein	1.97e+02
551	6	1.4	682	2	T12294	NADH dehydrogenase	1.97e+02	624	6	1.4	719	2	S25383	insecticidal protein	1.97e+02
552	6	1.4	683	2	T12295	NADH dehydrogenase	1.97e+02	625	6	1.4	721	2	T12212	parasporal crystal pr	1.97e+02
553	6	1.4	683	2	T12123	NADH dehydrogenase	1.97e+02	626	6	1.4	725	2	T05016	NADH dehydrogenase	1.97e+02
554	6	1.4	684	2	T13491	NADH dehydrogenase	1.97e+02	627	6	1.4	726	2	T12216	hyaluronan receptor	1.97e+02
555	6	1.4	684	2	T12151	NADH dehydrogenase	1.97e+02	628	6	1.4	726	2	T12215	NADH dehydrogenase	1.97e+02
556	6	1.4	684	2	T13695	NADH dehydrogenase su	1.97e+02	629	6	1.4	727	2	T12221	NADH dehydrogenase	1.97e+02
557	6	1.4	686	2	T13234	NADH dehydrogenase	1.97e+02	630	6	1.4	728	2	S04641	NADH dehydrogenase	1.97e+02
558	6	1.4	686	2	T13252	NADH dehydrogenase	1.97e+02	631	6	1.4	728	2	T13794	NADH dehydrogenase	1.97e+02
559	6	1.4	686	2	T13235	NADH dehydrogenase	1.97e+02	632	6	1.4	729	2	T12227	NADH dehydrogenase	1.97e+02
560	6	1.4	686	2	T13768	NADH dehydrogenase	1.97e+02	633	6	1.4	730	2	T12224	NADH dehydrogenase	1.97e+02
561	6	1.4	686	2	T13766	NADH dehydrogenase	1.97e+02	634	6	1.4	731	2	T14231	NADH dehydrogenase	1.97e+02
562	6	1.4	686	2	S33815	kinesin light chain 1	1.97e+02	635	6	1.4	731	2	T12226	NADH dehydrogenase	1.97e+02
563	6	1.4	686	2	T10969	DNA topoisomerase (AT	1.97e+02	636	6	1.4	732	2	T14233	NADH dehydrogenase	1.97e+02
564	6	1.4	686	2	S36727	kinesin light chain 1	1.97e+02	637	6	1.4	732	2	T13814	NADH dehydrogenase	1.97e+02
565	6	1.4	687	2	D57713	chloride channel CIC-	1.97e+02	638	6	1.4	732	2	T12194	NADH dehydrogenase	1.97e+02
566	6	1.4	688	2	T13242	NADH dehydrogenase	1.97e+02	639	6	1.4	733	2	T12213	NADH dehydrogenase	1.97e+02
567	6	1.4	688	2	T13237	NADH dehydrogenase	1.97e+02	640	6	1.4	734	2	T13785	NADH dehydrogenase	1.97e+02
568	6	1.4	688	2	T13243	NADH dehydrogenase	1.97e+02	641	6	1.4	735	2	E69139	hypothetical protein	1.97e+02
569	6	1.4	688	2	T13248	NADH dehydrogenase	1.97e+02	642	6	1.4	736	2	T12218	NADH dehydrogenase	1.97e+02
570	6	1.4	688	2	T13253	NADH dehydrogenase	1.97e+02	643	6	1.4	736	2	T12217	NADH dehydrogenase	1.97e+02
571	6	1.4	688	2	T13278	NADH dehydrogenase	1.97e+02	644	6	1.4	736	2	T12214	NADH dehydrogenase	1.97e+02
572	6	1.4	688	2	T09604	NADH dehydrogenase	1.97e+02	645	6	1.4	736	2	E71414	NADH dehydrogenase	1.97e+02
573	6	1.4	688	2	T13249	NADH dehydrogenase	1.97e+02	646	6	1.4	736	2	T12225	NADH dehydrogenase	1.97e+02
574	6	1.4	688	2	T13373	NADH dehydrogenase	1.97e+02	647	6	1.4	737	2	T12193	NADH dehydrogenase	1.97e+02
575	6	1.4	688	2	T13282	NADH dehydrogenase	1.97e+02	648	6	1.4	738	2	T14230	NADH dehydrogenase	1.97e+02
576	6	1.4	688	2	T09836	NADH dehydrogenase	1.97e+02	649	6	1.4	738	2	T12192	NADH dehydrogenase	1.97e+02
577	6	1.4	689	2	T13280	NADH dehydrogenase	1.97e+02	650	6	1.4	740	2	T12223	NADH dehydrogenase	1.97e+02
578	6	1.4	689	2	T13681	NADH dehydrogenase	1.97e+02	651	6	1.4	740	2	T12753	NADH dehydrogenase	1.97e+02
579	6	1.4	690	2	T12763	NADH dehydrogenase	1.97e+02	652	6	1.4	740	2	DENTN5	NADH dehydrogenase	1.97e+02
580	6	1.4	691	2	S28222	myeloperoxidase (EC 1	1.97e+02	653	6	1.4	741	2	T13791	NADH dehydrogenase	1.97e+02
581	6	1.4	692	2	T12293	NADH dehydrogenase	1.97e+02	654	6	1.4	742	2	VCBEHT	glycoprotein H precur	1.97e+02
582	6	1.4	693	2	T12587	NADH dehydrogenase su	1.97e+02	655	6	1.4	743	2	VCBEHC	glycoprotein H precur	1.97e+02
583	6	1.4	693	2	T149709	GTPase-activating pro	1.97e+02	656	6	1.4	747	2	S47327	chloride channel prot	1.97e+02
584	6	1.4	696	2	S44912	hypothetical protein	1.97e+02	657	6	1.4	747	2	T18294	gene clcd4 protein -	1.97e+02
585	6	1.4	697	2	T13754	NADH dehydrogenase	1.97e+02	658	6	1.4	747	2	W2BE45	gene 45 protein - hum	1.97e+02
586	6	1.4	697	2	T12563	large T antigen - lym	1.97e+02	659	6	1.4	755	2	R72061	eye cell development	1.97e+02
587	6	1.4	698	2	T12563	NADH dehydrogenase su	1.97e+02	660	6	1.4	760	2	A45174	chloride channel	1.97e+02
588	6	1.4	698	2	T12560	NADH dehydrogenase su	1.97e+02	661	6	1.4	760	2	T137242	anthranilate synthase	1.97e+02
589	6	1.4	698	2	T12559	NADH dehydrogenase su	1.97e+02	662	6	1.4	762	2	NNNC2	PRK1 protein - yeast	1.97e+02
590	6	1.4	698	2	T12565	NADH dehydrogenase su	1.97e+02	663	6	1.4	763	2	A29562	subtilisin-like prote	1.97e+02
591	6	1.4	698	2	T12564	NADH dehydrogenase su	1.97e+02	664	6	1.4	769	2	T05839	subtilisin-like prote	1.97e+02
592	6	1.4	698	2	T12567	NADH dehydrogenase su	1.97e+02	665	6	1.4	772	2	T05838	subtilisin-like prote	1.97e+02
593	6	1.4	698	2	T12569	NADH dehydrogenase su	1.97e+02	666	6	1.4	773	2	H70108	phenylalanine--tRNA 1	1.97e+02
594	6	1.4	698	2	T12590	NADH dehydrogenase su	1.97e+02	667	6	1.4	790	2	H71509	retrovirus-related po	1.97e+02
595	6	1.4	698	2	T12586	NADH dehydrogenase su	1.97e+02	668	6	1.4	806	2	T08932	hypothetical protein	1.97e+02
596	6	1.4	698	2	T12586	NADH dehydrogenase su	1.97e+02	669	6	1.4	814	2	GNSNIP	hypothetical protein	1.97e+02
597	6	1.4	698	2	T12588	NADH dehydrogenase su	1.97e+02	670	6	1.4	815	2	H69775	hypothetical protein	1.97e+02
598	6	1.4	698	2	T12588	NADH dehydrogenase su	1.97e+02	671	6	1.4	817	2	S53921	hypothetical protein	1.97e+02
599	6	1.4	699	2	T13772	NADH dehydrogenase su	1.97e+02	672	6	1.4	826	2	F64746	probable membrane pro	1.97e+02
600	6	1.4	699	2	T13778	NADH dehydrogenase su	1.97e+02	673	6	1.4	828	2	T08556	hypothetical protein	1.97e+02
601	6	1.4	699	2	G70142	DNA helicase (uvrD) h	1.97e+02	674	6	1.4	830	2	A57060	setine/threonine-spec	1.97e+02
602	6	1.4	700	2	T13470	NADH dehydrogenase su	1.97e+02	675	6	1.4	830	2	B44047	glycoprotein B precur	1.97e+02
603	6	1.4	700	2	T13726	NADH dehydrogenase su	1.97e+02	676	6	1.4	830	2	A44047	glycoprotein B precur	1.97e+02
604	6	1.4	700	2	T13763	NADH dehydrogenase su	1.97e+02	677	6	1.4	831	2	S39835	hypothetical protein	1.97e+02
605	6	1.4	700	2	T13702	NADH dehydrogenase su	1.97e+02	678	6	1.4	831	2	G71659	translational initiatio	1.97e+02
606	6	1.4	700	2	T13668	NADH dehydrogenase su	1.97e+02	679	6	1.4	839	2	F64171	hypothetical protein	1.97e+02
607	6	1.4	700	2	T12589	NADH dehydrogenase su	1.97e+02	680	6	1.4	840	2	H71114	probable cell divisio	1.97e+02

681	6	1.4	882	2	T05400	hypothetical protein	1.97e+02	754	6	1.4	1325	2	S64497	hypothetical protein	1.97e+02
682	6	1.4	882	2	T16198	hypothetical protein	1.97e+02	755	6	1.4	1332	2	F69732	PRK phage ORF xkd	1.97e+02
683	6	1.4	844	2	T50159	anion transporter - c	1.97e+02	756	6	1.4	1358	2	A29360	S14 protein - yeast	1.97e+02
684	6	1.4	888	2	A43810	band 3 anion transport	1.97e+02	757	6	1.4	1379	2	JC5778	apoptosis signal-regu	1.97e+02
685	6	1.4	882	1	A49346	aldehyde dehydrogenas	1.97e+02	758	6	1.4	1391	2	S50608	hypothetical protein	1.97e+02
686	6	1.4	869	1	S45757	replication licensing	1.97e+02	759	6	1.4	1429	2	S06434	homeotic protein lin-	1.97e+02
687	6	1.4	868	1	S49844	probable membrane pro	1.97e+02	760	6	1.4	1444	1	A30588	140K adhesin precurs	1.97e+02
688	6	1.4	872	2	B75073	ATP-dependent RNA hel	1.97e+02	761	6	1.4	1445	1	T10728	probable gag/pol poly	1.97e+02
689	6	1.4	885	2	S33015	hypothetical protein	1.97e+02	762	6	1.4	1473	2	S53599	tumor suppressor (AT	1.97e+02
690	6	1.4	885	2	S22389	acetylglutamate kinas	1.97e+02	763	6	1.4	1477	2	T13797	DNA topoisomerase	1.97e+02
691	6	1.4	892	2	H71558	probable initiation f	1.97e+02	764	6	1.4	1495	2	S27001	tumor suppressor prote	1.97e+02
692	6	1.4	896	2	H70233	hypothetical protein	1.97e+02	765	6	1.4	1497	2	S72250	alpha-2-macroglobulin	1.97e+02
693	6	1.4	909	2	S64038	probable membrane pro	1.97e+02	766	6	1.4	1548	1	DVANS	sex-determining trans	1.97e+02
694	6	1.4	919	2	IS3474	kinase receptor - ra	1.97e+02	767	6	1.4	1556	2	S59393	multidrug resistance	1.97e+02
695	6	1.4	919	2	JC5934	exostosin-related prot	1.97e+02	768	6	1.4	1589	1	RCBYC5	probable membrane pro	1.97e+02
696	6	1.4	919	2	JC5934	glutamate receptor GL	1.97e+02	769	6	1.4	1596	2	A35927	cell division control	1.97e+02
697	6	1.4	922	2	A30810	band 3 anion transport	1.97e+02	770	6	1.4	1602	2	H70988	190K DNA-binding prot	1.97e+02
698	6	1.4	925	2	A55748	protein kinase (EC 2.	1.97e+02	771	6	1.4	1608	2	S52586	probable polyketide s	1.97e+02
699	6	1.4	929	2	A25314	band 3 protein (EC 2.	1.97e+02	772	6	1.4	1678	2	S52586	clathrin heavy chain	1.97e+02
700	6	1.4	932	2	S76501	preprotein translocas	1.97e+02	773	6	1.4	1701	2	T09127	probable erythrocyte	1.97e+02
701	6	1.4	944	2	S66336	vacuolar protein-sort	1.97e+02	774	6	1.4	1736	2	S54784	sex-limited protein S	1.97e+02
702	6	1.4	946	1	JC5667	multidrug resistance	1.97e+02	775	6	1.4	1738	1	A29176	complement C4 precus	1.97e+02
703	6	1.4	953	2	S19427	probable membrane pro	1.97e+02	776	6	1.4	1745	2	A46431	tight junction associ	1.97e+02
704	6	1.4	955	2	A60990	alpha-amylase (EC 3.2	1.97e+02	777	6	1.4	1762	2	T03222	probable polyketide s	1.97e+02
705	6	1.4	956	2	JS0685	glutamate receptor ch	1.97e+02	778	6	1.4	1763	1	RRWF9	genome polyprotein -	1.97e+02
706	6	1.4	966	2	JH0826	glutamate ionotropic	1.97e+02	779	6	1.4	1774	2	B56101	collagen alpha 1(XVII	1.97e+02
707	6	1.4	973	2	F72076	polymorphic outer mem	1.97e+02	780	6	1.4	1894	2	JC4980	plexin.1 precursor -	1.97e+02
708	6	1.4	977	2	T16232	hypothetical protein	1.97e+02	781	6	1.4	2061	2	T13751	transcription factor -	1.97e+02
709	6	1.4	984	2	A41996	NF-kappa-B p50 subun	1.97e+02	782	6	1.4	2100	2	T03223	probable polyketide s	1.97e+02
710	6	1.4	985	1	VCLJSP	env polyprotein - hum	1.97e+02	783	6	1.4	2126	2	H70621	probable polyketide s	1.97e+02
711	6	1.4	987	2	S62752	probable DNA-directed	1.97e+02	784	6	1.4	2139	2	A35672	crumbs protein - frul	1.97e+02
712	6	1.4	992	2	A31666	hypothetical protein	1.97e+02	785	6	1.4	2157	2	S57461	protein-rich protein	1.97e+02
713	6	1.4	1002	2	T56963	transposase - Escheri	1.97e+02	786	6	1.4	2292	2	S55401	capsid polyprotein -	1.97e+02
714	6	1.4	1002	2	G70876	probable transmembran	1.97e+02	787	6	1.4	2292	1	GNNYE	genome polyprotein -	1.97e+02
715	6	1.4	1005	2	A42265	alpha-mannosidase (EC	1.97e+02	788	6	1.4	2292	1	GNNYE	genome polyprotein -	1.97e+02
716	6	1.4	1008	2	S72698	transport protein tpi	1.97e+02	789	6	1.4	2311	1	TVCHSR	kinase-related protei	1.97e+02
717	6	1.4	1026	2	A48895	paracrystalline surfa	1.97e+02	790	6	1.4	2366	2	S10317	toxlin B - Clostridium	1.97e+02
718	6	1.4	1039	2	S76747	hypothetical protein	1.97e+02	791	6	1.4	2367	2	S70172	toxlin B - Clostridium	1.97e+02
719	6	1.4	1040	2	T08190	COPII-like protein - A	1.97e+02	792	6	1.4	2524	2	A35844	Xorch protein - Afri	1.97e+02
720	6	1.4	1044	2	DVBEX3	translation elongatio	1.97e+02	793	6	1.4	2663	1	S28261	centromere protein E	1.97e+02
721	6	1.4	1044	2	S62926	probable membrane pro	1.97e+02	794	6	1.4	2723	2	T03221	probable polyketide s	1.97e+02
722	6	1.4	1050	2	S25363	translation elongatio	1.97e+02	795	6	1.4	2793	2	A64356	toxlin-like outer memb	1.97e+02
723	6	1.4	1051	2	A35761	cell surface glycopro	1.97e+02	796	6	1.4	2902	2	C71993	toxlin-like outer memb	1.97e+02
724	6	1.4	1055	2	H70951	hypothetical protein	1.97e+02	797	6	1.4	3020	2	A43932	muslin-2 precursor, in	1.97e+02
725	6	1.4	1056	2	A53767	tracheobronchial muc	1.97e+02	798	6	1.4	3187	2	JC5837	36AK Gold complex-as	1.97e+02
726	6	1.4	1064	2	S74861	hypothetical protein	1.97e+02	799	6	1.4	3268	2	S69625	hypothetical protein	1.97e+02
727	6	1.4	1070	1	RNNTR	DNA-directed RNA poly	1.97e+02	800	6	1.4	3411	1	GNNYV	genome polyprotein -	1.97e+02
728	6	1.4	1073	1	SYECP	cardamoyl phosphate s	1.97e+02	801	6	1.4	3411	1	GNNYV	genome polyprotein -	1.97e+02
729	6	1.4	1074	2	T04777	hypothetical protein	1.97e+02	802	6	1.4	3898	1	GNNVBP	genome polyprotein -	1.97e+02
730	6	1.4	1081	2	S15040	cellulotrophic drug resi	1.97e+02	803	6	1.4	3898	2	S58295	polyprotein - hog cho	1.97e+02
731	6	1.4	1087	1	S41797	cellulose 1,4-beta-ce	1.97e+02	804	6	1.4	3898	2	S57437	genome polyprotein -	1.97e+02
732	6	1.4	1113	2	S62904	calcium-regulated pot	1.97e+02	805	6	1.4	4092	1	S38128	dynein heavy chain, c	1.97e+02
733	6	1.4	1118	2	S46441	hypothetical protein	1.97e+02	806	6	1.4	4351	2	T00252	MEF1 protein - rat	1.97e+02
734	6	1.4	1120	2	T14275	myosin-like protein m	1.97e+02	807	6	1.4	4367	2	S72269	lysandine receptor is	1.97e+02
735	6	1.4	1132	2	JC4127	protein-tyrosine kina	1.97e+02	808	6	1.4	4969	2	A37113	tyrosine kinase recep	1.97e+02
736	6	1.4	1132	2	JM0091	Janus kinase (EC 2.7.	1.97e+02	809	6	1.4	5170	2	T15348	hypothetical protein	1.97e+02
737	6	1.4	1171	2	S57829	genome polyprotein -	1.97e+02	810	6	1.4	5639	2	S57242	twitcln - Caenorhabd	1.97e+02
738	6	1.4	1175	2	S51005	protein-tyrosine-phos	1.97e+02	811	6	1.4	26926	1	T18344	titin, cardiac muscle	1.97e+02
739	6	1.4	1176	2	IS5845	calcium-activated phos	1.97e+02	812	6	1.4	69	2	C72262	hypothetical protein	1.97e+02
740	6	1.4	1184	2	I49017	calcium-activated pot	1.97e+02	813	6	1.4	77	2	S76483	hypothetical protein	1.97e+02
741	6	1.4	1194	1	G70837	probable ABC transport	1.97e+02	814	6	1.4	82	2	E36787	hypothetical protein	1.97e+02
742	6	1.4	1196	2	A48206	calcium-activated pot	1.97e+02	815	6	1.4	86	2	S71636	acyl carrier protein	1.97e+02
743	6	1.4	1205	2	A55015	bumetanide-sensitive	1.97e+02	816	6	1.4	95	2	S55624	hypothetical protein	1.97e+02
744	6	1.4	1209	1	DNBEC4	DNA-binding protein -	1.97e+02	817	6	1.4	104	2	G49897	conserved hypotetica	1.97e+02
745	6	1.4	1212	2	A57187	bumetanide-sensitive	1.97e+02	818	6	1.4	114	2	S09753	hypothetical protein	1.97e+02
746	6	1.4	1234	2	S72640	endo-1,4-beta-xylanas	1.97e+02	819	6	1.4	118	2	B64630	hypothetical protein	1.97e+02
747	6	1.4	1246	2	JM0406	hypothetical protein	1.97e+02	820	6	1.4	122	2	S49638	transcription factor	1.97e+02
748	6	1.4	1274	2	JM0015	trp protein - fruit f	1.97e+02	821	6	1.4	125	2	S05042	transcription factor	1.97e+02
749	6	1.4	1275	2	TJ0092	trp protein - fruit f	1.97e+02	822	6	1.4	133	2	A41298	kinasin-like protein	1.97e+02
750	6	1.4	1285	2	T14171	ataxin-2 - mouse	1.97e+02	823	6	1.4	147	1	NR02	pancreatic ribonuclea	1.97e+02
751	6	1.4	1285	2	T14171	P-glycoprotein ppl	1.97e+02	824	6	1.4	152	2	T12249	major latex protein h	1.97e+02
752	6	1.4	1304	2	T14073	dynein lb heavy chain	1.97e+02	825	6	1.4	154	1	A55692	anaerobic ribonucleot	1.97e+02
753	6	1.4	1315	2	A56101	collagen alpha 1(XVII	1.97e+02	826	6	1.4	164	2	T04115	isocitrate lyase (EC	1.97e+02

827	5	1.1	168	2	S16800	hypothetical protein	4.87e+03	900	5	1.1	470	2	S30598	H+ transp. ATP s	4.87e+03
828	5	1.1	172	2	G70443	conserved hypothetical	4.87e+03	901	5	1.1	471	1	RKRRL2	ribulose-bisphosphate	4.87e+03
829	5	1.1	173	2	H69644	translation initiation	4.87e+03	902	5	1.1	472	2	JS00623	site-specific DNA-met	4.87e+03
830	5	1.1	180	2	E71929	heat shock protein	4.87e+03	903	5	1.1	473	2	S59984	hypd. protein - Rhodob	4.87e+03
831	5	1.1	180	2	C64584	heat shock protein	4.87e+03	904	5	1.1	473	2	A55975	gamma-aminobutyric ac	4.87e+03
832	5	1.1	184	1	F588	phaseolin - kidney be	4.87e+03	905	5	1.1	480	2	G36213	F3L protein - vaccini	4.87e+03
833	5	1.1	184	2	A42319	light-harvesting and	4.87e+03	906	5	1.1	498	1	VHIV61	nucleoprotein - Infl	4.87e+03
834	5	1.1	188	2	A42957	carbon monoxide-induc	4.87e+03	907	5	1.1	498	1	S11150	smc protein - Strept	4.87e+03
835	5	1.1	193	2	S70279	outer surface protein	4.87e+03	908	5	1.1	501	1	RGE008	sensor protein ubp	4.87e+03
836	5	1.1	205	2	S59048	phosphoribosylanthran	4.87e+03	909	5	1.1	510	2	A56142	phosphoglycerate muca	4.87e+03
837	5	1.1	208	2	B70174	hypothetical protein	4.87e+03	910	5	1.1	522	2	B71926	cag island protein -	4.87e+03
838	5	1.1	219	2	B43664	phosphoribosylanthran	4.87e+03	911	5	1.1	526	2	S34945	nitrogenase (EC 1.18	4.87e+03
839	5	1.1	225	2	S23568	adenylate kinase (EC	4.87e+03	912	5	1.1	527	2	A36695	catalase (EC 1.11.1.6	4.87e+03
840	5	1.1	241	2	F51211	cytoskeletal protein	4.87e+03	913	5	1.1	528	2	H70163	phenylalanine--trna	4.87e+03
841	5	1.1	247	1	PWPM46	H+ transp. ATP s	4.87e+03	914	5	1.1	529	2	S57345	m-impotin (nuclear p	4.87e+03
842	5	1.1	247	1	PWSP46	H+ transp. ATP s	4.87e+03	915	5	1.1	531	2	I38607	p53-binding protein 2	4.87e+03
843	5	1.1	248	2	S34995	surface lipoprotein p	4.87e+03	916	5	1.1	535	2	A44475	N-acetylglucosamine	4.87e+03
844	5	1.1	253	2	H72388	shikimate 5-dehydroge	4.87e+03	917	5	1.1	536	1	C64728	probable membrane pro	4.87e+03
845	5	1.1	253	2	T04435	hypothetical protein	4.87e+03	918	5	1.1	536	1	D70184	probable pyrrolone-5-	4.87e+03
846	5	1.1	262	2	S24727	ornithine carbamoylitr	4.87e+03	919	5	1.1	543	1	C70877	transcription factor	4.87e+03
847	5	1.1	265	2	C72287	hypothetical protein	4.87e+03	920	5	1.1	549	2	S53427	protein-tyrosine-phos	4.87e+03
848	5	1.1	268	2	E64613	cell division membran	4.87e+03	921	5	1.1	550	2	I55679	integral membrane pro	4.87e+03
849	5	1.1	270	2	S74993	hypothetical protein	4.87e+03	922	5	1.1	552	2	S53427	dihydroxyacid dehydrat	4.87e+03
850	5	1.1	273	2	A43862	29k peripheral membra	4.87e+03	923	5	1.1	553	2	RN256	hemagglutinin precurs	4.87e+03
851	5	1.1	278	2	G65165	DNA-damage-inducible	4.87e+03	924	5	1.1	563	1	HM1VSV	polymerase-associated	4.87e+03
852	5	1.1	288	2	B72272	liron-sulfur cluster-b	4.87e+03	925	5	1.1	568	2	RN256	GRSAG protein - tyrp	4.87e+03
853	5	1.1	295	2	JC5671	methionyl aminopeptid	4.87e+03	926	5	1.1	572	2	S14200	phosphotransferase sy	4.87e+03
854	5	1.1	296	2	I40264	outer surface protein	4.87e+03	927	5	1.1	572	2	B28474	ABC transporter, ATP	4.87e+03
855	5	1.1	303	2	JQ1386	hypothetical 33k prot	4.87e+03	928	5	1.1	577	2	C72275	type II secretion pat	4.87e+03
856	5	1.1	309	2	I41075	hypothetical protein	4.87e+03	929	5	1.1	585	2	T00212	hypothetical protein	4.87e+03
857	5	1.1	319	2	JH0135	site-specific DNA-met	4.87e+03	930	5	1.1	590	2	A35928	hypothetical 86k prot	4.87e+03
858	5	1.1	320	2	S75911	genome polypeptide	4.87e+03	931	5	1.1	597	2	B36789	cell division-regulated	4.87e+03
859	5	1.1	322	2	T11127	hypothetical protein	4.87e+03	932	5	1.1	601	2	A65120	glutathione-S-transfer	4.87e+03
860	5	1.1	325	2	H72329	NADH dehydrogenase (u	4.87e+03	933	5	1.1	615	2	D64714	cell division protein	4.87e+03
861	5	1.1	332	2	S06424	phenylalanine--trna	4.87e+03	934	5	1.1	616	2	T14235	NADH dehydrogenase su	4.87e+03
862	5	1.1	334	2	S47762	MHC class I histocomp	4.87e+03	935	5	1.1	640	2	S35734	DNA topoisomerase (AT	4.87e+03
863	5	1.1	334	2	D22735	hypothetical nox p	4.87e+03	936	5	1.1	645	1	SUBSMP	serine proteinase (EC	4.87e+03
864	5	1.1	341	2	H36841	E5R protein - variola	4.87e+03	937	5	1.1	649	2	S11163	endopeptidase Clp ATP	4.87e+03
865	5	1.1	344	2	S73555	MG415 homolog C12-orf	4.87e+03	938	5	1.1	652	2	S58666	protein kinase aspl	4.87e+03
866	5	1.1	344	2	T03499	integrase/recombinase	4.87e+03	939	5	1.1	668	2	D72278	histidine kinase - Ha	4.87e+03
867	5	1.1	345	2	S30579	succinate--COA ligase	4.87e+03	940	5	1.1	669	2	A50524	endo-1,4-beta-mannosi	4.87e+03
868	5	1.1	360	2	F63333	chorismate synthase (	4.87e+03	941	5	1.1	672	2	B45771	hypothetical protein	4.87e+03
869	5	1.1	363	1	A47620	3-isopropylmalate deh	4.87e+03	942	5	1.1	676	2	B72071	riboonuclease family	4.87e+03
870	5	1.1	364	1	ADCHB	fructose-bisphosphate	4.87e+03	943	5	1.1	679	2	R45771	2-5A-dependent RNAse	4.87e+03
871	5	1.1	365	1	S77963	MHC class I histocomp	4.87e+03	944	5	1.1	706	2	S28042	hemlin receptor precu	4.87e+03
872	5	1.1	365	1	A43324	3-isopropylmalate deh	4.87e+03	945	5	1.1	723	2	J02210	probable nucleic acid	4.87e+03
873	5	1.1	367	2	S65512	Rckbeta2 protein - ra	4.87e+03	946	5	1.1	725	2	A49613	enoyl-CoA hydratase (	4.87e+03
874	5	1.1	367	2	S65502	potassiun channel sha	4.87e+03	947	5	1.1	725	2	A57148	outer membrane protei	4.87e+03
875	5	1.1	373	2	JQ1646	SHL2 protein - human	4.87e+03	948	5	1.1	728	2	E69486	translation elongatio	4.87e+03
876	5	1.1	373	2	A69847	cystathionine gamma-s	4.87e+03	949	5	1.1	731	2	E36841	E2L protein - variola	4.87e+03
877	5	1.1	380	2	S75348	hypothetical protein	4.87e+03	950	5	1.1	747	2	A27892	translation initiatio	4.87e+03
878	5	1.1	381	2	S44094	beta-lactamase (EC 3	4.87e+03	951	5	1.1	754	2	A53679	endothelin convertin	4.87e+03
879	5	1.1	385	2	JC2298	RNA-binding protein H	4.87e+03	952	5	1.1	764	2	B54570	phenylalanine--trna	4.87e+03
880	5	1.1	386	1	KMECPM	chorismate mutase (EC	4.87e+03	953	5	1.1	764	2	S75407	probable DNA-directed	4.87e+03
881	5	1.1	386	1	C72013	succinyl-coa synthetase	4.87e+03	954	5	1.1	768	2	S04518	anthranilate synthase	4.87e+03
882	5	1.1	387	1	S26053	chromate mutase (EC	4.87e+03	955	5	1.1	781	2	A69312	DNA polymerase BI (po	4.87e+03
883	5	1.1	389	2	E71009	probable aspartate am	4.87e+03	956	5	1.1	788	1	S28302	ribonuclease-diphos	4.87e+03
884	5	1.1	393	2	D70858	hypothetical protein	4.87e+03	957	5	1.1	794	2	S73877	probable lipid-protein	4.87e+03
885	5	1.1	397	1	KMCMTC	major outer membrane	4.87e+03	958	5	1.1	803	1	A64070	endopeptidase La (EC	4.87e+03
886	5	1.1	402	2	A37049	myosin alpha heavy ch	4.87e+03	959	5	1.1	810	2	S49744	AMP deaminase (EC 3.5	4.87e+03
887	5	1.1	402	2	A70559	hypothetical protein	4.87e+03	960	5	1.1	824	2	T10020	leucine--trna ligase	4.87e+03
888	5	1.1	406	2	JS0343	tryptophan synthase (	4.87e+03	961	5	1.1	843	2	S44868	R05D3.7 protein - Cae	4.87e+03
889	5	1.1	407	2	C64167	hypothetical protein	4.87e+03	962	5	1.1	848	1	JC1351	transforming growth f	4.87e+03
890	5	1.1	417	2	A64380	phosphoglycerate kin	4.87e+03	963	5	1.1	852	2	D72230	conserved hypothetical	4.87e+03
891	5	1.1	418	2	S40824	hypothetical 48k prot	4.87e+03	964	5	1.1	904	2	S53836	DNA mismatch repair p	4.87e+03
892	5	1.1	422	2	S52790	glutamine--phenylpyp	4.87e+03	965	5	1.1	907	2	T04820	receptor tyrosine kin	4.87e+03
893	5	1.1	424	2	C64362	aconitate hydratase (	4.87e+03	966	5	1.1	913	2	A48280	surface-layer protein	4.87e+03
894	5	1.1	424	2	S09884	hypothetical protein	4.87e+03	967	5	1.1	917	2	S26365	progesterone receptor	4.87e+03
895	5	1.1	428	2	G70828	probable isocitrate 1	4.87e+03	968	5	1.1	933	1	ORHUP	probable cytochrome C	4.87e+03
896	5	1.1	429	2	T07809	S-receptor kinase (EC	4.87e+03	969	5	1.1	936	2	H1862	hypothetical protein	4.87e+03
897	5	1.1	433	2	G64594	hemolysin secretion p	4.87e+03	970	5	1.1	957	2	D64659	subtilisin-like prote	4.87e+03
898	5	1.1	460	2	C70576	probable mgtE protein	4.87e+03	971	5	1.1	962	2	JC5571	legumain-like prote	4.87e+03
899	5	1.1	466	2	JQ0077	gamma-aminobutylic ac	4.87e+03	972	5	1.1	965	2	S55658	legumain-like prote	4.87e+03

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973 5 1.1 985 1 DUBEL1 DNA-directed DNA poly 4.87e+03
974 5 1.1 1010 1 H+-transporting ATPas 4.87e+03
975 5 1.1 1020 2 A64641 cation efflux system 4.87e+03
976 5 1.1 1034 1 GNLICA pol polyprotein - hum 4.87e+03
977 5 1.1 1042 2 H70203 isoleucine--tRNA, 19g 4.87e+03
978 5 1.1 1072 2 A38457 integrin alpha 6 chal 4.87e+03
979 5 1.1 1156 2 A29125 parasporeal crystal br 4.87e+03
980 5 1.1 1175 2 C35815 myosin heavy chain 3 4.87e+03
981 5 1.1 1276 2 A34786 multidrug resistance 4.87e+03
982 5 1.1 1291 2 S05465 retrovirus-related po 4.87e+03
983 5 1.1 1318 1 Q08B1 membrane antigen p140 4.87e+03
984 5 1.1 1328 1 S04273 retrovirus-related re 4.87e+03
985 5 1.1 1358 2 A03905 genome polyprotein (v 4.87e+03
986 5 1.1 1371 1 VCBEM7 major capsid protein 4.87e+03
987 5 1.1 1409 1 OEFPCP copta polyprotein 4.87e+03
988 5 1.1 1464 1 S29159 glutamate receptor, N 4.87e+03
989 5 1.1 1588 1 BSVY1 ARO1 protein - yeast 4.87e+03
990 5 1.1 1694 2 J01896 hypothetical 191.1k p 4.87e+03
991 5 1.1 1729 2 A49282 fusion protein 1a/1b 4.87e+03
992 5 1.1 1734 2 A54602 microtubule-associate 4.87e+03
993 5 1.1 1869 1 S02771 myosin heavy chain A 4.87e+03
994 5 1.1 2188 2 A70984 probable polyketide s 4.87e+03
995 5 1.1 2201 2 S73014 polyketide synthase p 4.87e+03
996 5 1.1 2385 2 A32491 myosin heavy chain 1 4.87e+03
997 5 1.1 2469 2 H36812 hypothetical protein 4.87e+03
998 5 1.1 2796 2 JCA743 fatty acid synthase 4.87e+03
999 5 1.1 3524 2 S37431 ankyrin 2, neuronal 4.87e+03
1000 5 1.1 4452 1 YGHS62 gramicidin S syntheta 4.87e+03

```

## ALIGNMENTS

```

RESULT 1
ENTRY 1
TITLE A32694 #type complete
ORGANISM interferon alpha receptor precursor - human
DATE 22-Jun-1990 #sequence revision 22-Jun-1990 #text change
24-Sep-1998

```

```

ACCESSIONS
REFERENCE A32694
#authors Uze, G.; Lutfalla, G.; Gresser, I.
#journal Cell (1990) 60:225-234
#title Genetic transfer of a functional human interferon alpha
receptor into mouse cells: cloning and expression of its
cDNA.

```

```

#cross-references NUID:90124632

```

```

#accession A32694

```

```

#status preliminary

```

```

#molecule_type mRNA

```

```

#residues 1-557 #label UZE

```

```

#cross-references GB:J03171; NID:9184645; PID:906914

```

```

GENETICS GDB: IFNAR1; IFNAR; IFRC

```

```

#cross-references GDB:120078; OMIM:107450

```

```

#map position 21q22.1-21q22.1

```

```

KEYWORDS cytokine receptor; transmembrane protein

```

```

SUMMARY #length 557 #molecular_weight 63525; #checksum 7035

```

```

Query Match 100.0% Score 436; DB 2; Length 557;

```

```

Best Local Similarity 100.0% Pred. No. 0.00e+00; Indels 0; Gaps 0;

```

```

Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 1 MMYVLLGATTLVAVGVPMVLSAAGGKRLKSPKVEVDIIDNFIILMNRSDSEVGNT 60

```

```

Qy 1 MMYVLLGATTLVAVGVPMVLSAAGGKRLKSPKVEVDIIDNFIILMNRSDSEVGNT 60

```

```

Db 61 FSDYOKTGMDNWKILSCQNTSTKCNFSSILKNVEEIKIRIAKEKNTSSWTEVDSF 120

```

```

Qy 61 FSDYOKTGMDNWKILSCQNTSTKCNFSSILKNVEEIKIRIAKEKNTSSWTEVDSF 120

```

```

Db 61 FSDYOKTGMDNWKILSCQNTSTKCNFSSILKNVEEIKIRIAKEKNTSSWTEVDSF 120

```

```

Qy 61 FSDYOKTGMDNWKILSCQNTSTKCNFSSILKNVEEIKIRIAKEKNTSSWTEVDSF 120

```

```

Db 121 TPFRAOIGPPEVHLEADKALIVHISPGTKDSVMALDGLSFYSLLIMKSSGVEERI 180

```

```

Qy 121 TPFRAOIGPPEVHLEADKALIVHISPGTKDSVMALDGLSFYSLLIMKSSGVEERI 180

```

```

Db 121 TPFRAOIGPPEVHLEADKALIVHISPGTKDSVMALDGLSFYSLLIMKSSGVEERI 180

```

```

Qy 121 TPFRAOIGPPEVHLEADKALIVHISPGTKDSVMALDGLSFYSLLIMKSSGVEERI 180

```

```

Db 181 ENIYRHKIKYLSPEYTCYKAKALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240

```

```

Qy 181 ENIYRHKIKYLSPEYTCYKAKALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240

```

```

Db 241 NONVYLAQDYTAANNTPQVOMLAFLKRPNGHLKMKQIPDCENVKTKOCVFPQNVOK 300

```

```

Qy 241 NONVYLAQDYTAANNTPQVOMLAFLKRPNGHLKMKQIPDCENVKTKOCVFPQNVOK 300

```

```

Db 301 GYLIRVQASDQNTSFSSEIKFTEIOAFLPPVFNRISLSDSFHLYIGAPKOSGNT 360

```

```

Qy 301 GYLIRVQASDQNTSFSSEIKFTEIOAFLPPVFNRISLSDSFHLYIGAPKOSGNT 360

```

```

Db 361 VIQDPLIYEIIFMENTSNAERKIEKTDVTPMLKPLTYVCVAAHATMDEKLNKSSV 420

```

```

Qy 361 VIQDPLIYEIIFMENTSNAERKIEKTDVTPMLKPLTYVCVAAHATMDEKLNKSSV 420

```

```

Db 421 FSDVCEKTKPGNTSK 436

```

```

Qy 421 FSDVCEKTKPGNTSK 436

```

```

RESULT 2
ENTRY 2
TITLE SI7112 #type complete
ORGANISM interferon alpha/beta receptor - human
DATE 20-Feb-1995 #sequence revision 20-Feb-1995 #text change
30-May-1997

```

```

ACCESSIONS
REFERENCE SI7112
#authors Lutfalla, G.; Gardiner, X.Y.Z.; Proudoun, D.; Vielh, E.;
Mogensen, X.Y.Z.; Uze, G.
#submission Submitted to the EMBL data library, July 1991
#description The structure of the human interferon alpha/beta receptor
gene.

```

```

#accession SI7112

```

```

#status preliminary

```

```

#molecule_type DNA

```

```

#residues 1-545 #label LUT

```

```

#cross-references EMBL:X60459

```

```

GENETICS #introns 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 330/1; 369/3; 420/1;

```

```

KEYWORDS cytokine receptor; transmembrane protein

```

```

SUMMARY #length 545 #molecular_weight 62169 #checksum 672

```

```

Query Match 71.6% Score 312; DB 2; Length 545;

```

```

Best Local Similarity 100.0% Pred. No. 0.00e+00; Indels 0; Gaps 0;

```

```

Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 18 PVLVLSAAGGKRLKSPKVEVDIIDNFIILMNRSDSEVGNTSFSDYOKTGMDNWKILS 77

```

```

Qy 18 PVLVLSAAGGKRLKSPKVEVDIIDNFIILMNRSDSEVGNTSFSDYOKTGMDNWKILS 77

```

```

Db 78 GQNTSTKCNFSSILKNVEEIKIRIAKEKNTSSWTEVDSFDPFRAOIGPPEVHLEA 137

```

```

Qy 78 GQNTSTKCNFSSILKNVEEIKIRIAKEKNTSSWTEVDSFDPFRAOIGPPEVHLEA 137

```

```

Db 78 GQNTSTKCNFSSILKNVEEIKIRIAKEKNTSSWTEVDSFDPFRAOIGPPEVHLEA 137

```

```

Qy 78 GQNTSTKCNFSSILKNVEEIKIRIAKEKNTSSWTEVDSFDPFRAOIGPPEVHLEA 137

```

```

Db 138 EDKAVIHISPGTKDSVMALDGLSFYSLLIMKSSGVEERIENIYRHKIKYLSPE 197

```

```

Qy 138 EDKAVIHISPGTKDSVMALDGLSFYSLLIMKSSGVEERIENIYRHKIKYLSPE 197

```

```

Db 198 YCLAKKALLTSWKIGVSPVHCITTYENELPPENIEVSQNONVYLAQDYTAANN 257

```

```

Qy 198 YCLAKKALLTSWKIGVSPVHCITTYENELPPENIEVSQNONVYLAQDYTAANN 257

```

```

Db 258 OVOMLAFLKRPNGHLKMKQIPDCENVKTKOCVFPQNVOKGYLLRVAQSDQNTSF 317

```

```

Qy 258 OVOMLAFLKRPNGHLKMKQIPDCENVKTKOCVFPQNVOKGYLLRVAQSDQNTSF 317

```

```

Db 318 WSEIKFTEIO 329

```

```

Qy 318 WSEIKFTEIO 329

```

```

Db 318 WSEIKFTEIO 329

```

```

Qy 318 WSEIKFTEIO 329

```

RESULT 3  
ENTRY: S41602 #type fragments  
TITLE: Interferon alpha receptor 2 - human (fragments)  
ORGANISM: #formal\_name Homo sapiens #common\_name man  
DATE: 25-Dec-1994 #sequence\_revision 01-Dec-1995 #text\_change  
ACCESSIONS: S41602  
REFERENCE: #authors Abramovich, C.; Ratovitski, E.; Lundgren, E.; Revel, M.  
#journal FEBS Lett. (1994) 338:295-300  
#title Identification of mRNAs encoding two different soluble forms  
#cross-references MIMD:94139943  
#accession S41602  
#molecule\_type mRNA  
#residues 1-56 #label ABR  
KEYWORDS: cytokine receptor  
SUMMARY: #length 56 #checksum 845  
Query Match 3.7%; Score 16; DB 2; Length 56;  
Best Local Similarity 100.0%; Pred. No. 1.22e-22;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 PLUTVVCARAHMTDE 16  
QY 398 PLUTVVCARAHMTDE 413  
RESULT 4  
ENTRY: S27387 #type complete  
TITLE: Interferon alpha receptor type 1 precursor - bovine  
ORGANISM: #formal\_name Bos primigenius taurus #common\_name cattle  
DATE: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change  
ACCESSIONS: S27387; S33770  
REFERENCE: #authors Mouchel-Vieilh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.  
#journal FEBS Lett. (1992) 313:255-259  
#title Specific antiviral activities of the human alpha interferons  
#cross-references MIMD:93076908  
#accession S27387  
#status preliminary; nucleic acid sequence not shown  
#molecule\_type mRNA  
#residues 1-560 #label MOU  
#cross-references EMBL:X68443; NID:g431; PID:g432  
#experimental\_source MDR cells  
REFERENCE: S33770  
#authors Lhm, J.K.; Langer, J.A.  
#journal Blochim. Biophys. Acta (1993) 1173:314-319  
#title Cloning and characterization of a bovine alpha interferon  
#cross-references MIMD:93305725  
#accession S33770  
#status preliminary; nucleic acid sequence not shown  
#molecule\_type mRNA  
#residues 1-421, 'V', 423-560 #label LIM  
#cross-references EMBL:L06320; NID:g163187; PID:g163188  
#experimental\_source lung  
KEYWORDS: antiviral; cytokine receptor; transmembrane protein  
FEATURE: 1-24 #domain signal sequence #status predicted #label SIG  
15-560 #product interferon alpha receptor type 1 #status  
predicted #label MAT  
SUMMARY: #length 560 #molecular\_weight 63818 #checksum 4991  
Query Match 3.0%; Score 13; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 2.82e-14;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 397 LKPLTVVCARARA 409

QY 396 LKPLTVVCARARA 408  
RESULT 5  
ENTRY: A45283 #type complete  
TITLE: Interferon alpha/beta receptor - mouse  
ORGANISM: #formal\_name Mus musculus #common\_name house mouse  
DATE: 25-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change  
ACCESSIONS: A45283; I48423; I48425; I48426; I48427; I48428;  
I48429  
REFERENCE: #authors Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen,  
K.E.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:4774-4778  
#title Behavior of a cloned murine interferon alpha/beta receptor  
#cross-references MIMD:92262522  
#accession A45283  
#status preliminary  
#molecule\_type mRNA  
#residues 1-590 #label UZE  
#cross-references GB:M89641; NID:g194111; PID:g194112  
#note Sequence extracted from NCBI backbone (NCBIN:102354,  
NCBIP:102357)  
REFERENCE: I48423  
#authors Lutfalla, G.; Uze, G.  
#journal Gene (1994) 148:343-346  
#title Structure of the murine interferon alpha/beta  
#cross-references MIMD:95047447  
#accession I48423  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 118-125 #label RES  
#cross-references EMBL:U06237; NID:g497103; PID:g755810  
#accession I48424  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 127-224 #label RE2  
#cross-references EMBL:U06238; NID:g497104; PID:g755811  
#accession I48425  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 243-264 #label RE3  
#cross-references EMBL:U06239; NID:g497106; PID:g510261  
#accession I48426  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 265-375 #label RE4  
#cross-references EMBL:U06240; NID:g497108; PID:g510262  
#accession I48427  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 397-424 #label RE5  
#cross-references EMBL:U06241; NID:g497110; PID:g755812  
#accession I48428  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 426-445 #label RE6  
#cross-references EMBL:U06242; NID:g497112; PID:g755813  
#accession I48429  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type DNA  
#residues 473-590 #label RE7  
#cross-references EMBL:U06244; NID:g497114; PID:g510265  
GENETICS: IFNAR  
#gene 177/3; 331/1  
KEYWORDS: cytokine receptor; transmembrane protein  
SUMMARY: #length 590 #molecular\_weight 65776 #checksum 833



Query Match 2.58; Score 11; DB 2; Length 590;  
 Best Local Similarity 100.0%; Pred. No. 4.53e-09;  
 Matches 11; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

DB 363 YEIIEMTSN 373  
 |||||  
 QY 369 YEIIEMTSN 379

RESULT 6  
 ENTRY 700676 #type complete  
 TITLE hypothetical protein F6E13.9 - Arabidopsis thaliana  
 ORGANISM #formal\_name Arabidopsis thaliana #common\_name mouse-ear  
 cross

DATE 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change  
 30-Apr-1999

ACCESSIONS 700676  
 REFERENCE 214198

#authors Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby,  
 M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage,  
 A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.  
 #description Arabidopsis thaliana chromosome II BAC F6E13 genomic  
 sequence.

#accession T00676  
 #status translated from GB/EMBL/DBJ  
 #molecule\_type DNA  
 #residues 1-421 #label ROU  
 #cross-references EMBL:AC004005; NID:93212846; PID:93212853  
 #experimental\_source cultivar Columbia

GENETICS  
 #map\_position 2  
 #note F6E13.9  
 SUMMARY #length 421 #molecular\_weight 48397 #checksum 8249

Query Match 1.8%; Score 8; DB 2; Length 421;  
 Best Local Similarity 100.0%; Pred. No. 3.98e-02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 300 FLKRNPN 307  
 |||||  
 QY 265 FLKRNPN 272

RESULT 7  
 ENTRY T13710 #type fragment  
 TITLE protein-tyrosine kinase (EC 2.7.1.112) - fruit fly  
 ORGANISM #formal\_name Drosophila melanogaster (fragment)  
 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change  
 13-Aug-1999

ACCESSIONS T13710  
 REFERENCE 217703

#authors Ito, M.; Matsui, T.; Taniguchi, T.; Chihara, K.  
 #journal Gene (1994) 139:215-218  
 #title Alternative splicing generates two distinct transcripts for  
 the Drosophila melanogaster fibroblast growth factor  
 receptor homolog.

#accession T13710  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule\_type mRNA  
 #residues 1-1235 #label ITO  
 #cross-references EMBL:DI7550; NID:d1007694; PID:d1005014;  
 PDB:BA04486.1

KEYWORDS phosphotransferase;  
 SUMMARY #length 1235 #checksum 4817

Query Match 1.8%; Score 8; DB 2; Length 1235;  
 Best Local Similarity 100.0%; Pred. No. 3.98e-02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 731 TLVAVNG 738

QY 10 TLVAVNG 17  
 |||||

RESULT 8  
 ENTRY B26744 #type complete  
 TITLE megascollakinin - garden dagger wasp  
 ALTERNATE NAMES 6-Thr-bradykinin-Lys-Ala  
 ORGANISM #formal\_name Megascollia flayifrons #common\_name garden dagger  
 wasp

DATE 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change  
 02-Dec-1994

ACCESSIONS B26744; A28609  
 REFERENCE A34322

#authors Yasuhara, T.; Mantel, P.; Nakajima, T.; Plek, T.  
 #journal Toxicon (1987) 25:527-535  
 #title Two kinins isolated from an extract of the venom reservoirs  
 of the solitary wasp Megascollia flayifrons.

#cross-references MVID:87293024  
 #accession B26744  
 #molecule\_type protein  
 #residues 1-11 #label YAS

REFERENCE A28609  
 #authors Nakajima, T.; Plek, T.; Yasuhara, T.; Mantel, P.  
 #journal Toxicon (1988) 26:34  
 #title Two kinins isolated from the venom of Megascollia flayifrons.  
 #accession A28609  
 #molecule\_type protein  
 #residues 1-11 #label NAK

KEYWORDS bradykinin; presynaptic neurotoxin; venom  
 SUMMARY #length 11 #molecular\_weight 1273 #checksum 4943

Query Match 1.6%; Score 7; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 5 FTFPRKA 11  
 |||||  
 QY 120 FTFPRKA 126

RESULT 9  
 ENTRY PC4027 #type fragment  
 TITLE hypothetical protein 93 - Saccharopolyspora erythraea  
 ORGANISM #formal\_name Saccharopolyspora erythraea  
 21-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change  
 09-Sep-1997

ACCESSIONS PC4027  
 REFERENCE JC4089

#authors Zolchev, S.B.; Hutchinson, C.R.  
 #journal Gene (1995) 156:101-106  
 #title Cloning and heterologous expression of the genes encoding  
 nonspecific electron transport components for a cytochrome  
 P450 system of Saccharopolyspora erythraea involved in  
 erythromycin production.

#cross-references MVID:95255650  
 #accession PC4027  
 #molecule\_type DNA  
 #residues 1-93 #label ZOR  
 #cross-references GB:I3846; NID:9603921; PID:9603922  
 SUMMARY #length 93 #checksum 8543

Query Match 1.6%; Score 7; DB 2; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 48 TTLVAVA 54  
 |||||  
 QY 9 TTLVAVA 15

RESULT 10



```

ENTRY      /      SAVLDM      #type complete
TITLE      delta large antigen - hepatitis delta virus (strain Japanese
ALTERNATE_NAMES  Hdg1
ORGANISM    #formal_name hepatitis delta virus
DATE        31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
16-Jul-1999

ACCESSIONS A36409
REFERENCE   #authors  Imazeki, F.; Omata, M.; Ohno, M.
#journal    J. Virol. (1990) 64:5594-5599
#title      Heterogeneity and evolution rates of delta virus RNA
#cross-references MUID:91012805
#accession  A36409
#molecule_type genomic RNA
#residues   1195 #label TMA
#cross-references GB:D90190; GB:M58299; NID:9221691; PIDN:BAAL4214.1;
PID:d1014919; PID:9221692

CLASSIFICATION #superfamily hepatitis delta virus large antigen
KEYWORDS       core protein
FEATURE        2-195
#product delta large antigen #status predicted #label
#mat
SUMMARY         #length 195 #molecular_weight 21811 #checksum 7815

Query Match      1.6%: Score 7; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 116 AAGKNT 122
1111111
QY 24 AAGKNT 30

RESULT 11
ENTRY      B44459 #type fragment
TITLE      tropomyosin T, fast skeletal muscle splice form alpha - rabbit
ORGANISM    #formal_name Oryctolagus cuniculus #common_name domestic
            rabbit
DATE        30-Apr-1993 #sequence_revision 17-May-1996 #text_change
17-May-1996

ACCESSIONS B44459
REFERENCE   #authors  Pan, B.S.; Potter, J.D.
#journal    J. Biol. Chem. (1992) 267:23052-23056
#title      Two genetically expressed tropomyosin T fragments representing
            alpha and beta isoforms exhibit functional differences.
#cross-references MUID:93054628
#accession  B44459
#status     nucleic acid sequence not shown; not compared with
            conceptual translation
#molecule_type mRNA
#residues   1-234 #label PAN
#experimental_source neonatal skeletal muscle clone pT7
COMMENT      #note      sequence extracted from NCBI backbone (NCBIP:118207)
            The two carboxyl-terminal isoforms of tropomyosin T are designated
            alpha and beta. Alternative splicing to create varied
            amino-terminal isoforms adds considerable additional complexity
            to the expression of tropomyosin T.
CLASSIFICATION #superfamily tropomyosin T
KEYWORDS       alternative splicing; differentiation; skeletal muscle
SUMMARY         #length 234 #checksum 3857

Query Match      1.6%: Score 7; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 84 RIRAEKE 90
1111111
QY 103 RIRAEKE 109

```

```

RESULT 12
ENTRY      A44459 #type complete
TITLE      tropomyosin T, fast skeletal muscle splice form beta - rabbit
ORGANISM    #formal_name Oryctolagus cuniculus #common_name domestic
            rabbit
DATE        03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
13-Aug-1999

ACCESSIONS A44459
REFERENCE   #authors  Pan, B.S.; Potter, J.D.
#journal    J. Biol. Chem. (1992) 267:23052-23056
#title      Two genetically expressed tropomyosin T fragments representing
            alpha and beta isoforms exhibit functional differences.
#cross-references MUID:93054628
#accession  A44459
#status     nucleic acid sequence not shown; not compared with
            conceptual translation
#molecule_type mRNA
#residues   1-249 #label PAN
#experimental_source neonatal skeletal muscle clone PT5
COMMENT      #note      sequence extracted from NCBI backbone (NCBIP:118206)
            Putney, S.D.; Herlihy, W.C.; Schimmel, P.
            Nature (1983) 302:718-721
            A new tropomyosin T and cDNA clones for 13 different muscle
            proteins, found by shotgun sequencing.
#cross-references MUID:83167564
#accession  I46517
#status     translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues   207-226 #label PUT
#cross-references EMBL:V00901; NID:91744; PIDN:CAA24266.1; PID:929769

COMMENT      The two carboxyl-terminal isoforms of tropomyosin T are designated
            alpha and beta. Alternative splicing to create varied
            amino-terminal isoforms adds considerable additional complexity
            to the expression of tropomyosin T.
CLASSIFICATION #superfamily tropomyosin T
KEYWORDS       alternative splicing; differentiation; skeletal muscle
SUMMARY         #length 249 #molecular_weight 29683 #checksum 3853

Query Match      1.6%: Score 7; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 RIRAEKE 105
1111111
QY 103 RIRAEKE 109

RESULT 13
ENTRY      A34327 #type complete
TITLE      tropomyosin T, fast skeletal muscle, embryonic alpha (clone 501)
            - Japanese quail
ORGANISM    #formal_name Coturnix coturnix japonica #common_name Japanese
            quail
DATE        22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change
13-Aug-1999

ACCESSIONS A34327
REFERENCE   #authors  Bucher, E.A.; Charles de la Brousse, F.; Emerson Jr., C.P.
#journal    J. Biol. Chem. (1989) 264:12482-12491
#title      Developmental and muscle-specific regulation of avian fast
            skeletal tropomyosin T isoform expression by mRNA splicing.
#cross-references MUID:89308680
#accession  A34327
#status     preliminary
#molecule_type mRNA
#residues   1-249 #label BUC
#cross-references GB:M26599; NID:9213627; PIDN:AAA49505.1; PID:9213628;
GB:J05006

CLASSIFICATION #superfamily tropomyosin T
KEYWORDS       skeletal muscle

```

SUMMARY #length 249 #molecular-weight 29735 #checksum 5904

Query Match 1.6%; Score 7; DB 2; Length 249;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 101 RIRAEKE 107  
103 RIRAEKE 109

RESULT 14

ENTRY D31957 #type complete  
TITLE troponin T, skeletal muscle, isoform 4 - chicken  
ORGANISM #formal\_name Gallus gallus #common\_name chicken  
DATE 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 13-Aug-1999

ACCESSIONS D31957  
REFERENCE A92698  
#authors Smillie, L.B.; Golosinska, K.; Reinach, F.C.  
#journal J. Biol. Chem. (1988) 263:18816-18820  
#title Sequences of complete cDNAs encoding four variants of chicken skeletal muscle troponin T  
#cross-references M01D:89066672  
#accession D31957  
#molecule\_type mRNA  
#residues 1-251 #label SMI  
#cross-references GB:M2158; GB:J04198; NID:g212791; PIDN:AAA9103.1;

CLASSIFICATION #superfamily troponin T  
KEYWORDS alternative splicing; muscle; phosphoprotein; skeletal muscle  
SUMMARY #length 251 #molecular-weight 29648 #checksum 7133

Query Match 1.6%; Score 7; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 103 RIRAEKE 109  
103 RIRAEKE 109

RESULT 15

ENTRY B34327 #type complete  
TITLE troponin T, fast skeletal muscle, adult alpha (clone 605) - Japanese quail  
ORGANISM #formal\_name Coturnix coturnix japonica #common\_name Japanese quail  
DATE 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 13-Aug-1999

ACCESSIONS B34327  
REFERENCE B34327  
#authors Bucher, E.A.; Charles de la Brousse, F.; Emerson Jr., C.P.  
#journal J. Biol. Chem. (1989) 264:12482-12491  
#title Developmental and muscle-specific regulation of avian fast skeletal troponin T isoform expression by mRNA splicing.  
#cross-references M01D:89308680  
#accession B34327  
#status Preliminary  
#molecule\_type mRNA  
#residues 1-253 #label BUC  
#cross-references GB:M26600; NID:g213629; PIDN:AAA4506.1; PID:g213630;

CLASSIFICATION #superfamily troponin T  
KEYWORDS skeletal muscle  
SUMMARY #length 253 #molecular-weight 30098 #checksum 1070

Query Match 1.6%; Score 7; DB 2; Length 253;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 105 RIRAEKE 111  
11111111

Qy 103 RIRAEKE 109

RESULT 16

ENTRY B31957 #type complete  
TITLE troponin T, skeletal muscle, isoform 2 - chicken  
ORGANISM #formal\_name Gallus gallus #common\_name chicken  
DATE 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 13-Aug-1999

ACCESSIONS B31957  
REFERENCE A92698  
#authors Smillie, L.B.; Golosinska, K.; Reinach, F.C.  
#journal J. Biol. Chem. (1988) 263:18816-18820  
#title Sequences of complete cDNAs encoding four variants of chicken skeletal muscle troponin T  
#cross-references M01D:89066672  
#accession B31957  
#molecule\_type mRNA  
#residues 1-257 #label SMI  
#cross-references GB:M2155; GB:J04198; NID:g212787; PIDN:AAA9101.1;

CLASSIFICATION #superfamily troponin T  
KEYWORDS alternative splicing; muscle; phosphoprotein; skeletal muscle  
SUMMARY #length 257 #molecular-weight 30361 #checksum 7402

Query Match 1.6%; Score 7; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 109 RIRAEKE 115  
11111111

Qy 103 RIRAEKE 109

RESULT 17

ENTRY I53021 #type complete  
TITLE troponin T - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999

ACCESSIONS I53021  
REFERENCE I53021  
#authors Wu, Q.L.; Jha, P.K.; Raychowdhury, N.K.; Du, Y.; Leavis, P.C.; Sarkar, S.  
#journal DNA Cell Biol. (1994) 13:217-233  
#title Isolation and characterization of human fast skeletal beta troponin T cDNA: Comparative sequence analysis of isoforms and insight into the evolution of members of a multigene family.  
#cross-references M01D:94226695  
#accession I53021  
#status Preliminary; translated from GB/EMBL/DBJ  
#molecule\_type mRNA  
#residues 1-258 #label RES  
#cross-references GB:M21984; NID:g508854; PIDN:AAA36777.1; PID:g508855

GENETICS GDB:TNT3  
#cross-references GDB:350962; OMIM:600692  
#map\_position 11p15.5-11p15.5

CLASSIFICATION #superfamily troponin T  
SUMMARY #length 258 #molecular-weight 30596 #checksum 6005

Query Match 1.6%; Score 7; DB 2; Length 258;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 108 RIRAEKE 114  
11111111

Qy 103 RIRAEKE 109

RESULT 18

ENTRY C31957 #type complete

```

TITLE      tropoin T, skeletal muscle, isoform 3 - chicken
ORGANISM   #formal_name Gallus gallus #common_name chicken
DATE       31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
          13-Aug-1999

ACCESSIONS
#authors   A92698
#journal    J. Biol. Chem. (1988) 263:18816-18820
#title      Sequences of complete cDNAs encoding four variants of chicken
          "skeletal muscle tropoin T"
#cross-references MVID:89066672
#accession  C31957
          #molecule_type mRNA
          #residues 1-263 ##label SMI
          #cross-references GB:M22156; GB:004198; NID:g212789; PIDN:AAA49102.1;
          PTD:g212790

CLASSIFICATION
#superfamily tropoin T
#alternative splicing; muscle; phosphoprotein; skeletal muscle
#length 263 #molecular_weight 31142 #checksum 125
SUMMARY

Query Match 1.68; Score 7; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 3,73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 RIRAKE 121
    |||||
Oy 103 RIRAKE 109

RESULT 19
ENTRY    TPRBTS #type complete
TITLE    tropoin T, fast skeletal muscle - rabbit
CONTAINS tropoin T, fast skeletal muscle splice form 1; tropoin T,
          fast skeletal muscle splice form 2; tropoin T, fast
          skeletal muscle splice form 3
          #formal_name Oryctolagus cuniculus #common_name domestic
          rabbit
DATE      24-Apr-1984 #sequence_revision 17-May-1996 #text_change
          22-Jun-1999
ACCESSIONS
#authors   A03083; S03590; S03591; S03592; I46515; I46516
          A92220
#journal    Pearlstone, J.R.; Johnson, P.; Carpenter, M.R.; Smillie, L.B.
          J. Biol. Chem. (1977) 252:983-989
#title      Primary structure of rabbit skeletal muscle tropoin-T.
          Sequence determination of the NH-2-terminal fragment CB3
          and the complete sequence of tropoin-T:
          #cross-references MVID:77118575
          #accession A03083
          #molecule_type protein
          #residues 1-10,17-18,'E',20-48,50-266 ##label PE2
          #note      this is the final paper in a series.
          S03590
          #authors Briggs, M.M.; Schachar, F.
          #journal J. Mol. Biol. (1989) 206:245-249
          #title      N-terminal amino acid sequences of three functionally
          different tropoin T isoforms from rabbit fast skeletal
          muscle.
          #cross-references MVID:89199646
          #accession S03590
          #molecule_type protein
          #residues 1-10,17-53 ##label BRI
          #note      splice form 2
          S03591
          #accession
          #molecule_type protein
          #residues 1-53 ##label BR2
          #note      splice form 1
          S03592
          #accession
          #molecule_type protein
          #residues 1-21,39-53 ##label BR3

REFERENCE
#authors   Molr, A.J.G.; Cole, H.A.; Perry, S.V.
          #journal Biochem. J. (1977) 161:371-382
          #title      The phosphorylation sites of tropoin T from white skeletal

```

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muscle and the effects of interaction with tropomyosin C on
their phosphorylation by phosphorylase kinase.
#cross-references MWID:77157104
#contents annotation: phosphorylation sites
#note phosphorylation under in vivo conditions occurred at
#title positions that may not be accessible in tropomyosin complex
146471
#authors Putney, S.D.; Herlihy, W.C.; Schimmel, P.
#journal Nature (1983) 302:718-721
#title A new tropomyosin T and cDNA clones for 13 different muscle
# proteins, found by shotgun sequencing.
#cross-references MWID:83167564
#accession I46515
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 56-136 #label PUT
#cross-references EMBL:V00899; NID:q1740; PIDN:CAA24264.1; PID:929768
#accession I46516
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 240-266 #label PUT
#cross-references EMBL:V00900; NID:q1742; PIDN:CAA24265.1; PID:9833794
#title tropomyosin is a heterotrimer with one molecule each of tropomyosin
C (calcium binding component), tropomyosin I (inhibitory
component), and tropomyosin T (tropomyosin-binding component)
FUNCTION
#description binds the tropomyosin complex to tropomyosin; with tropomyosin
mediates contraction of vertebrate striated muscle in
response to calcium
#pathway muscle contraction
CLASSIFICATION
#superfamily: tropomyosin T
KEYWORDS acetylated amino end; alternative splicing; differentiation;
muscle contraction; phosphoprotein; skeletal muscle
FEATURE
1-266
#product tropomyosin T, fast skeletal muscle splice form 1
#status experimental #label MAT1\
#product tropomyosin T, fast skeletal muscle splice form 3
#status experimental #label MAT3\
#product tropomyosin T, fast skeletal muscle splice form 2
#status experimental #label MAT2\
#modified site acetylated amino end (Ser) #status
experimental\
#binding site phosphate (Ser) (covalent) (by tropomyosin T
kinase) #status experimental
#length 266 #molecular_weight 31426 #checksum 9215
SUMMARY
Query Match 1.6%; Score 7; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 116 RIRAKE 122.
|||
|||
Oy 103 RIRAKE 109
RESULT 20
ENTRY A24824 #type complete
TITLE tropomyosin T, fast skeletal muscle - rat
#formal_name Rattus norvegicus #common_name Norway rat
ORGANISM 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change
23-Feb-1997
DATE A24824
A24824
A24824
A24824
#Breitbart, R.E.; Nadal-Ginard, B.
#J. Mol. Biol. (1986) 188:313-324
#Complete nucleotide sequence of the fast skeletal tropomyosin T
#gene. Alternatively spliced exons exhibit unusual
#interspecies divergence.
#cross-references MWID:86281691
#accession A24824
#molecule_type DNA
#residues 1-272 #label BRE
GENETICS

```



COMMENT This protein is essential for symbiotic nitrogen fixation.  
 GENETICS  
 #gene fixB  
 #note operon contains fixA, fixB, fixC, and fixX genes  
 CLASSIFICATION  
 #superfamily electron transfer flavoprotein alpha chain  
 #electron transfer; flavoprotein; nitrogen fixation  
 KEYWORDS  
 #length 353 #molecular-weight 37786 #checksum 7176  
 SUMMARY  
 Query Match 1.6%; Score 7; DB 1; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 109 LIGATTL 115  
 OY 5 LIGATTL 11

RESULT 25  
 ENTRY S14071 #type complete  
 TITLE electron transfer flavoprotein alpha chain fixB homolog -  
 ORGANISM Azorhizobium caulinodans  
 #formal\_name Azorhizobium caulinodans  
 #cross-references EMBL:X55450; NID:g38695; PIDN:CA39092.1; PID:g38697  
 #length 369 #molecular-weight 39712 #checksum 897  
 KEYWORDS  
 #electron transfer; flavoprotein  
 #length 369 #molecular-weight 39712 #checksum 897  
 SUMMARY  
 Query Match 1.6%; Score 7; DB 1; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 125 LIGATTL 131  
 OY 5 LIGATTL 11

RESULT 26  
 ENTRY B32495 #type complete  
 TITLE Rep-1 protein B - mouse  
 ORGANISM #formal\_name Mus musculus #common\_name house mouse  
 #length 423 #molecular-weight 46977 #checksum 9992  
 DATE 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change  
 10-Sep-1997  
 ACCESSIONS  
 REFERENCE B32495  
 #authors Linton, J.P.; Yen, J.Y.J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; Kellems, R.E.; Crouse, G.F.  
 #journal Mol. Cell. Biol. (1989) 9:3058-3072  
 #title Dual bidirectional promoters at the mouse dhfr locus: cloning and characterization of two mRNA classes of the divergently transcribed Rep-1 gene.  
 #cross-references MUID:89384567  
 #accession B32495  
 #status preliminary  
 #molecule\_type mRNA  
 #residues 1-394 #label LIN  
 #cross-references GB:M24919; NID:g200703; PID:g200704; GB:J04244  
 KEYWORDS DNA binding  
 SUMMARY #length 394 #molecular-weight 44599 #checksum 606

Query Match 1.6%; Score 7; DB 2; Length 394;  
 Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 247 NKSYSVS 253  
 OY 416 NKSYSVS 422

RESULT 27  
 ENTRY I52590 #type complete  
 TITLE m3-B isoform - mouse  
 ORGANISM #formal\_name Mus sp. #common\_name mouse  
 #length 403 #molecular-weight 44824 #checksum 4331  
 DATE 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change  
 02-Aug-1996  
 ACCESSIONS  
 REFERENCE I52590  
 #authors Tchilian, E.Z.; Beverley, P.C.; Young, B.D.; Watt, S.M.  
 #journal Blood (1994) 83:3188-3198  
 #title Molecular cloning of two isoforms of the murine homolog of the myeloid CD3 antigen.  
 #cross-references MUID:94250900  
 #accession I52590  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule\_type mRNA  
 #residues 1-403 #label RES  
 #cross-references GB:S71345; NID:9551352; PID:9551353  
 #length 403 #molecular-weight 44824 #checksum 4331  
 SUMMARY  
 Query Match 1.6%; Score 7; DB 2; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 241 LVLVAVG 247  
 OY 11 LVLVAVG 17

RESULT 28  
 ENTRY T15309 #type complete  
 TITLE hypothetical protein B0286.3 - Caenorhabditis elegans  
 ORGANISM #formal\_name Caenorhabditis elegans  
 #length 423 #molecular-weight 46977 #checksum 9992  
 DATE 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change  
 20-Sep-1999  
 ACCESSIONS  
 REFERENCE T15309  
 #authors Johnson, D.  
 #journal submitted to the EMBL Data Library, November 1995  
 #description The sequence of C. elegans cosmid B0286.  
 #accession T15309  
 #status preliminary; translated from GB/EMBL/DBJ  
 #molecule\_type DNA  
 #residues 1-423 #label JOH  
 #cross-references EMBL:U39848; NID:g1053217; PID:g1053219;  
 #cross-references EMBL:AAA80690.1; CESP:B0286.3  
 #accession CESP:B0286.3  
 #status preliminary  
 #molecule\_type mRNA  
 #residues 1-394 #label LIN  
 #cross-references GB:M24919; NID:g200703; PID:g200704; GB:J04244  
 KEYWORDS DNA binding  
 SUMMARY #length 394 #molecular-weight 44599 #checksum 606

Query Match 1.6%; Score 7; DB 2; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 112 FLKRNPG 118  
 OY 265 FLKRNPG 271

RESULT 29  
 ENTRY S14147 #type complete  
 TITLE multifunctional purine biosynthesis protein - human

CONTAINS phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21);  
phosphoribosylaminoimidazole succinocarboxamide synthase (EC 6.3.2.6)  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 12-Jun-1998  
ACCESSIONS S14147  
REFERENCE S14147  
#authors Minet, M.; Lacroste, F.  
#journal Curr. Genet. (1990) 18:287-291  
#title Cloning and sequencing of a human cDNA coding for a multifunctional polypeptide of the purine pathway by complementation of the ade2-101 mutant in *Saccharomyces cerevisiae*.  
#cross-references MUID:91070616  
#accession S14147  
#status Preliminary  
#molecule\_type mRNA  
#residues 1-425 #label MIN  
#cross-references GB:X53793; MUID:928383; PID:928384  
GENETICS GDB:ADE2C1  
#gene #cross-references GDB:4627430  
#map\_position 8pter-8p23  
CLASSIFICATION #superfamily phosphoribosylaminoimidazole carboxylase  
KEYWORDS catalytic chain homology  
carbon-carbon lyase; carboxy-lyase; ligase; purine nucleotide biosynthesis  
FEATURE 266-397  
#domain phosphoribosylaminoimidazole carboxylase  
catalytic chain homology #label PCC  
SUMMARY #length 425 #molecular\_weight 47079 #checksum 3489  
Query Match 1.6%; Score 7; DB 2; Length 425;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 108 FLKRNPG 114  
QY 265 FLKRNPG 271  
RESULT 30  
ENTRY S55684 #type complete  
TITLE aminoimidazole ribonucleotide carboxylase - rat  
ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 29-Jan-1999  
ACCESSIONS S55684  
REFERENCE S55684  
#authors Iwahana, H.; Honda, S.; Tsujisawa, T.; Takahashi, Y.; Adzuma, K.; Katsushima, R.; Yamoka, T.; Moritani, M.; Yoshimoto, K.; Itakura, M.  
#journal Blochm. Biophys. Acta (1995) 1261:369-380  
#title Rat genomic structure of amidophosphoribosyltransferase, cDNA sequence of aminoimidazole ribonucleotide carboxylase, and cell cycle-dependent expression of these two physically linked genes.  
#cross-references MUID:95260861  
#accession S55684  
#status Preliminary  
#molecule\_type mRNA  
#residues 1-425 #label IWA  
#cross-references GB:D37979; MUID:9976251; PID:9976252  
CLASSIFICATION #superfamily phosphoribosylaminoimidazole carboxylase  
catalytic chain homology  
FEATURE 266-397  
#domain phosphoribosylaminoimidazole carboxylase  
catalytic chain homology #label PCC  
SUMMARY #length 425 #molecular\_weight 47096 #checksum 2993  
Query Match 1.6%; Score 7; DB 2; Length 425;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 108 FLKRNPG 114  
QY 265 FLKRNPG 271  
RESULT 31  
ENTRY A35641 #type complete  
TITLE 5-aminoimidazole ribonucleotide  
carboxylase-5-aminoimidazole-4-N-succinocarboxamide  
ribonucleotide - chicken  
ORGANISM #formal\_name Gallus gallus #common\_name chicken  
DATE 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 16-Dec-1998  
ACCESSIONS A35641  
REFERENCE A35641  
#authors Chen, Z.; Dixon, J.E.; Zalkin, H.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:3097-3101  
#title Cloning of a chicken liver cDNA encoding 5-aminoimidazole  
ribonucleotide carboxylase and  
5-aminoimidazole-4-N-succinocarboxamide ribonucleotide  
synthetase by functional complementation of *Escherichia coli* pur mutants.  
#cross-references MUID:90222176  
#accession A35641  
#status Preliminary  
#molecule\_type mRNA  
#residues 1-426 #label CHE  
#cross-references GB:M31764; MUID:9211193; PID:9211194  
CLASSIFICATION #superfamily phosphoribosylaminoimidazole carboxylase  
catalytic chain homology  
FEATURE 267-398  
#domain phosphoribosylaminoimidazole carboxylase  
catalytic chain homology #label PCC  
SUMMARY #length 426 #molecular\_weight 47240 #checksum 5538  
Query Match 1.6%; Score 7; DB 2; Length 426;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 109 FLKRNPG 115  
QY 265 FLKRNPG 271  
RESULT 32  
ENTRY S74801 #type complete  
TITLE ammonium transport protein - *Synechocystis* sp. (strain PCC 6803)  
ORGANISM #formal\_name *Synechocystis* sp.  
DATE 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 29-Sep-1999  
ACCESSIONS S74801  
REFERENCE S74322  
#authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugita, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naito, K.; Okumura, S.; Shimp, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.  
#journal DNA Res. (1996) 3:109-136  
#title Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.  
#cross-references MUID:97061201  
#accession S74801  
#status  
#molecule\_type DNA  
#residues 1-442 #label KAN  
nucleic acid sequence not shown; translation not shown

#cross-references EMBL:D90901; GB:AB001339; NID:91651897;  
 #note PIDN:BA016952.1; PID:d1017685; PID:g1652026  
 the nucleotide sequence was submitted to the EMBL Data  
 Library, June 1996

## GENETICS

#gene ant1  
 #superfamily ammonium transport protein ant1  
 #length 442 #molecular-weight 47172 #checksum 310

Query Match 1.68; Score 7; DB 2; Length 442;  
 Best Local Similarity 100.08; Pred. No. 3; 73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 277 LSNAAG 283  
 11111111  
 21 LSNAAG 27

## RESULT 33

ENTRY #type complete  
 TITLE 49.2K membrane protein - equine herpesvirus 1 (strain AB4p)  
 ORGANISM #formal\_name equine herpesvirus 1  
 #host Equus caballus (domestic horse)  
 DATE 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 16-Jul-1999

## ACCESSIONS

REFERENCE A36800  
 #authors Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.  
 #submission submitted to Genbank, March 1992  
 #description The DNA sequence of equine herpesvirus-1.  
 #accession G36800

#molecule\_type DNA  
 #residues 1-450 #label TEL

#cross-references GB:A86664; NID:g330791; PIDN:AB02487.1; PID:g330843

REFERENCE A41831  
 #authors Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.  
 #journal Virology (1992) 189:304-316  
 #title The DNA sequence of equine herpesvirus-1.  
 #cross-references NID:92295566  
 #contents annotation; possible protein-coding frames  
 #note neither amino acid nor nucleotide sequence is given

## GENETICS

#gene 52  
 #superfamily herpesvirus 51K protein  
 #transmembrane protein

## FEATURES

37-53 #domain transmembrane #status predicted #label TM1  
 111-127 #domain transmembrane #status predicted #label TM2  
 156-173 #domain transmembrane #status predicted #label TM3  
 179-195 #domain transmembrane #status predicted #label TM4  
 241-257 #domain transmembrane #status predicted #label TM5  
 271-287 #domain transmembrane #status predicted #label TM6  
 297-314 #domain transmembrane #status predicted #label TM7  
 341-358 #domain transmembrane #status predicted #label TM8  
 #length 450 #molecular-weight 49221 #checksum 9416

## SUMMARY

Query Match 1.68; Score 7; DB 1; Length 450;  
 Best Local Similarity 100.08; Pred. No. 3; 73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 109 TTVLVA 115  
 11111111  
 9 TTVLVA 15

## RESULT 34

ENTRY #type complete  
 TITLE multidrug resistance protein homolog - Archaeoglobus fulgidus  
 ORGANISM #formal\_name Archaeoglobus fulgidus  
 DATE 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 05-Jun-1998

ACCESSIONS G69392  
 ENTRY G69392  
 TITLE A69250  
 REFERENCE A69250

## #authors

Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwin, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kervatage, A.R.; Graham, D.E.; Kyriades, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs, T.; Arlrich, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Boyman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.

#journal Nature (1997) 390:364-370  
 #title The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Archaeoglobus fulgidus.

#cross-references NID:98049343

#accession G69392  
 #status preliminary; nucleic acid sequence not shown; translation not shown

#molecule\_type DNA  
 #residues 1-451 #label KLE

#cross-references GB:AE001025; GB:AE000782; NID:92689348; PID:g2649446;  
 TIGR:AP1144

Query Match 1.68; Score 7; DB 2; Length 451;  
 Best Local Similarity 100.08; Pred. No. 3; 73e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 KALLTS 11  
 11111111  
 203 KALLTS 209

## RESULT 35

ENTRY #type complete  
 TITLE T02100  
 #description hypothetical protein T3K9.4 - Arabidopsis thaliana  
 #formal\_name Arabidopsis thaliana #common\_name mouse-ear cross

DATE 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 23-Apr-1999

## ACCESSIONS

REFERENCE T02100  
 #authors Rounsley, S.D.; Kaul, S.; Llin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kervatage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.  
 #submission submitted to the EMBL Data Library, February 1999  
 #description Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence.  
 #accession T02100

#status translated from GB/EMBL/DBJ  
 #molecule\_type DNA  
 #residues 1-454 #label ROU

#cross-references EMBL:AC004261; NID:g4402695; PID:g3402699  
 #experimental\_source cultivar Columbia

## GENETICS

#map\_position 2  
 #inons 72/2; 156/1; 227/3; 235/3; 296/1; 337/1; 392/2; 407/1; 428/1  
 #lntons 73K9.4  
 #length 454 #molecular-weight 50448 #checksum 3623

## SUMMARY

Query Match 1.68; Score 7; DB 2; Length 454;  
 Best Local Similarity 100.08; Pred. No. 3; 73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 EKKTDV 15  
 11111111  
 386 EKKTDV 392

## RESULT 36

ENTRY #type complete  
 TITLE B75080  
 ENTRY B75080  
 TITLE hypothetical protein PAB0690 - Pyrococcus abyssi (strain

```

ORGANISM      #formal_name Pyrococcus abyssi
DATE          20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
ACCESSIONS    B75080
REFERENCE     A75001
#authors      anonymous, Genoscope
#submission   submitted to the EMBL Data Library, July 1999
#description   Pyrococcus abyssi genome sequence: insights into archaeal
               chromosome structure and evolution.
#accession    B75080
#status       preliminary
#molecule_type DNA
#residues     1-530 #label KAM
#cross-references GB:AJ248286; GB:AL096836; NID:95458366;
               PIDN:CA84943.1; PID:61515840; PID:95458455
#experimental_source strain Orsay

GENETICS
#gene         PAB0690
SUMMARY       #length 530 #molecular_weight 56829 #checksum 5873

Query Match   1.6% Score 7; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 445 CENKTT 451
OY 283 CENKTT 289

RESULT 37
ENTRY   B70682 #type complete
TITLE   probable nitrite reductase - Mycobacterium tuberculosis
         (strain H37RV)
ORGANISM #formal_name Mycobacterium tuberculosis
DATE     17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
         17-Jul-1998

ACCESSIONS B70682
REFERENCE  A70500
#authors   Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
           C.; Harris, D.; Gordon, S.V.; Eiglmeyer, K.; Gao, S.; Barry,
           III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.;
           Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
           Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
           Hornsby, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
           Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
           Skelton, S.; Squares, S.; Squires, R.; Sulston, J.E.;
           Taylor, K.; Whitehead, S.; Barrett, B.G.
#journal    Nature (1998) 393:537-544
#title      Deciphering the biology of Mycobacterium tuberculosis from
           the complete genome sequence.
#cross-references MIMD:98295987
#accession  B70682
#status     preliminary; nucleic acid sequence not shown;
           translation not shown
#molecule_type DNA
#residues   1-563 #label COL
#cross-references GB:Z61368; GB:AL123456; NID:93261656; PID:e279651;
           PID:91655669
#experimental_source strain H37RV

GENETICS
#gene       nifA
SUMMARY     #length 563 #molecular_weight 62997 #checksum 1223

Query Match   1.6% Score 7; DB 2; Length 563;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 48 ERIENIT 54
OY 178 ERIENIT 184

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RESULT 38
ENTRY   C71661 #type complete
TITLE   penicillin-binding protein (pbpA) RP565 - Rickettsia
         prowazekii.
ORGANISM #formal_name Rickettsia prowazekii
DATE     21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change
         26-Aug-1999
ACCESSIONS C71661
REFERENCE  A71630
#authors   Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.;
           Sichteritz-Ponten, T.; Alsmark, U.C.M.; Podowski, R.M.;
           Naestlund, A.K.; Eriksson, A.S.; Winkler, H.H.; Kurland,
           C.G.
#journal    Nature (1998) 396:133-140
#title      The genome sequence of Rickettsia prowazekii and the origin
           of mitochondria
#cross-references MIMD:99039499
#accession  C71661
#status     preliminary; nucleic acid sequence not shown;
           translation not shown
#molecule_type DNA
#residues   1-594 #label AND
#cross-references GB:AJ35272; GB:AJ235269; NID:93861033; PID:el342857;
           PID:93861113
#experimental_source strain Madrid E

GENETICS
#gene       pbpA1; RP565
CLASSIFICATION #superfamily penicillin-binding protein 3
SUMMARY       #length 594 #molecular_weight 67195 #checksum 9752

Query Match   1.6% Score 7; DB 2; Length 594;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 186 NIRSLSO 192
OY 338 NIRSLSO 344

RESULT 39
ENTRY   F64889 #type complete
TITLE   membrane protein maoC - Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE     12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
         13-Nov-1998
ACCESSIONS F64889
REFERENCE  A64720
#authors   Blatterer, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
           Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
           Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
           Kirpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
           Y.
#journal    Science (1997) 277:1453-1462
#title      The complete genome sequence of Escherichia coli K-12.
#cross-references MIMD:97426517
#accession  F64889
#status     nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues   1-681 #label BLAT
#cross-references GB:AF000236; GB:U00096; NID:91787652; PID:91787653;
           UWGP:D1387
#experimental_source strain K-12, substrain MG1655

FEATURE
301-317      #domain transmembrane #status predicted #label TM01\
588-604      #domain transmembrane #status predicted #label TM02
SUMMARY       #length 681 #molecular_weight 73002 #checksum 2628

Query Match   1.6% Score 7; DB 2; Length 681;
Best Local Similarity 100.0%; Pred. No. 3.73e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 587 VLSNAG 593

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OY : 20 VLSAAG.26  
 RESULT 40  
 ENTRY  
 TITLE  
 ORGANISM  
 DATE  
 ACCESSIONS  
 REFERENCE  
 #authors  
 G70559 #type complete  
 Probable uvrB protein - Mycobacterium tuberculosis (strain H37Rv)  
 #formal\_name Mycobacterium tuberculosis  
 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 26-Aug-1999  
 G70559  
 A70500  
 Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gao, S.; Barry, III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 #journal  
 #title  
 Nature (1998) 393:537-544  
 Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.  
 #cross-references M01D:98295987  
 #accession G70559  
 #status preliminary; nucleic acid sequence not shown;  
 translation not shown  
 #molecule\_type DNA  
 #residues 1-698 #label COL  
 #cross-references GB:295554; GB:AL123456; NID:93261771; PID:CA808886.1; PID:ej16899; PID:92113917  
 #experimental\_source strain H37Rv  
 GENETICS  
 #gene uvrB  
 #superfamily excludase ABC chain B; DEAD/H box helicase homology  
 KEYWORDS  
 ATP; P-loop  
 FEATURE  
 41-545  
 335-340  
 339-342  
 #domain DEAD/H box helicase homology #label DEAD\  
 #region nucleotide-binding motif A (P-loop)\  
 #region nucleotide-binding motif B\  
 #region DEXH motif  
 #length 698 #molecular\_weight 78070 #checksum 3125  
 SUMMARY  
 Query Match 1.6%; Score 7; DB 2; Length 698;  
 Best Local Similarity 100.0%; Pred. No. 3,73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 37 VVLGAT 43  
 OY 3 VVLGAT 9  
 RESULT 41  
 ENTRY  
 TITLE  
 ORGANISM  
 DATE  
 ACCESSIONS  
 REFERENCE  
 #authors  
 A32495 #type complete  
 rep-1 protein, form A - mouse  
 #formal\_name Mus musculus #common\_name house mouse  
 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 16-Feb-1997  
 A32495; A30939  
 A32495  
 Linton, J.P.; Yen, J.Y.J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; Kellems, R.E.; Crouse, G.F.  
 Mol. Cell. Biol. (1989) 9:3058-3072  
 Dual bidirectional promoters at the mouse dhfr locus: cloning and characterization of two mRNA classes of the divergently transcribed Rep-1 gene.  
 #cross-references M01D:89384567  
 #accession A32495  
 #molecule\_type mRNA  
 #residues 1-929 #label LIN  
 #cross-references GB:M24919; GB:004244  
 GENETICS  
 #gene  
 KEYWORDS  
 SUMMARY  
 rep-1  
 DNA binding  
 #length 929 #molecular\_weight 104652 #checksum 8244  
 Query Match 1.6%; Score 7; DB 2; Length 929;  
 Best Local Similarity 100.0%; Pred. No. 3,73e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 279 NKSSVES 285  
 OY 416 NKSSVES 422  
 RESULT 42  
 ENTRY  
 TITLE  
 ALTERNATE\_NAMES  
 ORGANISM  
 DATE  
 ACCESSIONS  
 REFERENCE  
 #authors  
 #journal  
 #title  
 #cross-references M01D:92011866  
 #accession A40021  
 #molecule\_type mRNA  
 #residues 1-1051 #label TAK  
 #cross-references GB:M59911; NID:9186496; PID:AAA36120.1; PID:g186497  
 JX0161  
 #journal  
 #title  
 J. Cell Biol. (1991) 115:257-266  
 Molecular cloning and expression of the cDNA for alpha-3 subunit of human alpha-3beta-1 (VLA-3), an integrin receptor for fibronectin, laminin, and collagen.  
 Hemler, M.E.; Murphy, E.; Pil, P.; Chen, C.; Ginsberg, M.H.; Takada, Y.; Murphy, E.; Pil, P.; Chen, C.; Ginsberg, M.H.; J. Cell Biol. (1991) 115:257-266  
 Molecular cloning and expression of the cDNA for alpha-3 subunit of human alpha-3beta-1 (VLA-3), an integrin receptor for fibronectin, laminin, and collagen.  
 #cross-references M01D:91331981  
 #accession JX0161  
 #molecule\_type mRNA  
 #residues 33-1051 #label TSU  
 #cross-references GB:PD01038; NID:9220140; PID:BAA00845.1; PID:d1001309; PID:g220141  
 JX0161  
 #journal  
 #title  
 J. Biol. Chem. (1991) 266:659-665  
 Identification of human galactoprotein b3, an oncogenic transformation-induced membrane glycoprotein, as VLA-3 alpha subunit: The primary structure of human integrin alpha 3.  
 #cross-references M01D:87204112  
 #accession C28018  
 #molecule\_type protein  
 #residues 33-46 #label TAZ  
 S44356  
 #journal  
 #title  
 EMBO J. (1994) 13:2044-2055  
 Molecular and biological characterization of fusion regulatory proteins (FRPs): anti-FRP mAbs induced HIV-mediated cell fusion via an integrin system.  
 #cross-references M01D:94244603  
 #accession S44356  
 #status preliminary  
 #molecule\_type protein  
 #residues 33-43, 'X', 45-49 #label OHT

GENETICS  
#gene GDB:ITGA3  
#map\_position 17q21.32-17q21.32  
#classification #superfamily integrin alpha-2b chain  
#keywords calcium binding; cell adhesion; duplication; glycoprotein; heterodimer; metal binding; transmembrane protein

FEATURE  
1-32  
33-871  
168-176  
241-249  
315-323  
378-386  
439-447  
874-1051  
992-1019  
86,107,265,500,511,  
573,605,656,697,  
841,857,926,935,  
969

SUMMARY  
#length 1051 #molecular\_weight 116611 #checksum 8842  
#binding\_site carbohydrate (asn) (covalent) #status predicted

Query Match 1.6%; Score 7; DB 2; Length 1051;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 994 LVLVAVG 1000  
11 LVLVAVG 17

RESULT 43  
ENTRY I55534 #type complete  
TITLE VLA-3 alpha subunit - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 29-Sep-1999

ACCESSIONS  
REFERENCE I55534  
#authors Takeuchi, K.; Hirano, K.; Tsuji, T.; Osawa, T.; Irimura, T.  
#journal J. Cell. Biochem. (1995) 57:371-377  
#title CDNA cloning of mouse VLA-3 alpha subunit.  
#cross-references MUID:95279462.  
#accession I55534

CLASSIFICATION  
#molecule\_type mRNA  
#residues 1-1053 #label RES  
#cross-references GB:D18867; NID:9220634; PIDN:BAA02980.1; PID:9220635  
#superfamily integrin alpha-2b chain  
SUMMARY #length 1053 #molecular\_weight 116744 #checksum 976

Query Match 1.6%; Score 7; DB 2; Length 1053;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 996 LVLVAVG 1002  
11 LVLVAVG 17

RESULT 44  
ENTRY JC4019 #type complete  
TITLE DNA mismatch repair protein rep-3 - mouse  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 21-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 17-Mar-1999  
ACCESSIONS JC4019; C32495  
REFERENCE JC4019  
#authors Liu, K.; Niu, L.; Linton, J.P.; Crouse, G.F.

#journal Gene (1994) 147:159-177  
#title Characterization of the mouse Rep-3 gene: Sequence similarities to bacterial and yeast mismatch-repair proteins.  
#cross-references MUID:95011610  
#accession JC4019  
#molecule\_type mRNA  
#residues 1-1126 #label L10  
#cross-references GB:L10295  
REFERENCE A32495  
#authors Linton, J.P.; Yen, J.Y.J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; Kellems, R.E.; Crouse, G.F.  
#journal Mol. Cell. Biol. (1994) 9:3058-3072  
#title Dual bidirectional promoters at the mouse dirr locus: cloning and characterization of two mRNA classes of the divergently transcribed Rep-1 gene.  
#cross-references MUID:89384567  
#accession C32495  
#status preliminary  
#molecule\_type mRNA  
#residues 47-60 #label L1N  
#cross-references GB:M24918; GB:J04244

GENETICS  
#gene Rep-3  
#introns 86/2; 159/3; 222/3; 261/3; 301/1; 349/3; 405/2; 443/2; 481/1; 546/2; 650/2; 706/1; 728/2; 767/2; 803/2; 840/2; 892/1; 998/3; 1055/2  
#note gene previously known as Rep-1  
SUMMARY #length 1126 #molecular\_weight 127207 #checksum 9169

Query Match 1.6%; Score 7; DB 2; Length 1126;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 293 NKSSVFS 299  
416 NKSSVFS 422

RESULT 45  
ENTRY G70600 #type complete  
TITLE hypothetical protein RV3910 - Mycobacterium tuberculosis (strain H37RV)  
ORGANISM #formal\_name Mycobacterium tuberculosis  
DATE 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 17-Jul-1998

ACCESSIONS  
REFERENCE G70600  
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gas, S.; Barry, III, C.E.; Tekala, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Hornsby, T.; Jagers, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.; Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
#journal Nature (1998) 393:537-544  
#title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.  
#cross-references MUID:98295987  
#accession G70600  
#status preliminary; nucleic acid sequence not shown; translation not shown

GENETICS  
#gene RV3910  
SUMMARY #length 1184 #molecular\_weight 123562 #checksum 6654

Tue Aug 22 08:32:28 2000

US-09-240-675-2.rpr

Page 21

Query Match 1.68; Score 7; DB 2; Length 1184;  
Best Local Similarity 100.0%; Pred. No. 3.73e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 113 LGATTL 119  
OY 5 LGATTL 11

Search completed: Mon Aug 21 10:31:39 2000  
Job time : 61 secs.

21 08 1980

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201 A 201  
67 s 67  
seq\_name: A\_Geneseq\_36:R14487

seq\_documentation\_block:  
ID R14487 standard; Protein: 436 AA.  
AC R14487;  
DE 16-JAN-1992 (first entry)  
DE Soluble Interferon alpha/beta receptor.  
KW IFN; autoimmune disease; graft rejection; histocompatibility.  
OS Homo sapiens.  
PN FR2657881-A.  
PD 09-APR-1991.  
PR 05-FEB-1990; FR-001298.  
PA (EUBR-) LAB EURO BIOTECHNO.  
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;  
PI Tovey M, Uze G;  
DR MPI; 91-31978/44.  
DR N-PSDB; 014239.  
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and  
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,  
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
PS Claim 2; Page 45; 52pp; French.  
CC The transmembrane and cytoplasmic domains of the native IFN receptor  
CC have been deleted to obtain a soluble, circulating form of the  
CC receptor. Potentially immunogenic epitopes have thus been eliminated.  
CC Derivatives obtained by substitution or deletion of this sequence  
CC are also claimed as are hybrid molecules comprising the soluble  
CC receptor (or deriv.) and an immunoglobulin such as IgG1.  
CC See also 014240.  
SQ Sequence 436 AA.

alignment\_scores:  
Quality: 340.00 Length: 67  
Ratio: 5.075 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x R14487

Align seg 1/1 to: R14487 from: 1 to: 436

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1 ATGATGCTGCTCTCTGGCGGAGACCCCTAGTCTGCTGCGCGTGGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuValAlaValG1 17
51 CCATGGCTGTGTCGCCAGCCGAGGTGGAATAAATCTAATCTCTCT 100
17 YPOTRPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGGTGACATCATAGATGACAACTTATCTGAGGTGGAAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
151 AGGAGCATGAGTCTGTGGGAATGTGACTTTTCATTCGATTATCAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlnL 67
201 A 201
67 s 67

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seq\_name: A\_Geneseq\_36:R28495

seq\_documentation\_block:

ID R28495 standard; Protein: 436 AA.  
AC R28495;  
DE 31-MAR-1993 (first entry)

DE Sequence of a soluble form of the interferon (IFN) receptor  
DE with a high affinity for IFN-alpha and -beta.  
KW Interferon receptor; alpha-interferon; beta-interferon.  
OS Synthetic.  
PN M09218626-A.  
PD 29-OCT-1992.  
PR 17-APR-1991; F00318.  
PA (EUBR-) LAB EURO BIOTECHNOLOGIE.  
PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,  
PI Tovey M, Uze G;  
DR MPI; 92-382110/46.  
DR N-PSDB; 030532.  
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha  
PT and beta - useful as immunosuppressants, for treating auto-immune  
PT diseases and transplant rejection  
PS Claim 2; Fig 1; 58pp; English.  
CC DNA encoding the water-soluble polypeptide with a high affinity for  
CC IFN-alpha and -beta is isolated by PCR, using appropriate  
CC oligonucleotides as primers and cloned cDNA as template. For example,  
CC bacteriophage lambda ZAP, containing the entire coding sequence of  
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos  
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495  
CC lacks the transmembrane and cytoplasmic domains. Both forms bind  
CC IFN in the same way as antibodies, so are immunosuppressants e.g. for  
CC treating autoimmune diseases and graft rejection. They lack the  
CC toxic side effects of known immunosuppressants such as steroids.  
SQ Sequence 436 AA.

alignment\_scores:  
Quality: 340.00 Length: 67  
Ratio: 5.075 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x R28495

Align seg 1/1 to: R28495 from: 1 to: 436

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1 ATGATGCTGCTCTCTGGCGGAGACCCCTAGTCTGCTGCGCGTGGG 50
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51 CCATGGCTGTGTCGCCAGCCGAGGTGGAATAAATCTAATCTCTCT 100
17 YPOTRPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
101 AAAAGTAGAGGTGACATCATAGATGACAACTTATCTGAGGTGGAAC 150
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50
151 AGGAGCATGAGTCTGTGGGAATGTGACTTTTCATTCGATTATCAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTrpGlnL 67
201 A 201
67 s 67

```

seq\_name: A\_Geneseq\_36:R71723

seq\_documentation\_block:

ID R71723 standard; Protein: 436 AA.  
AC R71723;  
DE 16-OCT-1995 (first entry)  
DE IFN receptor extracellular domain.  
KW IFN receptor; Interferon receptor; Interferon alpha;  
KW Interferon-beta; monoclonal antibody; Immunomodulator; AIDS.  
OS Homo sapiens.  
PN W09507716-A.  
PD 23-MAR-1995.  
PF 16-SEP-1994; E03114.

PR 17-SEP-1993, EP-402279.  
 PA (EMBL) LAB EURO BIOTECHNOLOGIE SA.  
 PI Benlizi E, Tovey MG.  
 DR WPI: 95-131187/17.  
 DR N-PSDB: 086457.  
 PT Compn. of monoclonal antibodies against interferon receptor  
 useful as immunomodulator, eg. for treating AIDS.  
 PS Disclosure: Fig. 2A-2B; 105pp; English.  
 CC A recombinant soluble form of the human interferon class I receptor  
 protein extracellular domain, given in R71723, was expressed in  
 CC either E. coli or COS cell hosts. The protein was used to raise  
 CC immunomodulatory monoclonal antibodies.  
 SO Sequence 436 AA.

alignment\_scores:  
 Quality: 340.00 Length: 67  
 Ratio: 5.075 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x R71723

Align seg 1/1 to: R71723 from: 1 to: 436

```

1  ARGATGTCGTCCTCTCTGGGCGGAGACCTAGTCGTCGCGCGTGGG 50
|||||
1  MetMetValValLeuLeuEnglYalAthrThrLeuValLeuValAlaValGl 17
51  CCCAAGGCGTGTGTCGCGAGCCGCGAGGTGAAAAATCTAAATCTCCTC 100
|||||
17  yProtrPValLeuSerAlaAlaAlaGlyLysAsnLeuLysSerProG 34
|||||
101  AAAAGTAGAGTCGACATCATGATGACACTTATCTCTGAGGTGGAGC 150
|||||
34  IntyValGluValAspIleIleAspAsnPhelIleLeuArgTrpAsn 50
|||||
151  AGGACCGATGAGTCGTCGCGAATGACTTTTCATTGCAATTATCAAAA 200
|||||
51  ArgSerAspGluSerValGlyLysValThrPheSerPheAspTyrGln 67
201  A 201
67 s 67

```

seq\_name: A\_Geneseq\_36:W21806

seq\_documentation\_block:

ID W21806 standard; Protein; 496 AA.

AC W21806;

DT 23-SEP-1997 (first entry)

DE Spliced-deleted interferon alpha-receptor form 2.

KM Interferon alpha-receptor; IFNAR.

OS Homo sapiens.

EH key

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

FT domain

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FT domain

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FT domain

FT domain

FT domain

PS Example 3; Fig 7; 46pp; English.  
 CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2  
 CC (W21806) is characterised by a double deletion when compared to  
 CC transmembrane IFNAR (W21804). The extracellular domain is  
 CC shortened by 6 amino acid residues and is followed by a truncated  
 CC intracellular domain. There is no transmembrane region. The amino  
 CC acid sequence is predicted from a cDNA clone (see also W73521) obtd.  
 CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR  
 CC splice-deleted forms 1 (see also W21805) and 2 may regulate the  
 CC response of human cells to IFNs, either by acting as IFN  
 CC antagonists or by regulating IFN activities. They can be expressed  
 CC in host cells and used to inhibit, modulate, or modify the  
 CC activities of IFNs alpha and beta in cells, tissues and organisms,  
 CC or for diagnostic purposes.  
 SO Sequence 496 AA.

alignment\_scores:  
 Quality: 340.00 Length: 67  
 Ratio: 5.075 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x W21806

Align seg 1/1 to: W21806 from: 1 to: 496

```

1  ARGATGTCGTCCTCTCTGGGCGGAGACCTAGTCGTCGCGCGTGGG 50
|||||
1  MetMetValValLeuLeuEnglYalAthrThrLeuValLeuValAlaValGl 17
51  CCCAAGGCGTGTGTCGCGAGCCGCGAGGTGAAAAATCTAAATCTCCTC 100
|||||
17  yProtrPValLeuSerAlaAlaAlaGlyLysAsnLeuLysSerProG 34
|||||
101  AAAAGTAGAGTCGACATCATGATGACACTTATCTCTGAGGTGGAGC 150
|||||
34  IntyValGluValAspIleIleAspAsnPhelIleLeuArgTrpAsn 50
|||||
151  AGGACCGATGAGTCGTCGCGAATGACTTTTCATTGCAATTATCAAAA 200
|||||
51  ArgSerAspGluSerValGlyLysValThrPheSerPheAspTyrGln 67
201  A 201
67 s 67

```

seq\_name: A\_Geneseq\_36:R11958

seq\_documentation\_block:

ID R11958 standard; Protein; 557 AA.

AC R11958;

DT 18-JUL-1991 (first entry)

DE Human alpha-interferon receptor protein.

KM Human alpha IFN; IFN agonists; antiviral; anti tumour agent;

OS Homo sapiens.

EH key

FT peptide

FT peptide

FT peptide

FT peptide

FT peptide

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FT peptide

FT peptide

CC nosis of viral diseases and tumours. Antibodies raised against  
 CC this protein can be used for blocking the receptor when required,  
 CC eg where overexpression of alpha-IFN is harmful. The Abs are  
 CC also useful for eg drug targeting. Variants of the protein,  
 CC having residue 164 (Thr) replaced by Arg and an Asp inserted  
 CC between residues 479 and 480, are also useful.  
 SO Sequence 557 AA;

## alignment\_scores:

Quality: 340.00 Length: 67  
 Ratio: 5.075 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x R1958

Align seg 1/1 to: R1958 from: 1 to: 557

```

1 ATGATGTCGTCCTCCTCGGCGCGAGACCTAGTCTGTCGCGCGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuAlaValAl 17
51 CCCATGGTGTGTCGCGAGCGCGAGGTGAAATAATCTCCTC 100
17 YPOTRYPAlleuSerAlaAlaAlaGlyGlyAsnLeuLysSerPro 34
101 AAAAGTAGAGTGCATCATAGTACGACCTTATCTGAGGTGAGAC 150
34 InLysValGluValAspIleIleAspAsnPhelleuArgTrpAsn 50
151 AGGAGCGATGCTGTCGGGAATGCTTTTCATTCGATTATCAAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67
201 A 201
67 s 67

```

seq\_name: A\_Geneseq\_36:R14488

## seq\_documentation\_block:

ID R14488 standard; Protein: 557 AA.  
 AC R14488;  
 DT 16-JAN-1992 (first entry)  
 DE Complete interferon-alpha/beta receptor.  
 KW IFN; autoimmune disease; graft rejection; histocompatibility.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT domain 437..457  
 FT /label= transmembrane  
 FT 458..557  
 FT /label= cytoplasmic  
 FN FR2657881-A;  
 PD 09-AUG-1991.  
 PR 05-FEB-1990; 001298.  
 PR 05-FEB-1990; FR-001298.  
 PA (EUBI-) LAB EURO BIOECHO.  
 EID P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;  
 Tovey M, Uze G;  
 WPI: 91-319778/44.  
 DR N-PSDB; Q14240.  
 PT New water-soluble polypeptide(s) with affinity for IFN-alpha and  
 PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,  
 PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
 PS Disclosure; Page 47; 52pp; French.  
 CC The invention covers derivatives of the interferon-alpha and/or beta  
 CC receptor obtained by deleting the transmembrane and cytoplasmic domains  
 CC of the native receptor or by substitution. Potentially immunogenic  
 CC epitopes are eliminated and the deriv. can be secreted from  
 CC transformed cells. Soluble deriv.s block the activity of IFN alpha/beta  
 CC and can be used to treat autoimmune diseases or to inhibit graft  
 CC rejection. See also Q14239.

SO Sequence 557 AA;

## alignment\_scores:

Quality: 340.00 Length: 67  
 Ratio: 5.075 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x R14488

Align Seg 1/1 to: R14488 from: 1 to: 557

```

1 ATGATGTCGTCCTCCTCGGCGCGAGACCTAGTCTGTCGCGCGG 50
1 MetMetValValLeuLeuGlyAlaThrThrLeuValLeuAlaValAl 17
51 CCCATGGTGTGTCGCGAGCGCGAGGTGAAATAATCTCCTC 100
17 YPOTRYPAlleuSerAlaAlaAlaGlyGlyAsnLeuLysSerPro 34
101 AAAAGTAGAGTGCATCATAGTACGACCTTATCTGAGGTGAGAC 150
34 InLysValGluValAspIleIleAspAsnPhelleuArgTrpAsn 50
151 AGGAGCGATGCTGTCGGGAATGCTTTTCATTCGATTATCAAAA 200
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67
201 A 201
67 s 67

```

seq\_name: A\_Geneseq\_36:R28496

## seq\_documentation\_block:

ID R28496 standard; Protein: 557 AA.  
 AC R28496;  
 DT 31-MAR-1993 (first entry)  
 DE Sequence of a soluble form of the interferon (IFN) receptor  
 DE with a high affinity for IFN-alpha and -beta.  
 KW Interferon receptor; alpha-interferon; beta-interferon.  
 OS Synthetic.  
 PN MO9218626-A.  
 PD 29-OCT-1992.  
 PR 17-APR-1991; F00318.  
 PR 17-APR-1991; WO-F00318.  
 PA (EUBI-) LAB EURO BIOECHOLOGIE.  
 EID P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,  
 Tovey M, Uze G;  
 WPI: 92-382110/46.  
 DR N-PSDB; Q30533.  
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha  
 PT and beta - useful as immunosuppressants, for treating auto-immune  
 PT diseases and transplant rejection  
 PS Claim 3; Fig 2; 58pp; English.  
 CC DNA encoding the water-soluble polypeptide with a high affinity for  
 CC IFN-alpha and -beta is isolated by PCR, using appropriate  
 CC oligonucleotides as primers and cloned cDNA as template. For example,  
 CC bacteriophage lambda ZAP, containing the entire coding sequence of  
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos  
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495  
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind  
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for  
 CC treating autoimmune diseases and graft rejection. They lack the  
 CC toxic side-effects of known immunosuppressants such as steroids.  
 SO Sequence 557 AA;

## alignment\_scores:

Quality: 340.00 Length: 67  
 Ratio: 5.075 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000



alignment\_block:  
US-09-240-675-1\_COPY\_27\_229 x R28496

Align seg 1/1 to: R28496 from: 1 to: 557

1 ATGATGGTGTCTCTGCGCGGAGACCCATGCTGCTGCGCGG 50  
1 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValAl 17  
51 CCCATGGGTGTCTGCGCGGAGACCCATGCTGCTGCGCGG 100  
17 yProtrpValLeuSerAlaAlaAlaGlyIlyAsnLeuLysSerPro 34  
101 AAAAGTAGAGTGCATCATGATGATGACACTTTCCTGAGTGAGAC 150  
34 IntyValGluValAspIleIleAspAspAspPheIleLeuArgTrpAsn 50  
151 AGAGCGATGAGTGTCTGCGGAGATGACTTTTCCTGATTATCAAA 200  
51 ArgSerAspGluSerValGlyLysValThrPheSerPheAspTyrGln 67

201 A 201

67 s 67

seq\_name: A\_Geneseq\_36:R42635

seq\_documentation\_block:

ID R42635 standard; Protein: 557 AA.  
AC R42635.  
DE 20-APR-1994 (first entry)  
DE Human interferon receptor.  
DE IFN-R; extracellular domain; monoclonal antibody; viral infection;  
KM cell proliferation; allograft rejection; systemic lupus erythematosus;  
KM psoriasis; multiple sclerosis; Behcet's Disease; aplastic anemia;  
KM Immunodeficiency; measles virus; Interferon-alpha-beta.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT domain 1. 436  
FT /label= extracellular\_domain  
FT /note= "soluble, immunogenic form of IFN-R"  
PD EP-563487-A.  
PD 06-OCT-1993.  
PF 31-MAR-1992; 400902.  
PF 31-MAR-1992; EP-400902.  
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.  
PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;  
DR WPI: 93-312951/40.  
DR N-PSDB; R42635.  
PT Monoclonal antibody to human interferon type-I receptor - having  
PT neutralising activity against human type I interferon, used for  
PT therapy and diagnosis  
PS Disclosure; Fig 3; 21pp; English.  
CC Monoclonal antibodies produced against soluble forms of the human  
CC interferon alpha-beta receptor based on the full-length human IFN-R  
CC sequence are claimed. The antibodies are useful for treatment and  
CC prophylaxis of disorders involving cell proliferation and/or viral  
CC infection.  
SQ Sequence 557 AA;

alignment\_scores:

Quality: 340.00 Length: 67  
Ratio: 5.075 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x R42635

Align seg 1/1 to: R42635 from: 1 to: 557

1 ATGATGGTGTCTCTGCGCGGAGACCCATGCTGCTGCGCGG 50

seq\_name: A\_Geneseq\_36:R75356

seq\_documentation\_block:

ID R75356 standard; Protein: 557 AA.  
AC R75356.  
DE 16-OCT-1995 (first entry)  
DE Human IFN receptor.  
DE IFN receptor; interferon receptor; interferon-alpha;  
KM Interferon-beta; monoclonal antibody; immunomodulator; AIDS.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT domain 1. 436  
FT /label= extracellular\_domain  
PD W09507716-A.  
PD 23-MAR-1995.  
PF 16-SEP-1994; E01114.  
PF 17-SEP-1993; EP-402279.  
PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.  
PI Benitzi EJ, Tovey MG;  
DR WPI: 95-131187/17.  
DR N-PSDB; 086458.  
PT Compns. of monoclonal antibodies against Interferon receptor -  
PT useful as immunomodulator, eg. for treating AIDS  
PS Disclosure; Fig 3A-2B; 105pp; English.  
CC The amino acid sequence of human interferon class I receptor is  
CC given in R75356. A recombinant soluble form of the extracellular  
CC domain of this receptor (R71723) has been used to raise  
CC immunomodulatory monoclonal antibodies.  
SQ Sequence 557 AA;

alignment\_scores:

Quality: 340.00 Length: 67  
Ratio: 5.075 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x R75356

Align seg 1/1 to: R75356 from: 1 to: 557

1 ATGATGGTGTCTCTGCGCGGAGACCCATGCTGCTGCGCGG 50  
1 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValAl 17  
51 CCCATGGGTGTCTGCGCGGAGACCCATGCTGCTGCGCGG 100  
17 yProtrpValLeuSerAlaAlaAlaGlyIlyAsnLeuLysSerPro 34  
101 AAAAGTAGAGTGCATCATGATGATGACACTTTCCTGAGTGAGAC 150  
34 IntyValGluValAspIleIleAspAspAspPheIleLeuArgTrpAsn 50  
151 AGAGCGATGAGTGTCTGCGGAGATGACTTTTCCTGATTATCAAA 200

|||||  
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67

201 A 201

67 s 67

seq\_name: A\_Geneseq\_36:W21804

seq\_documentation\_block:

ID: W21804 standard; Protein: 557 AA.

AC W21804:

DT 23-SEP-1997 (first entry)

DE Transmembrane Interferon alpha-receptor.

KW Interferon alpha-receptor; IFNAR.

OS Homo sapiens.

FT Key Location/Qualifiers

FT domain 1..436 Extracellular\_domain

FT domain 437..457

FT domain 458..557

FT domain /Label- Intracellular\_domain

FT domain

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PT Inhibiting, modulating or modifying the activities of Interferon(s)  
PS Disclosure; Fig 7; 46pp; English.  
CC Human transmembrane Interferon alpha receptor (IFNAR) (W21804)  
CC Includes a 21-amino acid transmembrane region. Novel, splice  
CC deleted IFNAR forms 1 (W21805) and 2 (W21806) have been detected  
CC that lack this transmembrane domain. These, soluble non-membrane  
CC bound polypeptides can be expressed in host cells and used to  
CC inhibit, modulate or modify the activities of Interferons alpha  
CC and beta in cells, tissues and organisms, or for diagnostic  
CC purposes.  
SQ Sequence 557 AA;

Alignment\_scores:

Quality: 340.00

Ratio: 5.075

Percent Similarity: 100.000

Percent Identity: 100.000

Length: 67

Gaps: 0

Align seg 1/1 to: W21804 from: 1 to: 557

1 ATGATGCTGCTCTCTGCGCGGAGACCTAGTCTGCTGCGCGGCGG 50  
1 MetMetValValLeuLeuValValThrThrLeuValValLeuValValVal 17  
51 CCCATGGGCTGCTGCGCGGAGCGGCGGAGGAAATCAATCAATCTCC 100  
17 yProTrpAlaLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 34  
101 AAAAAAGAGGTGACATCATAGATGACACTTTTCAATTCGATTAACAA 150  
34 InLyValGlyValAspIleLeuAspAspAsnPheIleLeuArgTrpAsn 50  
151 AGGACGATGATGCTGCTGCGGAGATGCTGCTTTTCAATTCGATTAACAA 200  
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67  
201 A 201

67 s 67

seq\_name: A\_Geneseq\_36:W93941

seq\_documentation\_block:

ID: W93941 standard; Protein: 1429 AA.

AC W93941:

DT 30-JUN-1999 (first entry)

DE Human bix protein.

KW Bix protein; breast cancer; nuclear receptor-binding auxiliary protein;  
anti-cancer; anti-proliferative; mitogen; transcription factor; human;  
tumour suppressor; ovarian cancer; proliferative disorder; treatment;  
immune tissue; prevention; reproductive tissue.

OS Homo sapiens.

FT Key Location/Qualifiers

FT domain 1..1544 AI

FT domain 1545..1999

FT domain 1999..2546

FT domain 2547..2548

FT domain 2549..2550

FT domain 2551..2552

FT domain 2553..2554

FT domain 2555..2556

FT domain 2557..2558

FT domain 2559..2560

FT domain 2561..2562

FT domain 2563..2564

FT domain 2565..2566

FT domain 2567..2568

FT domain 2569..2570

FT domain 2571..2572

FT domain 2573..2574

FT domain 2575..2576

FT domain 2577..2578

FT domain 2579..2580

FT domain 2581..2582

FT domain 2583..2584

FT domain 2585..2586

FT domain 2587..2588

FT domain 2589..2590

FT domain 2591..2592

FT domain 2593..2594

FT domain 2595..2596

FT domain 2597..2598

FT domain 2599..2600

FT domain 2601..2602

FT domain 2603..2604

FT domain 2605..2606

FT domain 2607..2608

FT domain 2609..2610

FT domain 2611..2612

FT domain 2613..2614

FT domain 2615..2616

FT domain 2617..2618

FT domain 2619..2620

FT domain 2621..2622

FT domain 2623..2624

FT domain 2625..2626

FT domain 2627..2628

FT domain 2629..2630

FT domain 2631..2632

FT domain 2633..2634

PT Breast cancer gene encoding a nuclear receptor-binding auxiliary  
protein, bix  
PS Claim 1b, Page 58-62; 69pp; English.  
CC This invention describes a novel human breast cancer gene encoding a  
nuclear receptor-binding auxiliary protein, bix. The bix encoded protein  
CC has anti-cancer, anti-proliferative and mitogenic activity and acts as a  
transcription factor and tumour suppressor. Levels of expression of bix  
CC can be detected using the primers, probes and antibodies (contained in  
the kit) to determine a predisposition to breast and ovarian cancer and  
CC other proliferative disorders of immune tissues. Vectors containing the  
CC bix gene can be used for prevention and treatment of cancers and  
proliferative diseases of mammalian reproductive and immune tissues.  
SQ Sequence 1429 AA;

Alignment\_scores:

Quality: 75.00

Ratio: 1.923

Percent Similarity: 52.703

Percent Identity: 41.892

Length: 74

Gaps: 5

Align seg 1/1 to: W93941 from: 1 to: 1429

Alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

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US-09-240-675-1\_COPY\_27\_229 x W93941

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US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

Alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

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US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

US-09-240-675-1\_COPY\_27\_229 x W93941

AC W93962;  
 DE 30-JUN-1999 (first entry)  
 DE Human brx immunogenic peptide 1.  
 KW Brx protein; breast cancer; nuclear receptor-binding auxiliary protein;  
 KW anti-cancer; anti-proliferative; mitogen; transcription factor; human;  
 KW tumour suppressor; ovarian cancer; proliferative disorder; treatment;  
 KW Immune tissue; prevention; reproductive tissue; immunogenic.  
 OS Homo sapiens.  
 PN MO9915544-A1.  
 PD 01-APR-1999.  
 PF 23-SEP-1998; US-019782.  
 PR 23-SEP-1997; US-059621.  
 PA (DRIC/) DRIGERS P H.  
 PA (RUBI/) RUBINO D M.  
 PA (SEGE/) SEGERS J.  
 PI Driggers PH, Rubino DM, Segers J;  
 WPI: 99-254688/21.  
 DR Breast cancer gene encoding a nuclear receptor-binding auxiliary  
 PT protein, brx  
 PS Disclosure; Page 29; 69pp; English.  
 CC This invention describes a novel human breast cancer gene encoding a  
 CC nuclear receptor-binding auxiliary protein, brx. The brx encoded protein  
 CC has anti-cancer, anti-proliferative and mitogenic activity and acts as a  
 CC transcription factor and tumour suppressor. Levels of expression of brx  
 CC can be detected using the primers, probes and antibodies (contained in  
 CC the kit) to determine a predisposition to breast and ovarian cancer and  
 CC other proliferative disorders of immune tissues. Vectors containing the  
 CC brx gene can be used for prevention and treatment of cancers and  
 CC proliferative diseases of mammalian reproductive and immune tissues.  
 SQ Sequence 30 AA;

alignment\_scores:  
 Quality: 62.00 Length: 33  
 Ratio: 3.263 Gaps: 2  
 Percent Similarity: 57.576 Percent Identity: 54.545

alignment\_block:  
 US-09-240-675-1\_COPY\_27\_229 x W93962 ..

Align seg 1/1 to: W93962 from: 1 to: 30

3 GATGCTGCTCCTCGGCGGACAGACCCCTAGTGTGCTGCCGCGGCGCC 52  
 |||||  
 3 AspGlyArgProSerTrp.....ProSerAlaArgArgCysSe 16  
 53 CATGGCTTGTCCGACGCCAGGTGGAATAATCTAAATCTCTCA 101  
 |||||  
 16 rArgGly.....SerArgThrIlePlyArgSerGlyArgSerSer 29

seq\_name: A\_Geneseq\_36:W52296

seq\_documentation\_block:  
 ID W52296 standard; Protein; 325 AA.  
 AC W52296;  
 DE 23-JUN-1998 (first entry)  
 DE CREB4 protein.  
 KW CREB4; interleukin-10; IL-10; IL-10 receptor; allograft rejection;  
 KW vaccine; photosensitivity; inflammation; autoimmune disease;  
 KW septic shock; immune response; organ rejection; gene therapy.  
 OS Homo sapiens.  
 PN MO9802542-A1.  
 PD 22-JAN-1998.  
 PF 17-JUL-1997; U12455.  
 PR 17-JUL-1996; US-683743.  
 PA (UYNE-) UNIV NEW JERSEY.  
 PI Kotenko SV, Pestka S;  
 WPI: 98-110590/10.  
 DR N-PS08: V19874.  
 PT New recombinant DNA - comprises sequences encoding interleukin-10  
 PT and CREB4 linked to operator, useful, e.g. preventing allograft  
 PT rejection  
 PS Claim 2; Page 7; 79pp; English.

CC This sequence is the human CREB4 sequence, DNA encoding it is used in the  
 CC recombinant DNA (I) of the invention. (I) comprises a sequence (S1)  
 CC encoding the interleukin-10 (IL-10) receptor (IL10R) and a sequence (S2)  
 CC encoding CREB4, both operably linked to expression control sequences.  
 CC Cells containing (I) may be used to identify agonists/antagonist of  
 CC IL-10. Agonists are potentially useful, e.g. for preventing allograft  
 CC rejection, as vaccine adjuvants, for treatment of photosensitivity,  
 CC inflammation, autoimmune disease and septic shock, while antagonists are  
 CC potentially useful for increasing immune responses against tumours,  
 CC viruses, bacteria and parasites (especially intracellular pathogens) and  
 CC for preventing organ rejection. A vector containing (I) is used to  
 CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses  
 CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a  
 CC signal. Antisense CREB4 sequences (especially ribozymes), can inhibit  
 CC IL-10 activity in cells. Antibodies specific for CREB4 are used to  
 CC measure and localise CREB4, for diagnosis of defective IL-10 activity.  
 CC Fragments of (I) are used as primers or probes to assay CREB4-specific  
 CC RNA. Agonists/antagonists may be administered parenterally, orally or  
 CC rectally especially by intravenous injection or directly into a tumour or  
 CC allograft.  
 SQ Sequence 325 AA;

alignment\_scores:  
 Quality: 61.50 Length: 54  
 Ratio: 1.922 Gaps: 1  
 Percent Similarity: 59.259 Percent Identity: 29.630

alignment\_block:  
 US-09-240-675-1\_COPY\_27\_229 x W52296 ..

Align seg 1/1 to: W52296 from: 1 to: 325

55 TGGGCTGTCTCCGACGCCAGGTGGAATAATCTAAATCT..... 96  
 ||| ||||| ||||| |||||  
 3 TrpSerLeuGlySerTrpLeuGlyGlyCysLeuLeuValSerAlaLeuG1 19  
 97 .....CCTCAAAAGTAGAGTCGACATCATGATGACAACT 133  
 |||||  
 19 yMetValProProGluAsnValArgMetAsnSerValAsnPhelysa 36  
 134 TTATCCTAGGTGGAACAGACGATGCTGTGGCAATGTGACTTT 183  
 |||||  
 36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52  
 184 TCATTTCATTAT 195  
 ::::|  
 53 ThrAlaGlnTyr 56

seq\_name: A\_Geneseq\_36:W07702

seq\_documentation\_block:  
 ID W07702 standard; Protein; 543 AA.  
 AC W07702;  
 DE 06-APR-1997 (first entry)  
 DE Mouse ETS2 repressor factor (ERF).  
 KW ERS2 repressor factor; ERF; transcriptional repressor;  
 KW tumour suppressor; tumour; cancer; oncoprotein; therapy.  
 OS Mus sp.  
 FH Key  
 FT domain Location/Qualifiers  
 FT 21..98 /label= "DNA binding domain"  
 FT /note= "ets-like DNA binding domain"  
 FT 466..525 /label= "Active\_repressor\_domain"  
 FT domain  
 PN MO9639517-A1.  
 PD 12-DEC-1996.  
 PF 04-JUN-1996; U10177.  
 PR 05-JUN-1995; US-469412.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PI Athanasiou MA, Beal GJ, Blair DG, Fisher RJ, Mavrothalassitis GJ,  
 PI Sgouras D N;  
 WPI: 97-043139/04.

DR N-PSDB: T47200.  
PT New DNA encoding ETS2 repressor factor - useful for reducing  
tumourigenicity, esp. oncogene associated tumour cells  
PS Disclosure; Page 70-72; 101pp; English.  
CC Murine ETS2 repressor factor (ERF) (W07702) is a member of the ETS  
family and acts as a transcriptional repressor in mammalian cells.  
CC Its amino acid sequence was deduced from the murine ERF gene  
(T47198). Human ERF (see also W07700) has also been identified.  
CC ERF has tumour suppressor activity. Chimeric molecules comprising  
the ERF repressor domain in combination with a heterologous  
transcription factor having a binding domain can be used to reduce  
tumourigenicity associated with inappropriate expression of  
transcription factors.  
SO Sequence 543 AA;

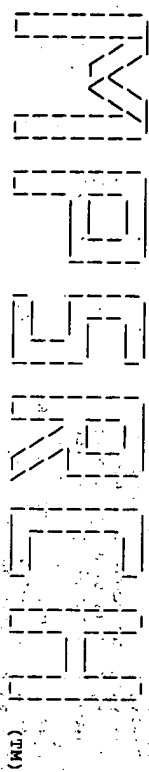
Alignment scores:  
Quality: 61.00 Length: 24  
Ratio: 3.389 Gaps: 0  
Percent Similarity: 75.000 Percent Identity: 45.833

## Alignment Block:

US-09-240-675-1\_COPY\_27\_229/rev x W07702

Align seg 1/1 to: W07702 from: 1 to: 543

82 TTCACCTCGGCTGGGAGAACACCCATGGGCCCGAGGAGAGACT 33  
||| :::::||||| ||:::|||||  
367 PhetyPhetylsleuclnProProleuglyArgArgGlnArgLalaI 383  
32 AGGTCGTGCGCCCGAGAGGA 11  
||:::|||||  
383 aglyclnlysalalProglygly 390



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MPearch\_p protein - protein database search, using Smith-Waterman algorithm  
Run on: Mon Aug 21 10:29:33 2000; Maspar time 12.38 seconds  
Tabular output not generated. 834,259 Million cell updates/sec

Title: >US-09-240-675-2  
Description: (1-436) from US09240675.pep  
Perfect score: 436  
Sequence: 1 MAAVLLATTLVLAAGVPMV.....KSSVFSADVCKTRPGNTSK 436

Scoring table: TABLE uniprottable  
Gap 60

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%  
Listing first 1000 summaries

Database: a-geneseq36  
1:geneseqp

Statistics: Mean 2.943; Variance 0.687; scale 4.285

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	436	100.0	436	1	R28495	0.00e+00
2	436	100.0	436	1	R14487	0.00e+00
3	436	100.0	557	1	R14488	0.00e+00
4	436	100.0	557	1	R11958	0.00e+00
5	436	100.0	557	1	R42635	0.00e+00
6	436	100.0	557	1	R28496	0.00e+00
7	385	88.3	557	1	R75356	0.00e+00
8	385	88.3	557	1	W21804	0.00e+00
9	376	86.2	434	1	W21805	0.00e+00
10	362	83.0	434	1	W21806	0.00e+00
11	318	72.9	436	1	R7123	0.00e+00
12	318	72.9	436	1	R7123	0.00e+00
13	318	72.9	436	1	R7123	0.00e+00
14	318	72.9	436	1	R7123	0.00e+00
15	318	72.9	436	1	R7123	0.00e+00
16	318	72.9	436	1	R7123	0.00e+00
17	318	72.9	436	1	R7123	0.00e+00
18	318	72.9	436	1	R7123	0.00e+00
19	318	72.9	436	1	R7123	0.00e+00
20	318	72.9	436	1	R7123	0.00e+00
21	318	72.9	436	1	R7123	0.00e+00
22	318	72.9	436	1	R7123	0.00e+00
23	318	72.9	436	1	R7123	0.00e+00

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	436	100.0	436	1	R28495	0.00e+00
2	436	100.0	436	1	R14487	0.00e+00
3	436	100.0	557	1	R14488	0.00e+00
4	436	100.0	557	1	R11958	0.00e+00
5	436	100.0	557	1	R42635	0.00e+00
6	436	100.0	557	1	R28496	0.00e+00
7	385	88.3	557	1	R75356	0.00e+00
8	385	88.3	557	1	W21804	0.00e+00
9	376	86.2	434	1	W21805	0.00e+00
10	362	83.0	434	1	W21806	0.00e+00
11	318	72.9	436	1	R7123	0.00e+00
12	318	72.9	436	1	R7123	0.00e+00
13	318	72.9	436	1	R7123	0.00e+00
14	318	72.9	436	1	R7123	0.00e+00
15	318	72.9	436	1	R7123	0.00e+00
16	318	72.9	436	1	R7123	0.00e+00
17	318	72.9	436	1	R7123	0.00e+00
18	318	72.9	436	1	R7123	0.00e+00
19	318	72.9	436	1	R7123	0.00e+00
20	318	72.9	436	1	R7123	0.00e+00
21	318	72.9	436	1	R7123	0.00e+00
22	318	72.9	436	1	R7123	0.00e+00
23	318	72.9	436	1	R7123	0.00e+00

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
24	318	72.9	436	1	R80024	2.94e+02
25	318	72.9	436	1	R84905	2.94e+02
26	318	72.9	436	1	R73033	2.94e+02
27	318	72.9	436	1	R71509	2.94e+02
28	318	72.9	436	1	R71510	2.94e+02
29	318	72.9	436	1	R15517	2.94e+02
30	318	72.9	436	1	R50181	2.94e+02
31	318	72.9	436	1	W40091	2.94e+02
32	318	72.9	436	1	W59202	2.94e+02
33	318	72.9	436	1	W78223	2.94e+02
34	318	72.9	436	1	W33605	2.94e+02
35	318	72.9	436	1	W5271	2.94e+02
36	318	72.9	436	1	W4756	2.94e+02
37	318	72.9	436	1	W58848	2.94e+02
38	318	72.9	436	1	W20172	2.94e+02
39	318	72.9	436	1	W29774	2.94e+02
40	318	72.9	436	1	W20533	2.94e+02
41	318	72.9	436	1	W60650	2.94e+02
42	318	72.9	436	1	R38777	2.94e+02
43	318	72.9	436	1	R26960	2.94e+02
44	318	72.9	436	1	R25524	2.94e+02
45	318	72.9	436	1	Y12709	2.94e+02
46	318	72.9	436	1	R38226	2.94e+02
47	318	72.9	436	1	W85613	2.94e+02
48	318	72.9	436	1	W19603	2.94e+02
49	318	72.9	436	1	W70219	2.94e+02
50	318	72.9	436	1	W29881	2.94e+02
51	318	72.9	436	1	W46489	2.94e+02
52	318	72.9	436	1	W58867	2.94e+02
53	318	72.9	436	1	W58869	2.94e+02
54	318	72.9	436	1	W71873	2.94e+02
55	318	72.9	436	1	W69389	2.94e+02
56	318	72.9	436	1	W28351	2.94e+02
57	318	72.9	436	1	W77774	2.94e+02
58	318	72.9	436	1	R50334	2.94e+02
59	318	72.9	436	1	W69423	2.94e+02
60	318	72.9	436	1	W10656	2.94e+02
61	318	72.9	436	1	R60359	2.94e+02
62	318	72.9	436	1	W55524	2.94e+02
63	318	72.9	436	1	W71872	2.94e+02
64	318	72.9	436	1	W69388	2.94e+02
65	318	72.9	436	1	W20849	2.94e+02
66	318	72.9	436	1	W54021	2.94e+02
67	318	72.9	436	1	R95609	2.94e+02
68	318	72.9	436	1	R80281	2.94e+02
69	318	72.9	436	1	R33259	2.94e+02
70	318	72.9	436	1	P82521	2.94e+02
71	318	72.9	436	1	W00679	2.94e+02
72	318	72.9	436	1	Y10948	2.94e+02
73	318	72.9	436	1	W55386	2.94e+02
74	318	72.9	436	1	Y05282	2.94e+02
75	318	72.9	436	1	W27087	2.94e+02
76	318	72.9	436	1	W60988	2.94e+02
77	318	72.9	436	1	W59129	2.94e+02
78	318	72.9	436	1	W59221	2.94e+02
79	318	72.9	436	1	R41231	2.94e+02
80	318	72.9	436	1	W28235	2.94e+02
81	318	72.9	436	1	W60592	2.94e+02
82	318	72.9	436	1	R05421	2.94e+02
83	318	72.9	436	1	R05772	2.94e+02
84	318	72.9	436	1	W20199	2.94e+02
85	318	72.9	436	1	R48743	2.94e+02
86	318	72.9	436	1	W02715	2.94e+02
87	318	72.9	436	1	W02720	2.94e+02
88	318	72.9	436	1	R48748	2.94e+02
89	318	72.9	436	1	W02718	2.94e+02
90	318	72.9	436	1	W02719	2.94e+02
91	318	72.9	436	1	R82689	2.94e+02
92	318	72.9	436	1	W55671	2.94e+02
93	318	72.9	436	1	R76767	2.94e+02
94	318	72.9	436	1	R76774	2.94e+02
95	318	72.9	436	1	R76772	2.94e+02
96	318	72.9	436	1	R76773	2.94e+02

97	6	1.4	300	1	R76745	FlmH protein derived f	2.94e+02	170	6	1.4	531	1	R07071	Sequence encoded by hu	2.94e+02
98	6	1.4	300	1	R76764	FlmH protein derived f	2.94e+02	171	6	1.4	538	1	W78755	Human EYF2.	2.94e+02
99	6	1.4	300	1	R76765	FlmH protein derived f	2.94e+02	172	6	1.4	539	1	W87799	Antipeptidase SLPD en	2.94e+02
100	6	1.4	300	1	R76771	FlmH protein derived f	2.94e+02	173	6	1.4	539	1	R80506	S. lividans protease p	2.94e+02
101	6	1.4	300	1	R76763	FlmH protein derived f	2.94e+02	174	6	1.4	546	1	W78756	Human EYF3.	2.94e+02
102	6	1.4	300	1	R76775	FlmH protein derived f	2.94e+02	175	6	1.4	548	1	R88842	E. coli llycMENA opero	2.94e+02
103	6	1.4	300	1	R76766	FlmH protein derived f	2.94e+02	176	6	1.4	548	1	W13731	E. coli llycMENA opero	2.94e+02
104	6	1.4	300	1	R76776	FlmH protein derived f	2.94e+02	177	6	1.4	548	1	W22460	Protein product of Eac	2.94e+02
105	6	1.4	300	1	R76768	FlmH protein derived f	2.94e+02	178	6	1.4	548	1	R86881	E. coli acetolactate s	2.94e+02
106	6	1.4	300	1	R76769	FlmH protein derived f	2.94e+02	179	6	1.4	552	1	W14287	E. coli theonine-deam	2.94e+02
107	6	1.4	300	1	R76770	FlmH protein derived f	2.94e+02	180	6	1.4	559	1	R13263	Human deleted in pancr	2.94e+02
108	6	1.4	301	1	R48639	Ryegrass Lol pV allere	2.94e+02	181	6	1.4	559	1	W78753	JMI-229 cell line t-Pa	2.94e+02
109	6	1.4	301	1	R71506	Lol pV (clone 12R). ma	2.94e+02	182	6	1.4	560	1	W38165	Human tyrosinase.	2.94e+02
110	6	1.4	301	1	R33555	Sequence of Lol p. Ib.1	2.94e+02	183	6	1.4	560	1	R83155	Human tyrosinase.	2.94e+02
111	6	1.4	304	1	R56480	I-19 B-lymphocyte derl	2.94e+02	184	6	1.4	563	1	R86989	Human tyrosinase.	2.94e+02
112	6	1.4	322	1	R23996	B-Hdgag-T recombinant p	2.94e+02	185	6	1.4	578	1	W26607	Thermosstable DNA poly	2.94e+02
113	6	1.4	322	1	R72736	Plasmidium falciparum	2.94e+02	186	6	1.4	592	1	W78754	Human EYF1-B.	2.94e+02
114	6	1.4	328	1	R76170	PMI2.	2.94e+02	187	6	1.4	593	1	W98782	Human EYF1-B.	2.94e+02
115	6	1.4	332	1	R76169	H. pylori ORF 29epi072	2.94e+02	188	6	1.4	595	1	W18097	Xenopus beta-signalin	2.94e+02
116	6	1.4	337	1	W74064	Absidia sporophora var	2.94e+02	189	6	1.4	602	1	R41228	CART-2 GABA transporter	2.94e+02
117	6	1.4	337	1	W7403	Absidia reiflexa lipase	2.94e+02	190	6	1.4	608	1	W26606	Thermosstable DNA poly	2.94e+02
118	6	1.4	338	1	W7403	Absidia reiflexa lipase	2.94e+02	191	6	1.4	608	1	R32657	PSI protein from C.mel	2.94e+02
119	6	1.4	338	1	W26690	Absidia reiflexa lipase	2.94e+02	192	6	1.4	657	1	R03926	T. cruzi HSP.	2.94e+02
120	6	1.4	338	1	W26691	Absidia reiflexa lipase	2.94e+02	193	6	1.4	658	1	W98873	H. pylori GPO 1739 pr	2.94e+02
121	6	1.4	338	1	W7401	Absidia corymbifera II	2.94e+02	194	6	1.4	664	1	R1606	Alcohol-oxidase.	2.94e+02
122	6	1.4	338	1	W26689	Absidia corymbifera II	2.94e+02	195	6	1.4	664	1	R1606	Recombinant alcohol ox	2.94e+02
123	6	1.4	341	1	W02599	G-protein coupled huma	2.94e+02	196	6	1.4	676	1	R89331	Tip adhesin protein an	2.94e+02
124	6	1.4	341	1	R48727	G-protein coupled huma	2.94e+02	197	6	1.4	693	1	W15140	Mammalian cell cycle r	2.94e+02
125	6	1.4	343	1	W60986	Streptococcus pneumoni	2.94e+02	198	6	1.4	719	1	W45089	Bacillus thuringiensis	2.94e+02
126	6	1.4	351	1	W20340	H. pylori secreted or	2.94e+02	199	6	1.4	719	1	R08081	81 kD endotoxin deduce	2.94e+02
127	6	1.4	351	1	W01052	Human umbilical vein e	2.94e+02	200	6	1.4	720	1	W19266	Lactobacillus amylovor	2.94e+02
128	6	1.4	371	1	R98113	Human lymphocyte cell	2.94e+02	201	6	1.4	725	1	W39165	Human RINAM protein.	2.94e+02
129	6	1.4	372	1	W36616	Celebs macaque Zcytor	2.94e+02	202	6	1.4	736	1	W97809	Human Grpase regulator	2.94e+02
130	6	1.4	373	1	W20833	H. pylori secreted or	2.94e+02	203	6	1.4	742	1	R47232	Cytomegalovirus Tome	2.94e+02
131	6	1.4	382	1	R03464	Transglutaminase type	2.94e+02	204	6	1.4	742	1	R21433	CMV Tome gH protein.	2.94e+02
132	6	1.4	385	1	P90551	Bovine substance K rec	2.94e+02	205	6	1.4	743	1	P70290	Human cytomegalovirus	2.94e+02
133	6	1.4	390	1	R25276	SCC antigen.	2.94e+02	206	6	1.4	760	1	W29490	Programmed cell death	2.94e+02
134	6	1.4	390	1	W15241	Psoriastatin type I.	2.94e+02	207	6	1.4	766	1	W55464	H. pylori ORF 07ap1121	2.94e+02
135	6	1.4	398	1	W80135	Human recombinant neur	2.94e+02	208	6	1.4	790	1	R95565	N. meningitidis seroly	2.94e+02
136	6	1.4	400	1	W80135	Human Doc2-alpha.	2.94e+02	209	6	1.4	798	1	W85013	Smad4-green fluorescen	2.94e+02
137	6	1.4	400	1	W80135	Human Doc2-alpha.	2.94e+02	210	6	1.4	806	1	W85013	Smad4-green fluorescen	2.94e+02
138	6	1.4	400	1	W80135	Human Doc2-alpha.	2.94e+02	211	6	1.4	854	1	R72855	A. nidulans FKSA.	2.94e+02
139	6	1.4	412	1	W71369	Brain-specific protein	2.94e+02	212	6	1.4	865	1	R75790	Murine predicted PMSL	2.94e+02
140	6	1.4	412	1	R74207	Death associated prote	2.94e+02	213	6	1.4	872	1	W26250	Thermolabile bacter the	2.94e+02
141	6	1.4	415	1	W22849	Human herpes virus pr	2.94e+02	214	6	1.4	909	1	W96254	Mouse semaphorin recep	2.94e+02
142	6	1.4	415	1	W22849	Human herpes virus pr	2.94e+02	215	6	1.4	909	1	W96254	Mouse semaphorin recep	2.94e+02
143	6	1.4	426	1	W55086	Streptococcus pneumoni	2.94e+02	216	6	1.4	911	1	R15355	Rat semaphorin recepto	2.94e+02
144	6	1.4	427	1	W80676	S. pneumoniae trigger	2.94e+02	217	6	1.4	911	1	R15355	Human erythrocyte memb	2.94e+02
145	6	1.4	437	1	R89329	TIP-adhesin protein.	2.94e+02	218	6	1.4	914	1	W96251	Mouse semaphorin recep	2.94e+02
146	6	1.4	438	1	R89333	Saccharomyces cerevisi	2.94e+02	219	6	1.4	916	1	W96251	Mouse semaphorin recep	2.94e+02
147	6	1.4	438	1	W01975	Saccharomyces cerevisi	2.94e+02	220	6	1.4	919	1	R50179	Secreted protein clone	2.94e+02
148	6	1.4	438	1	R71934	Sterol-delta-14-reduc	2.94e+02	221	6	1.4	925	1	W96308	Excitatory amino acid	2.94e+02
149	6	1.4	458	1	W20964	H. pylori cytoplasmic	2.94e+02	222	6	1.4	925	1	R92177	Neurotrophin-2.	2.94e+02
150	6	1.4	458	1	W55372	H. pylori ORF hp2el091	2.94e+02	223	6	1.4	925	1	R21606	SAK-a-serine-threonine	2.94e+02
151	6	1.4	459	1	W26529	Branched chain keto ac	2.94e+02	224	6	1.4	926	1	W96252	G6amylyase.	2.94e+02
152	6	1.4	465	1	W60723	36K antigen of Mycobac	2.94e+02	225	6	1.4	926	1	W96255	Mouse semaphorin recep	2.94e+02
153	6	1.4	466	1	Y00027	Enterococcus faecalis	2.94e+02	226	6	1.4	931	1	W96253	Human semaphorin recep	2.94e+02
154	6	1.4	471	1	W56742	Orphenomycos cellulase	2.94e+02	227	6	1.4	936	1	R33253	Mouse semaphorin recep	2.94e+02
155	6	1.4	485	1	Y00026	Enterococcus faecalis	2.94e+02	228	6	1.4	1026	1	R49014	Excitatory amino acid re	2.94e+02
156	6	1.4	488	1	W44322	Bacillus thuringiensis	2.94e+02	229	6	1.4	1026	1	R49014	Excitatory amino acid re	2.94e+02
157	6	1.4	508	1	W38167	Mutant human tyrosinas	2.94e+02	230	6	1.4	1026	1	R48993	rsaa S-lyase protein.	2.94e+02
158	6	1.4	526	1	W30705	Inositol-1-phosphate s	2.94e+02	231	6	1.4	1038	1	W37490	Caulobacter crescentus	2.94e+02
159	6	1.4	526	1	W79299	Inositol-1-phosphate s	2.94e+02	232	6	1.4	1038	1	W19766	Mouse Interleukin-1 re	2.94e+02
160	6	1.4	529	1	W75050	Fragment of human secr	2.94e+02	233	6	1.4	1088	1	Y00892	Hamster GAP b3 protein	2.94e+02
161	6	1.4	529	1	W03306	Tyrosinase melanoma an	2.94e+02	234	6	1.4	1088	1	Y00892	Isolucy-1-TRNA synthet	2.94e+02
162	6	1.4	529	1	W71234	Tyrosinase.	2.94e+02	235	6	1.4	1132	1	R77417	Human cell cycle prote	2.94e+02
163	6	1.4	529	1	R56309	Human tyrosinase actin	2.94e+02	236	6	1.4	1132	1	W33808	Human ataxin 2.	2.94e+02
164	6	1.4	529	1	W36519	Tyrosinase containing	2.94e+02	237	6	1.4	1139	1	W76425	Human JAK2 protein seq	2.94e+02
165	6	1.4	529	1	W00184	Human tyrosinase.	2.94e+02	238	6	1.4	1278	1	W88445	Human NCI1 (Niemann-P1	2.94e+02
166	6	1.4	529	1	R63623	Human tyrosinase prote	2.94e+02	239	6	1.4	1288	1	W92297	Mouse alpha-1 (XVIII)	2.94e+02
167	6	1.4	531	1	W38166	Normal human tyrosinas	2.94e+02	240	6	1.4	1388	1	W26328	Mouse alpha-1 collagen	2.94e+02
168	6	1.4	531	1	R79493	Human tyrosinase actin	2.94e+02	241	6	1.4	1319	1	W88446	Mouse NCI1 orthologue.	2.94e+02
169	6	1.4	531	1	W22083	Human SK29-MEL tyrosin	2.94e+02	242	6	1.4	1358	1	W18824	Human restrictin.	2.94e+02

243	6	1.4	1358	1	W35743	Recombinant human rest	2.94e+02	316	5	1.1	66	1	Y11767	Human 5' EST secreted	2.95e+03
244	6	1.4	1358	1	R99358	Human restricitin	2.94e+02	317	5	1.1	66	1	Y11767	Human 5' EST secreted	2.95e+03
245	6	1.4	1375	1	W27283	Apoptosis inducing pro	2.94e+02	318	5	1.1	68	1	Y13043	Human secreted protein	2.95e+03
246	6	1.4	1390	1	W21636	Grapevine leafrolli vlr	2.94e+02	319	5	1.1	69	1	W94650	Human secreted protein	2.95e+03
247	6	1.4	1398	1	W94839	Pyococcus furiosus pr	2.94e+02	320	5	1.1	70	1	W94650	Human secreted protein	2.95e+03
248	6	1.4	1398	1	W24124	Protease	2.94e+02	321	5	1.1	70	1	W94650	Human secreted protein	2.95e+03
249	6	1.4	1398	1	W87008	Human multidrug resist	2.94e+02	322	5	1.1	72	1	Y12811	Human 5' EST secreted	2.95e+03
250	6	1.4	1437	1	W80597	O. longistamata Xaz1	2.94e+02	323	5	1.1	73	1	Y12335	Human 5' EST secreted	2.95e+03
251	6	1.4	1445	1	W93585	H. pylori GPO 1484 pr	2.94e+02	324	5	1.1	73	1	Y12335	Human 5' EST secreted	2.95e+03
252	6	1.4	1484	1	W55686	Helicobacter polypepti	2.94e+02	325	5	1.1	77	1	R97830	Human 5' EST secreted	2.95e+03
253	6	1.4	1891	1	W22610	Platenolide synthase O	2.94e+02	326	5	1.1	78	1	Y12046	Human 5' EST secreted	2.95e+03
254	6	1.4	1891	1	W23720	Platenolide synthase O	2.94e+02	327	5	1.1	79	1	Y07970	Human secreted protein	2.95e+03
255	6	1.4	2353	1	R93933	Haemophilus adhesin p	2.94e+02	328	5	1.1	81	1	Y12435	Human 5' EST secreted	2.95e+03
256	6	1.4	2366	1	R95011	C. difficile toxin B	2.94e+02	329	5	1.1	82	1	Y13114	Human 5' EST secreted	2.95e+03
257	6	1.4	2366	1	W68388	Clostridium difficile	2.94e+02	330	5	1.1	82	1	Y13114	Human 5' EST secreted	2.95e+03
258	6	1.4	2893	1	W98828	H. pylori GPO 1484 pr	2.94e+02	331	5	1.1	83	1	W87983	Human 5' EST secreted	2.95e+03
259	6	1.4	2893	1	W71556	Helicobacter polypepti	2.94e+02	332	5	1.1	85	1	W94684	Human 5' EST secreted	2.95e+03
260	6	1.4	3398	1	R44430	erya region polypeptid	2.94e+02	333	5	1.1	85	1	W94684	Human 5' EST secreted	2.95e+03
261	6	1.4	3898	1	R10473	Hog cholera virus geno	2.94e+02	334	5	1.1	91	1	Y11610	Human 5' EST secreted	2.95e+03
262	5	1.1	7	1	W08842	Dolastatin-15 derivati	2.95e+03	335	5	1.1	92	1	W95346	Human 5' EST secreted	2.95e+03
263	5	1.1	8	1	W08835	Dolastatin-15 derivati	2.95e+03	336	5	1.1	96	1	Y12862	Human 5' EST secreted	2.95e+03
264	5	1.1	9	1	W08875	Predicted binding site	2.95e+03	337	5	1.1	96	1	Y12862	Human 5' EST secreted	2.95e+03
265	5	1.1	9	1	R87430	Human MHC class II bin	2.95e+03	338	5	1.1	96	1	W94885	Human 5' EST secreted	2.95e+03
266	5	1.1	9	1	W97918	Human MHC class II bin	2.95e+03	339	5	1.1	96	1	W94885	Human 5' EST secreted	2.95e+03
267	5	1.1	10	1	W97928	Human synaptonemal com	2.95e+03	340	5	1.1	97	1	Y12837	Human 5' EST secreted	2.95e+03
268	5	1.1	12	1	W07324	Collagen assembly inh1	2.95e+03	341	5	1.1	97	1	W00613	Human 5' EST secreted	2.95e+03
269	5	1.1	16	1	W98117	T-cell membrane protel	2.95e+03	342	5	1.1	97	1	R82458	Human 5' EST secreted	2.95e+03
270	5	1.1	17	1	W05607	Tetanus toxin helper T	2.95e+03	343	5	1.1	100	1	W28142	Human 5' EST secreted	2.95e+03
271	5	1.1	18	1	W03842	Activation domain of h	2.95e+03	344	5	1.1	103	1	W94883	Human 5' EST secreted	2.95e+03
272	5	1.1	21	1	W53348	Nephila clavipes spide	2.95e+03	345	5	1.1	103	1	W00614	Human 5' EST secreted	2.95e+03
273	5	1.1	21	1	W92319	E2A/bx1 immunogenic f	2.95e+03	346	5	1.1	103	1	W53025	Human 5' EST secreted	2.95e+03
274	5	1.1	21	1	R95023	Fragment #1 of 30 KD-1	2.95e+03	347	5	1.1	104	1	Y11335	Human 5' EST secreted	2.95e+03
275	5	1.1	23	1	R03068	Fragment of human secr	2.95e+03	348	5	1.1	104	1	R30010	Human 5' EST secreted	2.95e+03
276	5	1.1	24	1	R93066	Glycoprotein anchor se	2.95e+03	349	5	1.1	105	1	Y12249	Human 5' EST secreted	2.95e+03
277	5	1.1	24	1	R81561	Anchor sequence #2 of	2.95e+03	350	5	1.1	106	1	W67715	Human 5' EST secreted	2.95e+03
278	5	1.1	26	1	Y12058	Human 5' EST secreted	2.95e+03	351	5	1.1	106	1	W67715	Human 5' EST secreted	2.95e+03
279	5	1.1	28	1	W93833	Human 15S lipoxygenase	2.95e+03	352	5	1.1	107	1	W96714	Human 5' EST secreted	2.95e+03
280	5	1.1	29	1	W03012	Fragment of human secr	2.95e+03	353	5	1.1	107	1	W96714	Human 5' EST secreted	2.95e+03
281	5	1.1	29	1	Y12922	Amino acid sequence of	2.95e+03	354	5	1.1	107	1	R20590	Human 5' EST secreted	2.95e+03
282	5	1.1	29	1	W15659	Hepatocyte nuclear fac	2.95e+03	355	5	1.1	107	1	W07439	Human 5' EST secreted	2.95e+03
283	5	1.1	30	1	Y12545	Human 5' EST secreted	2.95e+03	356	5	1.1	107	1	W07439	Human 5' EST secreted	2.95e+03
284	5	1.1	33	1	W53349	Nephila clavipes spide	2.95e+03	357	5	1.1	110	1	W92773	Human 5' EST secreted	2.95e+03
285	5	1.1	33	1	W90039	N. crassa glutamate de	2.95e+03	358	5	1.1	111	1	W20254	Human 5' EST secreted	2.95e+03
286	5	1.1	35	1	Y12514	Human 5' EST secreted	2.95e+03	359	5	1.1	111	1	Y07876	Human 5' EST secreted	2.95e+03
287	5	1.1	35	1	Y12945	Amino acid sequence of	2.95e+03	360	5	1.1	112	1	Y09278	Human 5' EST secreted	2.95e+03
288	5	1.1	39	1	Y02740	Human secreted protein	2.95e+03	361	5	1.1	117	1	Y03266	Human 5' EST secreted	2.95e+03
289	5	1.1	41	1	Y11256	Streptococcus pneumoni	2.95e+03	362	5	1.1	119	1	Y12790	Human 5' EST secreted	2.95e+03
290	5	1.1	42	1	R71106	HEV antigenic peptide	2.95e+03	363	5	1.1	119	1	Y11396	Human 5' EST secreted	2.95e+03
291	5	1.1	44	1	Y12438	Human 5' EST secreted	2.95e+03	364	5	1.1	119	1	Y11895	Human 5' EST secreted	2.95e+03
292	5	1.1	44	1	Y12562	E. coli P1riase-alpha N	2.95e+03	365	5	1.1	120	1	W40417	Human 5' EST secreted	2.95e+03
293	5	1.1	44	1	R12912	Human 5' EST secreted	2.95e+03	366	5	1.1	122	1	Y00976	Human 5' EST secreted	2.95e+03
294	5	1.1	47	1	Y11935	Human 5' EST secreted	2.95e+03	367	5	1.1	122	1	Y11785	Human 5' EST secreted	2.95e+03
295	5	1.1	47	1	Y12566	Human 5' EST secreted	2.95e+03	368	5	1.1	123	1	W00617	Human 5' EST secreted	2.95e+03
296	5	1.1	47	1	W83947	Human secreted protein	2.95e+03	369	5	1.1	125	1	Y11240	Human 5' EST secreted	2.95e+03
297	5	1.1	47	1	Y02751	Human secreted protein	2.95e+03	370	5	1.1	125	1	P00289	Human 5' EST secreted	2.95e+03
298	5	1.1	48	1	Y11836	Human 5' EST secreted	2.95e+03	371	5	1.1	127	1	W96306	Human 5' EST secreted	2.95e+03
299	5	1.1	51	1	Y11272	Streptococcus pneumoni	2.95e+03	372	5	1.1	128	1	W67716	Human 5' EST secreted	2.95e+03
300	5	1.1	52	1	W95673	Pneumocystis carinii c	2.95e+03	373	5	1.1	128	1	R13519	Human 5' EST secreted	2.95e+03
301	5	1.1	52	1	Y03015	Fragment of human secr	2.95e+03	374	5	1.1	128	1	R54261	Human 5' EST secreted	2.95e+03
302	5	1.1	56	1	Y03015	Human secreted protein	2.95e+03	375	5	1.1	130	1	Y01487	Human 5' EST secreted	2.95e+03
303	5	1.1	57	1	W15202	Human secreted protein	2.95e+03	376	5	1.1	130	1	Y01487	Human 5' EST secreted	2.95e+03
304	5	1.1	57	1	W15202	Human secreted protein	2.95e+03	377	5	1.1	131	1	W97385	Human 5' EST secreted	2.95e+03
305	5	1.1	58	1	W74437	Human Galpha subunit N	2.95e+03	378	5	1.1	131	1	W88553	Human 5' EST secreted	2.95e+03
306	5	1.1	58	1	W74438	Human Galpha subunit N	2.95e+03	379	5	1.1	132	1	W88553	Human 5' EST secreted	2.95e+03
307	5	1.1	58	1	W69641	N-terminal region of G	2.95e+03	380	5	1.1	132	1	W88553	Human 5' EST secreted	2.95e+03
308	5	1.1	59	1	Y12866	Sequence of Elmeria ac	2.95e+03	381	5	1.1	135	1	W30891	Human 5' EST secreted	2.95e+03
309	5	1.1	60	1	R80103	Amino acid sequence of	2.95e+03	382	5	1.1	139	1	Y11233	Human 5' EST secreted	2.95e+03
310	5	1.1	61	1	Y10875	Human 5' EST secreted	2.95e+03	383	5	1.1	140	1	Y01641	Human 5' EST secreted	2.95e+03
311	5	1.1	62	1	Y11659	Human 5' EST secreted	2.95e+03	384	5	1.1	140	1	Y04885	Human 5' EST secreted	2.95e+03
312	5	1.1	64	1	Y12259	Human secreted protein	2.95e+03	385	5	1.1	142	1	Y05309	Human 5' EST secreted	2.95e+03
313	5	1.1	65	1	Y13169	Human secreted protein	2.95e+03	386	5	1.1	142	1	Y00975	Human 5' EST secreted	2.95e+03
314	5	1.1	66	1	Y12073	Human 5' EST secreted	2.95e+03	387	5	1.1	146	1	W80502	Human secreted protein	2.95e+03
315	5	1.1	66	1	W67875	Human secreted protein	2.95e+03	388	5	1.1	147	1	Y13074	Human secreted protein	2.95e+03

389	5	1.1	147	1	Y01642	A Brassica napus prote	2.95e+03	462	5	1.1	234	1	W74866	Human secreted protein	2.95e+03
390	5	1.1	148	1	W96307	Tango-69 type-II memb	2.95e+03	463	5	1.1	235	1	R01555	Pertussis toxin clone	2.95e+03
391	5	1.1	148	1	R99496	Genetic Met-X-Ob prot	2.95e+03	464	5	1.1	235	1	R01555	Pertussis toxin clone	2.95e+03
392	5	1.1	150	1	W93583	Mouse mAbPO4-gamma prot	2.95e+03	465	5	1.1	235	1	R01555	Pertussis toxin clone	2.95e+03
393	5	1.1	150	1	Y11199	S. pneumoniae protein	2.95e+03	466	5	1.1	237	1	W60441	Sensence-protein der	2.95e+03
394	5	1.1	150	1	Y02643	A. actinomycetemcomit	2.95e+03	467	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
395	5	1.1	150	1	W96144	Mouse TRAIIN-R (short f	2.95e+03	468	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
396	5	1.1	154	1	Y11119	S. pneumoniae IS12 pro	2.95e+03	469	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
397	5	1.1	158	1	W97248	Acyladenylation domain	2.95e+03	470	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
398	5	1.1	159	1	W97250	Acyladenylation domain	2.95e+03	471	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
399	5	1.1	160	1	W97250	Acyladenylation domain	2.95e+03	472	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
400	5	1.1	160	1	W97250	Acyladenylation domain	2.95e+03	473	5	1.1	237	1	W60441	Human LFA-3 antigen	2.95e+03
401	5	1.1	163	1	R37863	Deduced from clone Lam	2.95e+03	474	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
402	5	1.1	163	1	R37863	Human 5' EST secreted	2.95e+03	475	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
403	5	1.1	164	1	P70241	Polypeptide conferring	2.95e+03	476	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
404	5	1.1	164	1	P70241	Human H-rev 107-like p	2.95e+03	477	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
405	5	1.1	166	1	Y00974	CRCA-1 protein sequenc	2.95e+03	478	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
406	5	1.1	167	1	W46876	Protein sequence encod	2.95e+03	479	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
407	5	1.1	169	1	W88404	Human adult testis sec	2.95e+03	480	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
408	5	1.1	177	1	R98370	Mycobacterial AhpP pol	2.95e+03	481	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
409	5	1.1	178	1	R98370	H. pylori GHPO 1741 pr	2.95e+03	482	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
410	5	1.1	179	1	Y03772	S. aureus spoo2 polyp	2.95e+03	483	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
411	5	1.1	180	1	W98874	H. pylori GHPO 1741 pr	2.95e+03	484	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
412	5	1.1	182	1	Y07759	Human secreted protein	2.95e+03	485	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
413	5	1.1	186	1	W97109	Thermotable polypepti	2.95e+03	486	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
414	5	1.1	187	1	W20795	H. pylori outer membra	2.95e+03	487	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
415	5	1.1	190	1	R67238	Human glial cell grow	2.95e+03	488	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
416	5	1.1	190	1	W92757	US5856134 Seq ID 38	2.95e+03	489	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
417	5	1.1	191	1	Y00771	Human tag7 clone prote	2.95e+03	490	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
418	5	1.1	191	1	W64119	Human interferon recep	2.95e+03	491	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
419	5	1.1	192	1	R89548	Hepatitis C virus isol	2.95e+03	492	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
420	5	1.1	193	1	Y01410	Secreted protein encod	2.95e+03	493	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
421	5	1.1	193	1	P60463	Sequence of C-terminus	2.95e+03	494	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
422	5	1.1	193	1	Y10976	H. pylori ORF 01c1110	2.95e+03	495	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
423	5	1.1	194	1	P80624	AA sequence (IV) of po	2.95e+03	496	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
424	5	1.1	195	1	Y07105	Colon cancer associate	2.95e+03	497	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
425	5	1.1	196	1	W98411	H. pylori GHPO 267 pro	2.95e+03	498	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
426	5	1.1	197	1	W97134	Human guanlylate kinase	2.95e+03	499	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
427	5	1.1	198	1	W97135	Mouse guanlylate kinase	2.95e+03	500	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
428	5	1.1	200	1	W97625	Tomato prosystemin	2.95e+03	501	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
429	5	1.1	200	1	W99101	Tomato prosystemin	2.95e+03	502	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
430	5	1.1	200	1	W88109	A cockroach allergen d	2.95e+03	503	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
431	5	1.1	201	1	W93948	Human regulatory molec	2.95e+03	504	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
432	5	1.1	203	1	W97355	A partial HOOB059 poly	2.95e+03	505	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
433	5	1.1	205	1	W88400	Human foetal brain sec	2.95e+03	506	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
434	5	1.1	206	1	Y07222	MTN6-derived G protein	2.95e+03	507	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
435	5	1.1	207	1	Y07115	MO3904265 Seq ID No: 6	2.95e+03	508	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
436	5	1.1	208	1	Y05432	Mouse BAK protein sequ	2.95e+03	509	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
437	5	1.1	209	1	Y11177	S. pneumoniae N-(5'-ph	2.95e+03	510	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
438	5	1.1	211	1	Y05433	Human BAK protein sequ	2.95e+03	511	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
439	5	1.1	212	1	W92389	Human TR-interacting p	2.95e+03	512	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
440	5	1.1	213	1	W92526	Human GSTH protein	2.95e+03	513	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
441	5	1.1	213	1	P30199	Sequence encoded by VP	2.95e+03	514	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
442	5	1.1	213	1	P30373	Sequence of viral pro	2.95e+03	515	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
443	5	1.1	214	1	W93580	Mouse mAbPO4-alpha (sho	2.95e+03	516	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
444	5	1.1	214	1	W98145	Mouse TRAIIN-R (long fr	2.95e+03	517	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
445	5	1.1	215	1	Y06983	Recombinant pCO-8pt	2.95e+03	518	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
446	5	1.1	216	1	Y05280	EGF-8 homologue pRO533	2.95e+03	519	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
447	5	1.1	216	1	Y13353	Amino acid sequence of	2.95e+03	520	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
448	5	1.1	217	1	W97318	A HOOB059 polypeptide	2.95e+03	521	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
449	5	1.1	218	1	W04323	Ancyllostoma secreted p	2.95e+03	522	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
450	5	1.1	218	1	W98656	H. pylori GHPO 453 pro	2.95e+03	523	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
451	5	1.1	219	1	W80455	Human CD53 antigen	2.95e+03	524	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
452	5	1.1	219	1	W89152	Human CD53 antigen	2.95e+03	525	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
453	5	1.1	219	1	W92524	Human h4-IBSV recepto	2.95e+03	526	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
454	5	1.1	219	1	W92524	Human h4-IBSV recepto	2.95e+03	527	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
455	5	1.1	221	1	W80645	S. pneumoniae protein	2.95e+03	528	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
456	5	1.1	222	1	W20138	H. pylori cell envelop	2.95e+03	529	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
457	5	1.1	222	1	Y02661	Human secreted protein	2.95e+03	530	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
458	5	1.1	230	1	Y00195	Enterococcus faecalis	2.95e+03	531	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
459	5	1.1	230	1	W37993	Mutant Aspergillus ory	2.95e+03	532	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
460	5	1.1	232	1	Y04284	Mouse APRIL protein se	2.95e+03	533	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03
461	5	1.1	233	1	P80728	Sequence of human tumo	2.95e+03	534	5	1.1	244	1	W95053	Human CD7 antigen	2.95e+03



535	5	1.1	320	1	P10034	Sequence of VPI encode	2.95e+03	608	5	1.1	402	1	Y06894	Murine IL-2/19 fusion	2.95e+03
536	5	1.1	320	1	W06585	B. lactofermentum diam	2.95e+03	609	5	1.1	404	1	P303154	Bacterial xylanase pro	2.95e+03
537	5	1.1	323	1	W95685	Brexitella nidulans Cd	2.95e+03	610	5	1.1	405	1	P20202	Sequence encoded by pf	2.95e+03
538	5	1.1	324	1	W95684	Aleliomyces capsulata	2.95e+03	611	5	1.1	406	1	Y05393	Human TIE ligand NLR p	2.95e+03
539	5	1.1	326	1	W99066	Streptococcus pneumonia	2.95e+03	612	5	1.1	407	1	W65458	Human growth different	2.95e+03
540	5	1.1	327	1	Y05529	Soybean vesicleone redu	2.95e+03	613	5	1.1	409	1	W03442	G. max truncated SBP2	2.95e+03
541	5	1.1	327	1	W08483	Sequence of ovine IL-1	2.95e+03	614	5	1.1	409	1	W94247	C. albicans tyrosyl tr	2.95e+03
542	5	1.1	329	1	W08356	Partial human DMX-101	2.95e+03	615	5	1.1	409	1	R47256	Pre-pro-BMP4	2.95e+03
543	5	1.1	331	1	W98971	Alcaligenes sp. protei	2.95e+03	616	5	1.1	411	1	W93576	Human hsp80 protein	2.95e+03
544	5	1.1	332	1	R22213	Sequence of Interleukin	2.95e+03	617	5	1.1	411	1	W83321	Human Apo-2 protein	2.95e+03
545	5	1.1	332	1	R22218	Sequence of Interleukin	2.95e+03	618	5	1.1	411	1	W93608	Human IL-12R	2.95e+03
546	5	1.1	333	1	W99386	S. erythrae dtdp-4-Net	2.95e+03	619	5	1.1	411	1	Y00932	Human DR5 protein sequ	2.95e+03
547	5	1.1	334	1	W95103	Truncated p27/p16 fusi	2.95e+03	620	5	1.1	412	1	Y11085	H. pylori ORF hp05157	2.95e+03
548	5	1.1	334	1	W19631	Human mitogen activate	2.95e+03	621	5	1.1	412	1	W88437	Disease associated pro	2.95e+03
549	5	1.1	334	1	W97669	Human tyrosine kinase	2.95e+03	622	5	1.1	412	1	W82738	Human CpG/R6 variant	2.95e+03
550	5	1.1	335	1	W97110	Thermotoga maritima	2.95e+03	623	5	1.1	413	1	W73348	Rabbit alpha-d globin	2.95e+03
551	5	1.1	336	1	W88330	Manihotyl transferase 1	2.95e+03	624	5	1.1	413	1	W72835	Rabbit alpha-d globin	2.95e+03
552	5	1.1	337	1	Y07754	Human secreted protein	2.95e+03	625	5	1.1	415	1	R22211	Sequence of Interleukin	2.95e+03
553	5	1.1	338	1	W88361	Human lymphocyte activ	2.95e+03	626	5	1.1	415	1	R22217	Sequence of Interleukin	2.95e+03
554	5	1.1	338	1	W22503	Ubiquitin-ribosomal-40	2.95e+03	627	5	1.1	416	1	W93579	Mouse MAP4-alpha (lon	2.95e+03
555	5	1.1	338	1	Y04123	Caspase activated nuc1	2.95e+03	628	5	1.1	416	1	W92993	S. aureus f1x protein	2.95e+03
556	5	1.1	342	1	W97783	Human HIV/SIV receptor	2.95e+03	629	5	1.1	417	1	Y00927	Calreticulin	2.95e+03
557	5	1.1	347	1	W20595	H. pylori cytoplasmic	2.95e+03	630	5	1.1	417	1	W83388	Caenorhabditis elegans	2.95e+03
558	5	1.1	348	1	W95104	Truncated p27/p16 fusi	2.95e+03	631	5	1.1	417	1	R67000	Staphylococcus epiderm	2.95e+03
559	5	1.1	350	1	Y00934	Human DR5 protein sequ	2.95e+03	632	5	1.1	419	1	W99120	Streptococcus pneumoni	2.95e+03
560	5	1.1	351	1	W93072	HIV isolate WVP-5180/9	2.95e+03	633	5	1.1	419	1	W97682	Staphylococcus aureus	2.95e+03
561	5	1.1	353	1	W88346	Salmonella enterica O	2.95e+03	634	5	1.1	419	1	W81073	Amino acid sequence of	2.95e+03
562	5	1.1	353	1	W98041	Bacillus peptidase 1	2.95e+03	635	5	1.1	419	1	W01504	Wtld-type human pancre	2.95e+03
563	5	1.1	354	1	W04344	Chamaecyparis obtusa p	2.95e+03	636	5	1.1	419	1	W97680	Staphylococcus aureus	2.95e+03
564	5	1.1	355	1	W64307	Mycobacterium tubercul	2.95e+03	637	5	1.1	419	1	W93360	Wo 99/07855 Seq ID 2	2.95e+03
565	5	1.1	355	1	W83010	Human neural cell adhe	2.95e+03	638	5	1.1	420	1	R22215	Sequence of human inte	2.95e+03
566	5	1.1	355	1	Y05000	Mycobacterium specie	2.95e+03	639	5	1.1	422	1	W88360	Human lymphocyte activ	2.95e+03
567	5	1.1	356	1	Y05310	S. aureus protein sequ	2.95e+03	640	5	1.1	423	1	W96262	Sequence of human inte	2.95e+03
568	5	1.1	357	1	W60231	Bacillus thuringiensis	2.95e+03	641	5	1.1	426	1	W93937	Br13a polypeptide	2.95e+03
569	5	1.1	360	1	W97621	Human neutrophil relat	2.95e+03	642	5	1.1	427	1	R4186	S. anthracis desosam	2.95e+03
570	5	1.1	362	1	W97364	Amino acid sequence of	2.95e+03	643	5	1.1	429	1	Y06993	5-ethylpyridylsulfonate	2.95e+03
571	5	1.1	362	1	W46460	Rat ADP-ribosylarginin	2.95e+03	644	5	1.1	432	1	Y06891	Rat eukaryotic transla	2.95e+03
572	5	1.1	362	1	W97620	Mouse neutrophil relat	2.95e+03	645	5	1.1	433	1	Y03770	Human varts peptide fr	2.95e+03
573	5	1.1	363	1	W95109	Amino acid sequence of	2.95e+03	646	5	1.1	434	1	W73959	Human TP3 protein	2.95e+03
574	5	1.1	363	1	Y07116	Lung cancer associated	2.95e+03	647	5	1.1	438	1	W93151	C. saccharolyticum end	2.95e+03
575	5	1.1	363	1	W84654	G-protein coupled rece	2.95e+03	648	5	1.1	440	1	R2628	Cladosporium heliatum	2.95e+03
576	5	1.1	364	1	Y06992	Glycolytic enzyme aldo	2.95e+03	649	5	1.1	440	1	R32479	Peroxisome proliferato	2.95e+03
577	5	1.1	365	1	W95106	Human p16p27 fusion pr	2.95e+03	650	5	1.1	440	1	Y00194	Enterococcus faecalis	2.95e+03
578	5	1.1	365	1	W95096	Human p16p27 fusion pr	2.95e+03	651	5	1.1	440	1	W99597	Mouse peroxisome prol	2.95e+03
579	5	1.1	368	1	R11466	Prepro-polygalacturona	2.95e+03	652	5	1.1	441	1	R41780	Streptococcus pyogenes	2.95e+03
580	5	1.1	370	1	W98733	H. pylori GHP 923 pro	2.95e+03	653	5	1.1	443	1	W92948	W0990587 Seq ID 8	2.95e+03
581	5	1.1	370	1	W98490	H. pylori GHP 1038 pr	2.95e+03	654	5	1.1	443	1	W16120	Diclielobacter nodosus	2.95e+03
582	5	1.1	371	1	W60677	Transcription factor E	2.95e+03	655	5	1.1	444	1	Y03649	Human 7-transmembrane	2.95e+03
583	5	1.1	373	1	W05033	Recombinant pCO-11PL P	2.95e+03	656	5	1.1	444	1	W93371	Human HCNV inducible g	2.95e+03
584	5	1.1	374	1	W05033	Brevibacterium flavum	2.95e+03	657	5	1.1	444	1	W92975	G. max truncated SBP1	2.95e+03
585	5	1.1	377	1	W78124	Chimeric receptor agon	2.95e+03	658	5	1.1	445	1	W92975	H. pylori ORF hp05157	2.95e+03
586	5	1.1	377	1	W75063	Human secreted protein	2.95e+03	659	5	1.1	445	1	Y11065	Human hsp80 protein	2.95e+03
587	5	1.1	379	1	Y04830	Mycobacterium specie	2.95e+03	660	5	1.1	450	1	W06090	Human TAP-1-binding pro	2.95e+03
588	5	1.1	379	1	Y13345	Amino acid sequence of	2.95e+03	661	5	1.1	452	1	W98334	H. pylori GHP 1733 pr	2.95e+03
589	5	1.1	380	1	Y00877	Human JAPH-2 protein s	2.95e+03	662	5	1.1	457	1	W97844	Rat bone mineralisatio	2.95e+03
590	5	1.1	380	1	W95095	Human JAPH-2 protein s	2.95e+03	663	5	1.1	457	1	W97844	Rat bone mineralisatio	2.95e+03
591	5	1.1	380	1	W33603	Human p16p27 fusion pr	2.95e+03	664	5	1.1	457	1	W97844	Rat bone mineralisatio	2.95e+03
592	5	1.1	381	1	W33603	Human p16p27 fusion pr	2.95e+03	665	5	1.1	457	1	W97844	Rat bone mineralisatio	2.95e+03
593	5	1.1	381	1	W71015	Human p16p27 fusion pr	2.95e+03	666	5	1.1	459	1	Y00873	Toxin A immunogenic fr	2.95e+03
594	5	1.1	383	1	W17143	Human p16p27 fusion pr	2.95e+03	667	5	1.1	459	1	Y00873	Toxin A immunogenic fr	2.95e+03
595	5	1.1	383	1	W17143	Human p16p27 fusion pr	2.95e+03	668	5	1.1	460	1	Y00873	Toxin A immunogenic fr	2.95e+03
596	5	1.1	386	1	W17148	Human p16p27 fusion pr	2.95e+03	669	5	1.1	460	1	Y00873	Toxin A immunogenic fr	2.95e+03
597	5	1.1	388	1	W05306	Helicobacter polypepti	2.95e+03	670	5	1.1	461	1	W96984	Recombinant pCO-8CKs p	2.95e+03
598	5	1.1	388	1	W98375	S. aureus protein sequ	2.95e+03	671	5	1.1	463	1	R14530	Usp45 protein	2.95e+03
599	5	1.1	389	1	Y01090	H. pylori GHP 1138 pr	2.95e+03	672	5	1.1	463	1	W88315	O antigen fliptase inv	2.95e+03
600	5	1.1	390	1	W97585	Rice ribosomal protein	2.95e+03	673	5	1.1	464	1	W88435	Disease associated pro	2.95e+03
601	5	1.1	391	1	W95094	An ACT-1 polypeptide	2.95e+03	674	5	1.1	467	1	W59992	Silicothecin family me	2.95e+03
602	5	1.1	394	1	W69713	Human p27-p16 fusion p	2.95e+03	675	5	1.1	467	1	R46792	Phytase	2.95e+03
603	5	1.1	396	1	R29281	Streptomyces clavulige	2.95e+03	676	5	1.1	468	1	W92952	W0990587 Seq ID 12	2.95e+03
604	5	1.1	396	1	R44747	Human pre-pro-BMP-2A	2.95e+03	677	5	1.1	471	1	Y00878	Succrose fatty acid est	2.95e+03
605	5	1.1	396	1	R89680	Osteogenic protein CBM	2.95e+03	678	5	1.1	476	1	P50584	Tabacco ribulose-dipho	2.95e+03
606	5	1.1	397	1	R89680	Human osteogenic prote	2.95e+03	679	5	1.1	479	1	W96320	Glutathione reductase	2.95e+03
607	5	1.1	397	1	R43588	Ragweed Pollen Allerge	2.95e+03	680	5	1.1	480	1	Y03184	Topoisomerase II blndi	2.95e+03
608	5	1.1	397	1	W80212	Human cardiac and panc	2.95e+03						Y04109	Staphylococcus aureus	2.95e+03
609	5	1.1	397	1	W88300	Galactosyl transferase	2.95e+03						Y04108	Staphylococcus aureus	2.95e+03

681	1.1	481	1	Y04145	Rat Tango-76 protein	2.95e+03	754	5	1.1	612	1	W62929	Murine H1AP-2 protein	2.95e+03
682	1.1	482	1	W88321	E. coli O157 antigen p	2.95e+03	755	5	1.1	614	1	W98113	T-cell membrane protel	2.95e+03
683	1.1	485	1	Y00895	Rat GMEB-2' protein se	2.95e+03	756	5	1.1	614	1	W98113	T-cell membrane protel	2.95e+03
684	1.1	487	1	Y11008	H. pylori ORF hp6p060	2.95e+03	757	5	1.1	619	1	Y06980	Recombinant p50-11CKS	2.95e+03
685	1.1	489	1	R66220	ADP-glucose-pyrophosph	2.95e+03	758	5	1.1	619	1	W89271	Granulocyte Ehrlichia	2.95e+03
686	1.1	489	1	W90341	G. max SBP2 protein	2.95e+03	759	5	1.1	621	1	W98548	H. pylori GHP0.1588 pr	2.95e+03
687	1.1	490	1	Y06978	Recombinant p50-9CKS p	2.95e+03	760	5	1.1	621	1	R37870	Soluble KE2 protease	2.95e+03
688	1.1	491	1	P70464	Sequence of gpv encode	2.95e+03	761	5	1.1	621	1	Y01402	Secreted protein encod	2.95e+03
689	1.1	493	1	W49070	Streptococcus pneumonia	2.95e+03	762	5	1.1	623	1	R15298	Varicella zoster virus	2.95e+03
690	1.1	496	1	W96815	Smad7 protein used to	2.95e+03	763	5	1.1	625	1	W47023	Arabidopsis thaliana S	2.95e+03
691	1.1	497	1	W93362	C. trichomatis Cys5 pro	2.95e+03	764	5	1.1	626	1	W98010	BCG Ag85B antigen phag	2.95e+03
692	1.1	497	1	P60456	Sequence of aldehyde d	2.95e+03	765	5	1.1	631	1	W43105	C. thermophilum scaffo	2.95e+03
693	1.1	498	1	W80439	Feline herpesvirus IE	2.95e+03	766	5	1.1	641	1	W93364	Mouse calpain CAP6 pr	2.95e+03
694	1.1	500	1	R12769	Cl inhibitor muten	2.95e+03	767	5	1.1	642	1	W82741	806.077 heavy chain Rd	2.95e+03
695	1.1	500	1	W18212	Recombinant Cl inhibi	2.95e+03	768	5	1.1	643	1	W82739	Clone pNG4/ASB7VH-1952	2.95e+03
696	1.1	501	1	W93490	Rat L-alpha-OHase prot	2.95e+03	769	5	1.1	647	1	W00926	Human cyclin D1-human	2.95e+03
697	1.1	503	1	W75500	Canine oral papillomav	2.95e+03	770	5	1.1	647	1	W82747	Plasid pUC19/muASB7-R	2.95e+03
698	1.1	506	1	Y04840	MYCOPACTERIUM SPECIES	2.95e+03	771	5	1.1	652	1	R63808	Human amphotrophic ret	2.95e+03
699	1.1	506	1	Y01313	Glutamine-oxoglutarate	2.95e+03	772	5	1.1	659	1	W93387	Human HEV ORF 2 protel	2.95e+03
700	1.1	507	1	W93491	Mouse L-alpha-OHase pr	2.95e+03	773	5	1.1	660	1	W93395	Human HEV ORF 2 protel	2.95e+03
701	1.1	507	1	R47517	MEV EPO receptor	2.95e+03	774	5	1.1	660	1	W93391	Human HEV ORF 2 protel	2.95e+03
702	1.1	507	1	W92894	Murine L-alpha-hydroxy	2.95e+03	775	5	1.1	660	1	W93394	Human HEV ORF 2 protel	2.95e+03
703	1.1	509	1	W47533	Amino acid sequence of	2.95e+03	776	5	1.1	660	1	W93393	Human HEV ORF 2 protel	2.95e+03
704	1.1	510	1	W93304	Xenopus activin recept	2.95e+03	777	5	1.1	660	1	W93396	Human HEV ORF 2 protel	2.95e+03
705	1.1	511	1	P81180	Sequence of alpha-amyli	2.95e+03	778	5	1.1	660	1	W93392	Swine HEV ORF 2 protel	2.95e+03
706	1.1	511	1	R23997	Immunogenic secretory	2.95e+03	779	5	1.1	660	1	W93388	Human HEV ORF 2 protel	2.95e+03
707	1.1	513	1	R54214	L-lactis branched amin	2.95e+03	780	5	1.1	660	1	W93388	Human HEV ORF 2 protel	2.95e+03
708	1.1	513	1	R80508	S. lividans protease p	2.95e+03	781	5	1.1	660	1	W93388	Human HEV ORF 2 protel	2.95e+03
709	1.1	514	1	W88426	Chlamydia pneumoniae s	2.95e+03	782	5	1.1	660	1	W93390	Human HEV ORF 2 protel	2.95e+03
710	1.1	516	1	W59448	Pea ADP-glucose pyroph	2.95e+03	783	5	1.1	661	1	W47274	Human B-cell activatio	2.95e+03
711	1.1	517	1	W94393	Variant ADP-glucose py	2.95e+03	784	5	1.1	662	1	W81502	Dead Box X (DBX) gene	2.95e+03
712	1.1	518	1	W94392	Variant ADP-glucose py	2.95e+03	785	5	1.1	666	1	W82745	Fusion protein (806.07	2.95e+03
713	1.1	524	1	W90339	G. max SBP1 protein	2.95e+03	786	5	1.1	672	1	W96957	Staphylococcus aureus	2.95e+03
714	1.1	526	1	W97814	Human butyrophilin	2.95e+03	787	5	1.1	673	1	W82742	Plasid pNG4/55.1scfV/	2.95e+03
715	1.1	527	1	W78914	Bovine butyrophilin pr	2.95e+03	788	5	1.1	675	1	W63354	P. damselae bst protein	2.95e+03
716	1.1	529	1	W96321	Human catalase sequenc	2.95e+03	789	5	1.1	675	1	W74500	Amino acid sequence of	2.95e+03
717	1.1	529	1	Y00894	Rat GMEB-2 protein seq	2.95e+03	790	5	1.1	675	1	W74499	Amino acid sequence of	2.95e+03
718	1.1	530	1	R14405	Protein 1 (1.3-fucosyl	2.95e+03	791	5	1.1	676	1	W93832	Human 15S lipoygenase	2.95e+03
719	1.1	531	1	W47002	Glutathione-S-transfer	2.95e+03	792	5	1.1	678	1	W96954	Human adenosine nucleo	2.95e+03
720	1.1	532	1	W80446	Human intracellular ad	2.95e+03	793	5	1.1	679	1	W96998	The gibbon ape leukem	2.95e+03
721	1.1	532	1	W86193	Human intracellular ad	2.95e+03	794	5	1.1	685	1	W04209	Mouse 2.5A-dependent R	2.95e+03
722	1.1	543	1	W92498	Glycine max protoporph	2.95e+03	795	5	1.1	686	1	W17597	Mutant streptavidin/liu	2.95e+03
723	1.1	544	1	R82213	Talaromyces flavus glu	2.95e+03	796	5	1.1	687	1	Y07111	Bacillus Cfrase varian	2.95e+03
724	1.1	547	1	W57261	Human Nramp1 protein	2.95e+03	797	5	1.1	692	1	W93890	Colon cancer associate	2.95e+03
725	1.1	548	1	W93671	Mutant firefly lucifer	2.95e+03	798	5	1.1	696	1	W93890	Human Hc3 protein	2.95e+03
726	1.1	548	1	R30803	Thermotable luciferas	2.95e+03	799	5	1.1	704	1	R41249	Human neutrophil relat	2.95e+03
727	1.1	548	1	W04212	Luciola lateralis luci	2.95e+03	800	5	1.1	708	1	R13355	B. ohenensis Alal8 cycl	2.95e+03
728	1.1	552	1	Y13373	Amino acid sequence of	2.95e+03	801	5	1.1	711	1	W73025	Amino acid sequence of	2.95e+03
729	1.1	552	1	W93666	Chimeric firefly lucif	2.95e+03	802	5	1.1	712	1	W80485	Helicobacter pylori 76	2.95e+03
730	1.1	560	1	W97859	Streptococcus pneumonia	2.95e+03	803	5	1.1	713	1	W97617	Islet cell antibody an	2.95e+03
731	1.1	560	1	W95088	Response regulator cog	2.95e+03	804	5	1.1	720	1	Y05452	Human neutrophil relat	2.95e+03
732	1.1	563	1	Y00893	Human GMEB-1 protein s	2.95e+03	805	5	1.1	720	1	W97618	Human heparin-like f	2.95e+03
733	1.1	565	1	W96316	Acidic leucine aminope	2.95e+03	806	5	1.1	722	1	W73107	Human neutrophil relat	2.95e+03
734	1.1	570	1	P94046	1-plastin protein deri	2.95e+03	807	5	1.1	726	1	W95636	B. f. toxin protein 211	2.95e+03
735	1.1	571	1	W96315	Acidic leucine aminope	2.95e+03	808	5	1.1	727	1	W93798	Rhodotermus marinus D	2.95e+03
736	1.1	571	1	W78491	S. coelicolor AbsAI pro	2.95e+03	809	5	1.1	729	1	W97694	Human VRRP-1 (VR2) cap	2.95e+03
737	1.1	571	1	Y00093	Enterococcus faecalis	2.95e+03	810	5	1.1	730	1	W13669	Staphylococcus aureus	2.95e+03
738	1.1	575	1	W83389	Caenorhabditis elegans	2.95e+03	811	5	1.1	732	1	W97207	C-proteinase encoded b	2.95e+03
739	1.1	576	1	R61067	Murine IL-1 receptor p	2.95e+03	812	5	1.1	735	1	W49096	A triehalose phosphor	2.95e+03
740	1.1	582	1	W81077	Amino acid sequences o	2.95e+03	813	5	1.1	745	1	W80357	Human I-kappa-B kinase	2.95e+03
741	1.1	582	1	Y01364	Human protein with Zn	2.95e+03	814	5	1.1	746	1	W80322	Human IKK-alpha	2.95e+03
742	1.1	585	1	R41359	Tumour associated 90K	2.95e+03	815	5	1.1	748	1	W98877	Bacillus thuringiensis	2.95e+03
743	1.1	589	1	P60303	Sequence encoded by th	2.95e+03	816	5	1.1	748	1	W98877	H. pylori GHP0.1750 pr	2.95e+03
744	1.1	590	1	Y04736	PDZ domain-containing	2.95e+03	817	5	1.1	754	1	W89272	Granulocyte Ehrlichia	2.95e+03
745	1.1	591	1	W97384	A catalytic telomerase	2.95e+03	818	5	1.1	754	1	W98210	Amyloid precursor prot	2.95e+03
746	1.1	592	1	W97359	A 6-transmembrane prot	2.95e+03	819	5	1.1	761	1	W99790	Desulfurococcus M1 TL	2.95e+03
747	1.1	592	1	W82661	A. thaliana L-galacton	2.95e+03	820	5	1.1	762	1	Y00939	Desulfurococcus M1 TL	2.95e+03
748	1.1	593	1	Y00092	Enterococcus faecalis	2.95e+03	821	5	1.1	766	1	Y00870	S. tuberosum isomylas	2.95e+03
749	1.1	596	1	W94459	Human neurofibromatost	2.95e+03	822	5	1.1	770	1	W97996	Human amyloid precuro	2.95e+03
750	1.1	596	1	W92643	Rat anti-oestrogen tire	2.95e+03	823	5	1.1	771	1	W97798	Aspergillus oryzae pro	2.95e+03
751	1.1	603	1	R74620	Human lung tumour Polo	2.95e+03	824	5	1.1	785	1	Y06890	Human varts protein	2.95e+03
752	1.1	603	1	Y05277	P. roqueforti beta-fir	2.95e+03	825	5	1.1	787	1	W81064	Amino acid sequence of	2.95e+03
753	1.1	606	1	Y00129	Enterococcus faecalis	2.95e+03	826	5	1.1	788	1	W75919	C-proteinase sequence	2.95e+03

827	5	1.1	789	1	W80321	Bacillus thuringiensis	2.95e+03	900	5	1.1	1059	1	Y13393	Amino acid sequence of	2.95e+03
828	5	1.1	789	1	W80320	Bacillus thuringiensis	2.95e+03	901	5	1.1	1060	1	W69314	STIMAC339 genome pol p	2.95e+03
829	5	1.1	789	1	W46863	Bacillus thuringiensis	2.95e+03	902	5	1.1	1070	1	W08747	Human colon carcinoma	2.95e+03
830	5	1.1	793	1	W81065	Amino acid sequence of	2.95e+03	903	5	1.1	1074	1	Y00186	Enterococcus faecalis	2.95e+03
831	5	1.1	800	1	W83165	Rat orphan tyrosine ki	2.95e+03	904	5	1.1	1074	1	Y00206	Enterococcus faecalis	2.95e+03
832	5	1.1	802	1	Y04922	Myobacterium species	2.95e+03	905	5	1.1	1077	1	W95559	A partial hepatitis A	2.95e+03
833	5	1.1	803	1	Y07113	Myobacterium species	2.95e+03	906	5	1.1	1077	1	W95559	Human calcium channel	2.95e+03
834	5	1.1	809	1	W19521	B. cereus VIP(A) sgn	2.95e+03	907	5	1.1	1079	1	W63154	Human calcium channel	2.95e+03
835	5	1.1	811	1	W39521	Human regulatory molec	2.95e+03	908	5	1.1	1081	1	W81600	Candida albicans CANIK	2.95e+03
836	5	1.1	815	1	Y04926	Myobacterium species	2.95e+03	909	5	1.1	1103	1	W63153	Human calcium channel	2.95e+03
837	5	1.1	823	1	W80972	Amino acid sequence of	2.95e+03	910	5	1.1	1106	1	W63153	Human calcium channel	2.95e+03
838	5	1.1	823	1	W80972	Sequence encoded by 3k	2.95e+03	911	5	1.1	1120	1	W63153	Human calcium channel	2.95e+03
839	5	1.1	831	1	W79961	Thermus flavus DNA pol	2.95e+03	912	5	1.1	1130	1	W13395	Human calcium channel	2.95e+03
840	5	1.1	832	1	W80428	DNA polymerase enzyme	2.95e+03	913	5	1.1	1132	1	W05178	H-late large tumour su	2.95e+03
841	5	1.1	832	1	W74089	Human Hpr-1 protein se	2.95e+03	914	5	1.1	1146	1	W90251	Human catalytic telome	2.95e+03
842	5	1.1	840	1	W93570	Human conductin protel	2.95e+03	915	5	1.1	1148	1	W47544	Caenorhabditis elegans	2.95e+03
843	5	1.1	840	1	W93569	Human conductin protel	2.95e+03	916	5	1.1	1148	1	W47544	Alternative cryIF/cryI	2.95e+03
844	5	1.1	843	1	W93799	Chicken VRI capsalain	2.95e+03	917	5	1.1	1155	1	W83393	Bacillus thuringiensis	2.95e+03
845	5	1.1	843	1	W93799	BRCA1 mutant from pati	2.95e+03	918	5	1.1	1176	1	R88117	CryE(d) protein	2.95e+03
846	5	1.1	844	1	R81484	Enterococcus faecalis	2.95e+03	919	5	1.1	1208	1	W47035	Bacillus thuringiensis	2.95e+03
847	5	1.1	851	1	Y00172	Enterococcus faecalis	2.95e+03	920	5	1.1	1208	1	R81520	BRCA1 mutant from samp	2.95e+03
848	5	1.1	851	1	Y00172	Enterococcus faecalis	2.95e+03	921	5	1.1	1216	1	W14497	Urease protein	2.95e+03
849	5	1.1	851	1	Y00176	Enterococcus faecalis	2.95e+03	922	5	1.1	1220	1	W03664	IBC-1 protein conferrl	2.95e+03
850	5	1.1	853	1	W81079	Amino acid sequence of	2.95e+03	923	5	1.1	1239	1	Y04734	Protein containing PDZ	2.95e+03
851	5	1.1	854	1	R44957	Feline immunodefience	2.95e+03	924	5	1.1	1255	1	W67673	Mouse mla Rho targett	2.95e+03
852	5	1.1	855	1	R51251	Staphylococcus aureus	2.95e+03	925	5	1.1	1262	1	W13505	B. bronchiseptica aden	2.95e+03
853	5	1.1	857	1	W97702	Staphylococcus aureus	2.95e+03	926	5	1.1	1262	1	W97098	HIS tagged thiorodoxin	2.95e+03
854	5	1.1	862	1	W87971	Toxin A immunogenic fr	2.95e+03	927	5	1.1	1285	1	W47000	RTU DNA polymerase C s	2.95e+03
855	5	1.1	862	1	Y07064	Renal cancer associate	2.95e+03	928	5	1.1	1285	1	R28890	Mouse Per gene product	2.95e+03
856	5	1.1	866	1	W93656	Staphylococcus aureus	2.95e+03	929	5	1.1	1291	1	R28890	Protein encoded by the	2.95e+03
857	5	1.1	868	1	Y00935	A. degensii DNA polym	2.95e+03	930	5	1.1	1291	1	Y06810	Enterococcus faecalis	2.95e+03
858	5	1.1	873	1	Y06985	Murine developmental t	2.95e+03	931	5	1.1	1301	1	Y00130	Enterococcus faecalis	2.95e+03
859	5	1.1	876	1	Y04883	M. prunae DNA polymera	2.95e+03	932	5	1.1	1301	1	Y00130	Adenyl cyclase type 9	2.95e+03
860	5	1.1	877	1	Y00938	Bacillus cereus 100 KD	2.95e+03	933	5	1.1	1305	1	W88525	Aldehyde oxidase prote	2.95e+03
861	5	1.1	884	1	R63793	Myobacterium species	2.95e+03	934	5	1.1	1358	1	W57838	Sequence encoded by hu	2.95e+03
862	5	1.1	886	1	Y04884	Human brain-specific t	2.95e+03	935	5	1.1	1370	1	P60005	Toxin 17a.	2.95e+03
863	5	1.1	887	1	Y07286	Human dystroglycan CDN	2.95e+03	936	5	1.1	1385	1	R28889	BR toxin 17a.	2.95e+03
864	5	1.1	895	1	R80231	Human axlin.	2.95e+03	937	5	1.1	1401	1	R28803	Murine MWRN polypeptid	2.95e+03
865	5	1.1	900	1	W93264	Human Hg38 protein.	2.95e+03	938	5	1.1	1401	1	W97841	Leuotoxin 101.	2.95e+03
866	5	1.1	907	1	W93889	A. ligilum ABI protel	2.95e+03	939	5	1.1	1403	1	W97574	Enterococcus faecalis	2.95e+03
867	5	1.1	915	1	W80263	Rat metabotropic gluta	2.95e+03	940	5	1.1	1416	1	Y00211	Human brr protein.	2.95e+03
868	5	1.1	921	1	R80479	Neutrophilin.	2.95e+03	941	5	1.1	1429	1	W93941	Enterococcus faecalis	2.95e+03
869	5	1.1	921	1	W96247	Human semaphorin recep	2.95e+03	942	5	1.1	1448	1	Y00210	Human brr protein.	2.95e+03
870	5	1.1	922	1	W96309	Mouse semaphorin recep	2.95e+03	943	5	1.1	1481	1	W95160	Canine ribosome recept	2.95e+03
871	5	1.1	923	1	W96246	Chlamydia pneumoniae s	2.95e+03	944	5	1.1	1508	1	R89721	hCPS1.	2.95e+03
872	5	1.1	928	1	W88421	M. catarrhalis strain	2.95e+03	945	5	1.1	1500	1	W96706	Human slit 1 mature pr	2.95e+03
873	5	1.1	930	1	W88424	Human placenta calcium	2.95e+03	946	5	1.1	1508	1	W96706	Human BAT protein.	2.95e+03
874	5	1.1	941	1	W68205	Human AOMF05 proteln.	2.95e+03	947	5	1.1	1522	1	Y04138	Topoisomerase II. bindl	2.95e+03
875	5	1.1	944	1	W43310	Human AOMF05 proteln.	2.95e+03	948	5	1.1	1522	1	Y03183	Mouse multidrug resist	2.95e+03
876	5	1.1	949	1	W93905	Human AOMF05 proteln.	2.95e+03	949	5	1.1	1528	1	W74472	Mouse multidrug resist	2.95e+03
877	5	1.1	949	1	W93905	Human AOMF05 proteln.	2.95e+03	950	5	1.1	1528	1	W99895	Human multidrug resist	2.95e+03
878	5	1.1	951	1	W93965	Human AOMF05 proteln.	2.95e+03	951	5	1.1	1528	1	W99895	Human multidrug resist	2.95e+03
879	5	1.1	951	1	W93965	Human AOMF05 proteln.	2.95e+03	952	5	1.1	1528	1	R95333	Human multidrug resist	2.95e+03
880	5	1.1	951	1	W93965	Human AOMF05 proteln.	2.95e+03	953	5	1.1	1528	1	W90182	Human multidrug resist	2.95e+03
881	5	1.1	951	1	W93965	Human AOMF05 proteln.	2.95e+03	954	5	1.1	1531	1	W74471	Human multidrug resist	2.95e+03
882	5	1.1	955	1	R42245	Human p50 protein DNA	2.95e+03	955	5	1.1	1531	1	W74471	Human multidrug resist	2.95e+03
883	5	1.1	955	1	R42245	Human p50 protein DNA	2.95e+03	956	5	1.1	1531	1	W74471	Human multidrug resist	2.95e+03
884	5	1.1	970	1	W89409	Maize phosphoenolpyruv	2.95e+03	957	5	1.1	1531	1	W99894	Human multidrug resist	2.95e+03
885	5	1.1	974	1	W64221	Human secreted protein	2.95e+03	958	5	1.1	1531	1	W99894	Human multidrug resist	2.95e+03
886	5	1.1	975	1	W93167	Human ZGBB1 protein.	2.95e+03	959	5	1.1	1534	1	W96707	Protein sequence of th	2.95e+03
887	5	1.1	985	1	W06786	ILTV glycoprotein 960.	2.95e+03	960	5	1.1	1635	1	W04139	Human slit 1 protein.	2.95e+03
888	5	1.1	986	1	W13670	C-proteinase encoded b	2.95e+03	961	5	1.1	1635	1	W34624	Human C3 protein mutan	2.95e+03
889	5	1.1	990	1	R84660	Myobacterium tubercul	2.95e+03	962	5	1.1	1661	1	W34625	Human C3 protein mutan	2.95e+03
890	5	1.1	994	1	W37904	Myobacterium tubercul	2.95e+03	963	5	1.1	1752	1	W70991	Human class II PI3 kin	2.95e+03
891	5	1.1	1005	1	W93955	Sequence of pol protel	2.95e+03	964	5	1.1	1863	1	Y07031	Breast cancer associat	2.95e+03
892	5	1.1	1014	1	W97039	A secreted blood stage	2.95e+03	965	5	1.1	1863	1	R81514	BRCA1 mutant from samp	2.95e+03
893	5	1.1	1018	1	W97039	BRCA1 mutant from samp	2.95e+03	966	5	1.1	1863	1	R81514	BRCA1 mutant from samp	2.95e+03
894	5	1.1	1024	1	R81515	Human DDP protein.	2.95e+03	967	5	1.1	1863	1	W79665	BRCA1 (om11) protein s	2.95e+03
895	5	1.1	1025	1	W93361	Human DDP protein.	2.95e+03	968	5	1.1	1878	1	W81170	Human BAX2-alpha prote	2.95e+03
896	5	1.1	1025	1	Y04659	L-lactis HsdR subunit	2.95e+03	969	5	1.1	2007	1	Y04732	Protein containing PDZ	2.95e+03
897	5	1.1	1042	1	W19765	Human Interleukin-1 re	2.95e+03	970	5	1.1	2037	1	R04032	Full length T4 encoded	2.95e+03
898	5	1.1	1042	1	W93489	Human SPA-1 protein.	2.95e+03	971	5	1.1	2070	1	Y04733	Protein containing PDZ	2.95e+03
899	5	1.1	1045	1	W86354	Human DNAX toll-like r	2.95e+03	972	5	1.1	2089	1	W08333	Cyclothella cryptica ac	2.95e+03

973	5	1.1	2161	1	M87724	Ruprestis stem pitting	2.95e+03
974	5	1.1	2183	1	M48709	Measles virus Zagreb v	2.95e+03
975	5	1.1	2193	1	M48708	Measles virus Moraten	2.95e+03
976	5	1.1	2193	1	M48710	Measles virus ATK-Civa	2.95e+03
977	5	1.1	2233	1	M48711	HPV-3 JS isolate wild	2.95e+03
978	5	1.1	2283	1	M98149	Bacillus subtilis meta	2.95e+03
979	5	1.1	2332	1	M33323	Procoagulant active hu	2.95e+03
980	5	1.1	2343	1	M80989	Canine factor VIII	2.95e+03
981	5	1.1	2352	1	M11438	Active factor VIII C a	2.95e+03
982	5	1.1	2352	1	M11439	Active factor VIII C a	2.95e+03
983	5	1.1	2478	1	R04031	Full length T4 encoded	2.95e+03
984	5	1.1	2471	1	M88481	Candida albicans histi	2.95e+03
985	5	1.1	2860	1	M63651	Hepatitis G virus E2	2.95e+03
986	5	1.1	2873	1	M92755	US5856134 Seq ID 15	2.95e+03
987	5	1.1	2910	1	M89458	Hepatitis G virus vari	2.95e+03
988	5	1.1	2910	1	M92789	US5856134 Seq ID 183	2.95e+03
989	5	1.1	2963	1	M56444	Fragment HgJ1789 of a	2.95e+03
990	5	1.1	2969	1	M56449	Fragment KJ32(2Y) of a	2.95e+03
991	5	1.1	3030	1	M98022	Infectious hepatitis C	2.95e+03
992	5	1.1	3011	1	R20111	Non-A, non-B viral gen	2.95e+03
993	5	1.1	3011	1	M98020	Infectious hepatitis C	2.95e+03
994	5	1.1	3011	1	M34480	HCV polypeptide	2.95e+03
995	5	1.1	3011	1	M98021	Infectious hepatitis C	2.95e+03
996	5	1.1	3096	1	Y06919	Hexaploid wheat DBE pa	2.95e+03
997	5	1.1	3119	1	M72204	HSV-2 strain S85 Cont1	2.95e+03
998	5	1.1	3165	1	R38889	Sequence encoded by OR	2.95e+03
999	5	1.1	3366	1	R43662	DE1-S273/90 (BCACC V9	2.95e+03
1000	5	1.1	3801	1	M31949	Human b2 protein assoc	2.95e+03

## ALIGNMENTS

RESULT 1  
ID R28495 standard; Protein: 436 AA.

AC R28495;  
DT 31-MAR-1993 (first entry)  
DE Sequence of a soluble form of the interferon (IFN) receptor  
with a high affinity for IFN-alpha and -beta.  
KM Interferon receptor; alpha-interferon; beta-interferon.  
OS Synthetic.  
PN WO9218626-A.  
PD 29-OCT-1992.  
PE 17-APR-1991; F00318.  
PR 17-APR-1991; WO-F00318.  
PA (EUBI-) LAB EURO BIOTECHNOLOGIE.  
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,  
PI Tovey M, Uze G;  
DR MPI: 92-382110/46.  
DR N-PSDB: Q30532.  
PT Water soluble polypeptide(s) strongly bind interferon(s) alpha  
and beta - useful as immunosuppressants, for treating auto-immune  
PT diseases and transplant rejection  
PS Claim 2; Fig 1; 58pp; English.  
CC DNA encoding the water-soluble polypeptide with a high affinity for  
IFN-alpha and -beta is isolated by PCR, using appropriate  
CC oligonucleotides as primers and cloned cDNA as template. For example,  
CC bacteriophage lambda ZAP, containing the entire coding sequence of  
CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos  
CC Q30534 and Q30535. R28496 represents the complete receptor. R28495  
CC lacks the transmembrane and cytoplasmic domains. Both forms bind  
CC IFN in the same way as antibodies so are immunosuppressants e.g. for  
CC treating autoimmune diseases and graft rejection. They lack the  
CC toxic side-effects of known immunosuppressants such as steroids.  
SQ Sequence 436 AA;

Query Match 100.0%; Score 436; DB 1; Length 436;

Best Local Similarity 100.0%; Pred. No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVLLGATTLVAVGPVWLSAAGKMLKSPQKVEVDIIDNFTLRNRSDESGVNT 60  
1 MMVLLGATTLVAVGPVWLSAAGKMLKSPQKVEVDIIDNFTLRNRSDESGVNT 60  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	61	ESPDYOKTGDMNWKISGCONITSTKCNFSLKLNVEERIKLRREKNTSSWYVDSE	120
Qy	61	FSFDYOKTGDMNWKISGCONITSTKCNFSLKLNVEERIKLRREKNTSSWYVDSE	120
Db	121	TPFRKAQIGPPEVHEAEKKAIVIHISPTKDSVMMALDGLSTYSLLIMKSSGVEERI	180
Qy	121	TPFRKAQIGPPEVHEAEKKAIVIHISPTKDSVMMALDGLSTYSLLIMKSSGVEERI	180
Db	181	ENIYSNRKIKYKSPETTYCLKVAALITSMKIGVSPVNCIKTVEENLPPENIEVSQ	240
Qy	181	ENIYSNRKIKYKSPETTYCLKVAALITSMKIGVSPVNCIKTVEENLPPENIEVSQ	240
Db	241	NOVYVLMKDYTNAMFQVOMLAFLKRPNGNLTKYKQIPDCEKTKQCFPQVNRK	300
Qy	241	NOVYVLMKDYTNAMFQVOMLAFLKRPNGNLTKYKQIPDCEKTKQCFPQVNRK	300
Db	301	GYLLRVQASDGNSTFSESEIEKFEIOAFLPVPFNRLSDSFHYIYGAPKSGNTP	360
Qy	301	GYLLRVQASDGNSTFSESEIEKFEIOAFLPVPFNRLSDSFHYIYGAPKSGNTP	360
Db	361	VIODYPLIIEIIFEMTSSNAERKIKKIDVYVNLKPLTYCVKRAHMDKLNKSSV	420
Qy	361	VIODYPLIIEIIFEMTSSNAERKIKKIDVYVNLKPLTYCVKRAHMDKLNKSSV	420
Db	421	ESDVGCEKTKPGNTSK 436	
Qy	421	ESDVGCEKTKPGNTSK 436	

RESULT 2  
ID R14487 standard; Protein: 436 AA.

AC R14487;  
DT 16-JAN-1992 (first entry)  
DE Soluble Interferon-alpha/beta receptor.  
KM IFN; autoimmune disease; graft rejection; histocompatibility.  
OS Homo sapiens.  
PN FR2657881-A.  
PD 09-AUG-1991.  
PE 05-FEB-1990; 001298.  
PR 05-FEB-1990; FR-001298.  
PA (EUBI-) LAB EURO BIOTECHNO.  
PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;  
PI Tovey MG, Uze G;  
DR MPI: 91-319778/44.  
DR N-PSDB: Q14239.  
PT New water-soluble polypeptide(s) with affinity for IFN-alpha and  
PT beta - used to treat e.g. lupus erythematosus, Behcet's disease,  
PT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
PS Claim 2; Page 45; 52pp; French.  
CC The transmembrane and cytoplasmic domains of the native IFN receptor  
CC have been deleted to obtain a soluble, circulating form of the  
CC receptor. Potentially immunogenic epitopes have thus been eliminated.  
CC Derivatives obtained by substitution or deletion of this sequence  
CC are also claimed as are hybrid molecules comprising the soluble  
CC receptor (or deriv.) and an immunoglobulin such as IgG1.  
SQ See also Q14240.  
SQ Sequence 436 AA;

Query Match 100.0%; Score 436; DB 1; Length 436;

Best Local Similarity 100.0%; Pred. No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVLLGATTLVAVGPVWLSAAGKMLKSPQKVEVDIIDNFTLRNRSDESGVNT 60  
1 MMVLLGATTLVAVGPVWLSAAGKMLKSPQKVEVDIIDNFTLRNRSDESGVNT 60  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 61 FSPDYOKTGDMNWKISGCONITSTKCNFSLKLNVEERIKLRREKNTSSWYVDSE 120  
61 FSPDYOKTGDMNWKISGCONITSTKCNFSLKLNVEERIKLRREKNTSSWYVDSE 120

DB 121 TPFRKAQIGPPEVHEAEKKAIVIHISPTKDSVMMALDGLSTYSLLIMKSSGVEERI 180  
121 TPFRKAQIGPPEVHEAEKKAIVIHISPTKDSVMMALDGLSTYSLLIMKSSGVEERI 180

DB 181 ENIYSNRKIKYKSPETTYCLKVAALITSMKIGVSPVNCIKTVEENLPPENIEVSQ 240  
181 ENIYSNRKIKYKSPETTYCLKVAALITSMKIGVSPVNCIKTVEENLPPENIEVSQ 240

DB 241 NOVYVLMKDYTNAMFQVOMLAFLKRPNGNLTKYKQIPDCEKTKQCFPQVNRK 300  
241 NOVYVLMKDYTNAMFQVOMLAFLKRPNGNLTKYKQIPDCEKTKQCFPQVNRK 300

DB 301 GYLLRVQASDGNSTFSESEIEKFEIOAFLPVPFNRLSDSFHYIYGAPKSGNTP 360  
301 GYLLRVQASDGNSTFSESEIEKFEIOAFLPVPFNRLSDSFHYIYGAPKSGNTP 360

DB 361 VIODYPLIIEIIFEMTSSNAERKIKKIDVYVNLKPLTYCVKRAHMDKLNKSSV 420  
361 VIODYPLIIEIIFEMTSSNAERKIKKIDVYVNLKPLTYCVKRAHMDKLNKSSV 420

DB 421 ESDVGCEKTKPGNTSK 436  
421 ESDVGCEKTKPGNTSK 436

RESULT 3  
 ID R14488 standard; Protein; 557 AA.  
 AC R14488;  
 DE 16-JAN-1992 (first entry)  
 DE Complete interferon-alpha/beta receptor.  
 KW IFN; autoimmune disease; graft rejection; histocompatibility.  
 OS Homo sapiens.  
 FH Key.  
 FT domain  
 FT location/Qualifiers  
 FT 437..457  
 FT /label= transmembrane  
 FT 458..557  
 FT /label= cytoplasmic  
 PN ER2657881-A;  
 PN 09-AUG-1991.  
 PF 05-FEB-1990; 001298.  
 PR 05-FEB-1990; PR-001298.  
 PA (EUBI-) LAB EURO BIOTECHNO.  
 PI Eld P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;  
 PI Tovey NG, Uze G;  
 PI WPI; 91-319778/44.  
 RDR N-PSDB; Q14240.  
 SPT New water-soluble polypeptide(s) with affinity for IFN-alpha and  
 SPT beta, used to treat e.g. lupus erythematosus, Behcet's disease,  
 SPT aplastic anaemia, diabetes mellitus, rheumatoid arthritis, etc.  
 SPT disclosure; Page 47; 52pp; French.  
 SPT The invention covers derivatives of the interferon-alpha and/or beta  
 SPT receptor obtained by deleting the transmembrane and cytoplasmic domains  
 SPT of the native receptor or by substitution. Potentially immunogenic  
 SPT epitopes are eliminated and the deriv. can be secreted from  
 SPT transformed cells. Soluble deriv.s block the activity of IFN alpha/beta  
 SPT and can be used to treat autoimmune diseases or to inhibit graft  
 SPT rejection. See also Q14239.  
 SPT Sequence 557 AA;  
 SPT 50

ID	Accession	Protein	Length	Start	End	Score	Value	Label	Peptide	Location/Qualifiers
1	AC	R11958 standard; Protein; 557 AA.	557	1	557	100	100	100	100	100
2	AC	R11958; 18-JUL-1991 (first entry)	557	1	557	100	100	100	100	100
3	DE	Human alpha-interferon receptor protein.	557	1	557	100	100	100	100	100
4	KW	Human alpha IFN; IFN agonists; antiviral; anti tumour agent;	557	1	557	100	100	100	100	100
5	OS	drug targeting.	557	1	557	100	100	100	100	100
6	OS	Homo sapiens.	557	1	557	100	100	100	100	100
7	FH	Key	557	1	557	100	100	100	100	100
8	FT	peptide	557	1	557	100	100	100	100	100
9	FT	1..27	557	1	557	100	100	100	100	100
10	PD	WO9105862.A.	557	1	557	100	100	100	100	100
11	PD	02-MAY-1991.	557	1	557	100	100	100	100	100
12	PF	19-OCT-1990; F00758.	557	1	557	100	100	100	100	100
13	PR	20-OCT-1989; FR-013770.	557	1	557	100	100	100	100	100
14	PA	(CNRS ) CNRS CENT NAT RECH SCI.	557	1	557	100	100	100	100	100
15	PI	Mogenssen KE, Uze G, Lutfalla G, Gresser I;	557	1	557	100	100	100	100	100
16	DR	WPI; 91-148/40/20.	557	1	557	100	100	100	100	100
17	DR	N-PSDB; 011701.	557	1	557	100	100	100	100	100
18	PT	New human alpha-interferon receptor protein - useful for testing	557	1	557	100	100	100	100	100
19	PT	interferon agonists and in treatment or diagnosis	557	1	557	100	100	100	100	100
20	PS	Disclosure; fig 4; 30pp; French.	557	1	557	100	100	100	100	100
21	CC	This recombinant human alpha-interferon (IFN) receptor protein is	557	1	557	100	100	100	100	100
22	CC	useful for the testing of IFN agonists and for treatment and diag-	557	1	557	100	100	100	100	100
23	CC	nosis of viral diseases and tumours. Antibodies raised against	557	1	557	100	100	100	100	100
24	CC	this protein can be used for blocking the receptor when required,	557	1	557	100	100	100	100	100
25	CC	also where overexpression of alpha-IFN is harmful. The Abs are	557	1	557	100	100	100	100	100
26	CC	also useful for eg drug targeting. Variants of the protein,	557	1	557	100	100	100	100	100
27	CC	having residue 164 (Thr) replaced by Arg and an Asp inserted	557	1	557	100	100	100	100	100
28	CC	between residues 479 and 480, are also useful.	557	1	557	100	100	100	100	100
29	Sequence	557 AA;	557	1	557	100	100	100	100	100

	Query Match	100.08;	Score 436;	Dg 1;	Length 557;
	Best Local Similarity 100.08;		Pred. No. 0.00e+00;		
	Matches 436;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0
Db	1 MMVVLGATTLVLAVGVPMVLASAAAGKKLKSPOKVEVDIIDDNFLRMNRSDSEVGNVT				60
Oy	1 MMVVLGATTLVLAVGVPMVLASAAAGKKLKSPOKVEVDIIDDNFLRMNRSDSEVGNVT				60
Db	61 FEFDDYQKTMGNWIKLSCGQNTSTKCNFSSHLKLVYEIKRLIRAEKENTSSMYEVDSE				120
Oy	61 FEFDDYQKTMGNWIKLSCGQNTSTKCNFSSHLKLVYEIKRLIRAEKENTSSMYEVDSE				120
Db	121 PPRKAGQGPPEVHLAEADKAIYHISPGTDSYMMALDGLSFYSLLIKNSSGVEERI				180
Oy	121 PPRKAGQGPPEVHLAEADKAIYHISPGTDSYMMALDGLSFYSLLIKNSSGVEERI				180
Db	181 ENISRRHIIYLSSETTYCLKVKRAALLTSKIGIYSVPHCIKTTVENELPPPEIEIYSVQ				240
Oy	181 ENISRRHIIYLSSETTYCLKVKRAALLTSKIGIYSVPHCIKTTVENELPPPEIEIYSVQ				240
Db	241 NQNVLVKMDYYANMTPQVQYOMLHAFLKRNQNNILYKKKQILPDCENVKTTQCVFPQNVFK				300

OY 241 NONVLMKDYTNAMTFVOYOMLHAFLEKRNNGNHLKMKOIPDCENVTQCVFPONVFQK 300  
 DB 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKSGNTP 360  
 OY 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKSGNTP 360  
 DB 361 VIODYPLIYEIEMTNSNKRKIEKKTDTVPNKLPLVYCVKARAHMDEKLKSSV 420  
 OY 361 VIODYPLIYEIEMTNSNKRKIEKKTDTVPNKLPLVYCVKARAHMDEKLKSSV 420  
 DB 421 FSDVCEKTRPGNTSK 436  
 OY 421 FSDVCEKTRPGNTSK 436  
 RESULT 5  
 ID R28496 standard; Protein; 557 AA.  
 AC R42635;  
 DT 20-APR-1994 (first entry)  
 DE Human interferon receptor.  
 KW IFN-R; extracellular domain; monoclonal antibody; viral infection;  
 cell proliferation; allograft rejection; systemic lupus erythematosus;  
 psoriasis; multiple sclerosis; Behcet's Disease; aplastic anaemia;  
 immunodeficiency; measles virus; interferon-alpha-beta.  
 OS Homo sapiens.  
 PI Key Location/Qualifiers  
 FT domain 1..436  
 FT label= extracellular domain  
 FT /note= soluble; immunogenic form of IFN-R  
 EP-563487-A.  
 PD 06-OCT-1993.  
 PF 31-MAR-1992: 400902.  
 PR 31-MAR-1992: EP-400902.  
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.  
 PI Benoit P, Maguire D, Meyer F, Plavec I, Tovey MG;  
 DR MPI'93-312951/40.  
 DR P-PSDB; R42635.  
 PT Monoclonal antibody to human interferon type-I receptor - having  
 neutralising activity against human type I interferon, used for  
 therapy and diagnosis  
 PS Disclosure: Fig 3; 21pp; English.  
 CC Monoclonal antibodies produced against soluble forms of the human  
 CC interferon alpha-beta receptor based on the full-length human IFN-R  
 CC sequence are claimed. The antibodies are useful for treatment and  
 CC prophylaxis of disorders involving cell proliferation and/or viral  
 CC infection.  
 SQ Sequence 557 AA;  
 Query Match 100.0%; Score 436; DB 1; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 MMYVLLGATTLVAVANGPWVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60  
 OY 1 MMYVLLGATTLVAVANGPWVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60  
 DB 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSKLNTYEETIKLIRAEKENTSSWYEDSF 120  
 OY 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSKLNTYEETIKLIRAEKENTSSWYEDSF 120  
 DB 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSKLNTYEETIKLIRAEKENTSSWYEDSF 120  
 OY 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSKLNTYEETIKLIRAEKENTSSWYEDSF 120  
 DB 121 TPRKAOIGPPEVHLEADKAIVIHISPGTKDSVMALDGLSTYSLLIMKNSGVEERI 180  
 OY 121 TPRKAOIGPPEVHLEADKAIVIHISPGTKDSVMALDGLSTYSLLIMKNSGVEERI 180  
 DB 121 TPRKAOIGPPEVHLEADKAIVIHISPGTKDSVMALDGLSTYSLLIMKNSGVEERI 180  
 OY 121 TPRKAOIGPPEVHLEADKAIVIHISPGTKDSVMALDGLSTYSLLIMKNSGVEERI 180  
 DB 181 ENTYSRRIKIKLSPETTYCLAKVAALLTSKIGVSPVHCIKTTVENELPPENIEVSQ 240  
 OY 181 ENTYSRRIKIKLSPETTYCLAKVAALLTSKIGVSPVHCIKTTVENELPPENIEVSQ 240  
 DB 241 NONVLMKDYTNAMTFVOYOMLHAFLEKRNNGNHLKMKOIPDCENVTQCVFPONVFQK 300  
 OY 241 NONVLMKDYTNAMTFVOYOMLHAFLEKRNNGNHLKMKOIPDCENVTQCVFPONVFQK 300

DB 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKSGNTP 360  
 OY 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKSGNTP 360  
 DB 361 VIODYPLIYEIEMTNSNKRKIEKKTDTVPNKLPLVYCVKARAHMDEKLKSSV 420  
 OY 361 VIODYPLIYEIEMTNSNKRKIEKKTDTVPNKLPLVYCVKARAHMDEKLKSSV 420  
 DB 421 FSDVCEKTRPGNTSK 436  
 OY 421 FSDVCEKTRPGNTSK 436  
 RESULT 6  
 ID R28496 standard; Protein; 557 AA.  
 AC R28496;  
 DT 31-MAR-1993 (first entry)  
 DE Sequence of a soluble form of the interferon (IFN) receptor  
 DE with a high affinity for IFN-alpha and -beta.  
 KW Interferon receptor; alpha-interferon; beta-interferon.  
 OS Synthetic.  
 PN M09218626-A.  
 PD 29-OCT-1992.  
 PF 17-APR-1991: F00318.  
 PR 17-APR-1991: M0-F00318.  
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE.  
 PI Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE,  
 PI Tovey M, Uze G;  
 DR MPI'92-382110/46.  
 DR N-PSDB; Q30533.  
 PT Water soluble polypeptide(s) strongly bind interferon(s) alpha  
 PT and beta - useful as immunosuppressants, for treating auto-immune  
 PT diseases and transplant rejection  
 PS Claim 3; Fig 2; 58pp; English.  
 CC DNA encoding the water-soluble polypeptide with a high affinity for  
 CC IFN-alpha and -beta is isolated by PCR, using appropriate  
 CC oligonucleotides as primers and cloned cDNA as template. For example,  
 CC bacteriophage lambda ZAP, containing the entire coding sequence of  
 CC the IFN-alpha and -beta receptor (Q30533), was incubated with oligos  
 CC Q30534 and Q30535. R28496 represents the complete receptor. R28495  
 CC lacks the transmembrane and cytoplasmic domains. Both forms bind  
 CC IFN in the same way as antibodies so are immunosuppressants e.g. for  
 CC treating autoimmune diseases and graft rejection. They lack the  
 CC toxic side-effects of known immunosuppressants such as steroids.  
 SQ Sequence 557 AA;  
 Query Match 100.0%; Score 436; DB 1; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 MMYVLLGATTLVAVANGPWVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60  
 OY 1 MMYVLLGATTLVAVANGPWVLSAAGGNLKSPOKVEVDIIDNFIILRNRSDESIGNVT 60  
 DB 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSKLNTYEETIKLIRAEKENTSSWYEDSF 120  
 OY 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSKLNTYEETIKLIRAEKENTSSWYEDSF 120  
 DB 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSKLNTYEETIKLIRAEKENTSSWYEDSF 120  
 OY 61 FSPDYOKTGDMNLIKSGCONITSTKCNFSSKLNTYEETIKLIRAEKENTSSWYEDSF 120  
 DB 121 TPRKAOIGPPEVHLEADKAIVIHISPGTKDSVMALDGLSTYSLLIMKNSGVEERI 180  
 OY 121 TPRKAOIGPPEVHLEADKAIVIHISPGTKDSVMALDGLSTYSLLIMKNSGVEERI 180  
 DB 121 TPRKAOIGPPEVHLEADKAIVIHISPGTKDSVMALDGLSTYSLLIMKNSGVEERI 180  
 OY 121 TPRKAOIGPPEVHLEADKAIVIHISPGTKDSVMALDGLSTYSLLIMKNSGVEERI 180  
 DB 181 ENTYSRRIKIKLSPETTYCLAKVAALLTSKIGVSPVHCIKTTVENELPPENIEVSQ 240  
 OY 181 ENTYSRRIKIKLSPETTYCLAKVAALLTSKIGVSPVHCIKTTVENELPPENIEVSQ 240  
 DB 241 NONVLMKDYTNAMTFVOYOMLHAFLEKRNNGNHLKMKOIPDCENVTQCVFPONVFQK 300  
 OY 241 NONVLMKDYTNAMTFVOYOMLHAFLEKRNNGNHLKMKOIPDCENVTQCVFPONVFQK 300  
 DB 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKSGNTP 360  
 OY 301 GYLLRQASDGNNTSFWSEIKFDEIOAFLLPVPFNISLSDSFHIYIGAPKSGNTP 360





RESULT 9  
ID W21805 standard; Protein; 434 AA.  
AC W21805;  
DE 23-SEP-1997 (first entry)  
DE Spliced-deleted interferon alpha-receptor form 1.  
DE Interferon alpha-receptor; IFNAR.  
OS Homo sapiens.  
FH Key: location/Qualifiers  
FT domain 1. 427  
FT /label= Extracellular domain  
FT /note= "Comprises amino acids 1-427 of the  
FT transmembrane IFNAR"  
FT domain 428. 434  
FT /label= S-domain  
PN AU9475977-A.  
PD 11-MAY-1995.  
PE 20-OCT-1994; 075977.  
PR 24-OCT-1993; IL-107378.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
PA (ABRA/ ) ABRAMOVICH C.  
PI Abramovich C, Ratovitski E, Revel M.  
PI WPI; 95-200634/27.  
PT New mammalian soluble interferon alpha-receptor forms - used for  
PT inhibiting, modulating or modifying the activities of interferon(s)  
PS Example 2; Fig 7; 46pp; English.  
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 1.  
CC (W21805) is characterised by a new domain (S) which follows an  
CC end-deleted extracellular domain when compared to transmembrane  
CC IFNAR (W21804). There is no transmembrane domain. The amino acid  
CC sequence is predicted from a cDNA clone (see also T73520) obtd.  
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR  
CC splice-deleted forms 1 and 2 (see also W21806) probably regulate  
CC the response of human cells to IFNs, either by acting as IFN  
CC antagonists or by regulating the activity of the multiple IFN  
CC subtypes. They can be expressed in host cells and used to inhibit,  
CC modulate or modify the activities of IFNs alpha and beta in cells,  
CC tissues and organisms, or for diagnostic purposes.  
SQ Sequence 434 AA.

Query Match 86.2%; Score 376; DB 1; Length 434;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 426; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 MMYVLGATTLVLA VGPWVLSAAGKLNKSPKVEVDIIDNFILRNMSDSVGNVT 60  
QY 1 MMYVLGATTLVLA VGPWVLSAAGKLNKSPKVEVDIIDNFILRNMSDSVGNVT 60  
DB 61 FSPDYQKGMNWKISGCONITSTKCNFSSLKNTVEIKLRIRAKENTSSVYEDSF 120  
QY 61 FSPDYQKGMNWKISGCONITSTKCNFSSLKNTVEIKLRIRAKENTSSVYEDSF 120  
DB 121 TPFKRAOIGPPEVLEADKAIIVHISPGTKDSYVMAALDGLSFYSLILMNSSGVEERI 180  
QY 121 TPFKRAOIGPPEVLEADKAIIVHISPGTKDSYVMAALDGLSFYSLILMNSSGVEERI 180  
DB 121 TPFKRAOIGPPEVLEADKAIIVHISPGTKDSYVMAALDGLSFYSLILMNSSGVEERI 180  
QY 121 TPFKRAOIGPPEVLEADKAIIVHISPGTKDSYVMAALDGLSFYSLILMNSSGVEERI 180  
DB 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCCKTTVENELPPENIEVSQ 240  
QY 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCCKTTVENELPPENIEVSQ 240  
DB 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCCKTTVENELPPENIEVSQ 240  
QY 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCCKTTVENELPPENIEVSQ 240  
DB 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKQIPDCENVTQOCVFPOANTFOK 300  
QY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKQIPDCENVTQOCVFPOANTFOK 300  
DB 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKQIPDCENVTQOCVFPOANTFOK 300  
QY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKQIPDCENVTQOCVFPOANTFOK 300  
DB 301 GYLLLRVQASDGNNTSPWSEIEIKFDEIOAFLLPVENIRSLSDSFHYIGAPROSGNTP 360  
QY 301 GYLLLRVQASDGNNTSPWSEIEIKFDEIOAFLLPVENIRSLSDSFHYIGAPROSGNTP 360  
DB 301 GYLLLRVQASDGNNTSPWSEIEIKFDEIOAFLLPVENIRSLSDSFHYIGAPROSGNTP 360  
QY 301 GYLLLRVQASDGNNTSPWSEIEIKFDEIOAFLLPVENIRSLSDSFHYIGAPROSGNTP 360  
DB 361 VIQDYPLLEYIEIFEMNTSNAERKIIIEKTDVTYVNLKPLFYCYKARAHMDELKNSV 420  
QY 361 VIQDYPLLEYIEIFEMNTSNAERKIIIEKTDVTYVNLKPLFYCYKARAHMDELKNSV 420  
DB 421 FSDAVCE 427

RESULT 10  
ID W21806 standard; Protein; 496 AA.  
AC W21806;  
DE 23-SEP-1997 (first entry)  
DE Spliced-deleted interferon alpha-receptor form 2.  
DE Interferon alpha-receptor; IFNAR.  
OS Homo sapiens.  
FH Key: location/Qualifiers  
FT domain 1. 419  
FT /label= Extracellular domain  
FT /note= "Comprises amino acid residues 1-413 and  
FT 422-427 of transmembrane IFNAR"  
FT domain 420. 496  
FT /label= Intracellular domain  
FT /note= "Comprises amino acids 481-557 of  
FT transmembrane IFNAR"  
PN AU9475977-A.  
PD 11-MAY-1995.  
PE 20-OCT-1994; 075977.  
PR 24-OCT-1993; IL-107378.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
PA (ABRA/ ) ABRAMOVICH C.  
PI Abramovich C, Ratovitski E, Revel M.  
PI WPI; 95-200634/27.  
PT New mammalian soluble interferon alpha-receptor forms - used for  
PT inhibiting, modulating or modifying the activities of interferon(s)  
PS Example 3; Fig 7; 46pp; English.  
CC Novel splice-deleted interferon alpha-receptor (IFNAR) form 2  
CC (W21806) is characterised by a double deletion when compared to  
CC transmembrane IFNAR (W21804). The extracellular domain is  
CC shortened by 6 amino acid residues and is followed by a truncated  
CC intracellular domain. There is no transmembrane region. The amino  
CC acid sequence is predicted from a cDNA clone (see also T73521) obtd.  
CC from human myeloma U266 cells. Soluble, non-membrane bound IFNAR  
CC splice-deleted forms 1 (see also W21805) and 2 may regulate the  
CC response of human cells to IFNs, either by acting as IFN  
CC antagonists or by regulating IFN activities. They can be expressed  
CC in host cells and used to inhibit, modulate or modify the  
CC activities of IFNs alpha and beta in cells, tissues and organisms,  
CC or for diagnostic purposes.  
SQ Sequence 496 AA.

Query Match 83.0%; Score 362; DB 1; Length 496;  
Best Local Similarity 99.8%; Pred. No. 0.00e+00;  
Matches 412; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 MMYVLGATTLVLA VGPWVLSAAGKLNKSPKVEVDIIDNFILRNMSDSVGNVT 60  
QY 1 MMYVLGATTLVLA VGPWVLSAAGKLNKSPKVEVDIIDNFILRNMSDSVGNVT 60  
DB 61 FSPDYQKGMNWKISGCONITSTKCNFSSLKNTVEIKLRIRAKENTSSVYEDSF 120  
QY 61 FSPDYQKGMNWKISGCONITSTKCNFSSLKNTVEIKLRIRAKENTSSVYEDSF 120  
DB 121 TPFKRAOIGPPEVLEADKAIIVHISPGTKDSYVMAALDGLSFYSLILMNSSGVEERI 180  
QY 121 TPFKRAOIGPPEVLEADKAIIVHISPGTKDSYVMAALDGLSFYSLILMNSSGVEERI 180  
DB 121 TPFKRAOIGPPEVLEADKAIIVHISPGTKDSYVMAALDGLSFYSLILMNSSGVEERI 180  
QY 121 TPFKRAOIGPPEVLEADKAIIVHISPGTKDSYVMAALDGLSFYSLILMNSSGVEERI 180  
DB 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCCKTTVENELPPENIEVSQ 240  
QY 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCCKTTVENELPPENIEVSQ 240  
DB 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCCKTTVENELPPENIEVSQ 240  
QY 181 ENTYSRKIRKLSPEYTYCLKVKAAALTSKIGYSPVHCCKTTVENELPPENIEVSQ 240  
DB 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKQIPDCENVTQOCVFPOANTFOK 300  
QY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKQIPDCENVTQOCVFPOANTFOK 300  
DB 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKQIPDCENVTQOCVFPOANTFOK 300  
QY 241 NONTVLMKDYTYANMTFOVOMLHAFKRNPGNHLKMKQIPDCENVTQOCVFPOANTFOK 300  
DB 301 GYLLLRVQASDGNNTSPWSEIEIKFDEIOAFLLPVENIRSLSDSFHYIGAPROSGNTP 360  
QY 301 GYLLLRVQASDGNNTSPWSEIEIKFDEIOAFLLPVENIRSLSDSFHYIGAPROSGNTP 360  
DB 301 GYLLLRVQASDGNNTSPWSEIEIKFDEIOAFLLPVENIRSLSDSFHYIGAPROSGNTP 360  
QY 301 GYLLLRVQASDGNNTSPWSEIEIKFDEIOAFLLPVENIRSLSDSFHYIGAPROSGNTP 360



Db 361 VIDDYPIYIIFWNTSNKRIEKTIVYVNLKPLVYCVKARAHNDE 413  
 361 VIDDYPIYIIFWNTSNKRIEKTIVYVNLKPLVYCVKARAHNDE 413

RESULT 11  
 ID R71723 standard; Protein: 436 AA.

AC R71723;  
 DE IFN receptor extracellular domain.  
 KM IFN receptor; Interferon receptor; Interferon-alpha.  
 KW Interferon-beta; monoclonal antibody; Immunomodulator; AIDS.  
 OS Homo sapiens.  
 PN W09507716-A.  
 PD 23-MAR-1995.  
 PF 16-SEP-1994; E03114.  
 PR 17-SEP-1993; EP-402279.  
 PA (EUBI-) LAB EURO BIOTECHNOLOGIE SA.  
 PI Benizri EJ, Tovey MG;  
 DR WPI: 95-131187/17.  
 N-PEDB; 086457.  
 CC Compn. of monoclonal antibodies against interferon receptor  
 PT useful as immuno-modulator, eg. for treating AIDS.  
 PS Disclosure; Fig.2A-2B; 105pp; English.  
 CC A recombinant soluble form of the human interferon class I receptor  
 CC protein extracellular domain, given in R71723, was expressed in  
 CC either E. coli or COS cell hosts. The protein was used to raise  
 CC immunodulatory monoclonal antibodies.  
 SO Sequence 436 AA;

Query Match 72.9%; Score 318; DB 1; Length 436;  
 Best Local Similarity 99.7%; Pred. No. 0.00e+00;  
 Matches 368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MNVVLGATTVLVAVGPNVLSAAGKRLKSPQVEVVIDNFIILNRNSDESIGNVT 60  
 1 MNVVLGATTVLVAVGPNVLSAAGKRLKSPQVEVVIDNFIILNRNSDESIGNVT 60  
 Db 61 FSPDYOKTGMNMKILSGCONITSTKCNFSSSLKLVNVEEIKIRIREKNTSSWYVDSE 120  
 61 FSPDYOKTGMNMKILSGCONITSTKCNFSSSLKLVNVEEIKIRIREKNTSSWYVDSE 120  
 QY 61 FSPDYOKTGMNMKILSGCONITSTKCNFSSSLKLVNVEEIKIRIREKNTSSWYVDSE 120  
 Db 121 TPFRAQIGPPEVHLAEADKAIVIHISPTKDSVMALDGLSEFTSLIMKSSGVEERI 180  
 121 TPFRAQIGPPEVHLAEADKAIVIHISPTKDSVMALDGLSEFTSLIMKSSGVEERI 180  
 QY 121 TPFRAQIGPPEVHLAEADKAIVIHISPTKDSVMALDGLSEFTSLIMKSSGVEERI 180  
 Db 181 ENIYSRHKIYKISPEYTCYKAKAALLTSWKIGVYSPVHCITTVENELRPENIEVSQ 240  
 181 ENIYSRHKIYKISPEYTCYKAKAALLTSWKIGVYSPVHCITTVENELRPENIEVSQ 240  
 QY 181 ENIYSRHKIYKISPEYTCYKAKAALLTSWKIGVYSPVHCITTVENELRPENIEVSQ 240  
 Db 241 NONVTLKMDYTYANNTFOVOMLHFLKRNPNHLYKMKQIPDCEVNTKQCFPQNVK 300  
 241 NONVTLKMDYTYANNTFOVOMLHFLKRNPNHLYKMKQIPDCEVNTKQCFPQNVK 300  
 QY 241 NONVTLKMDYTYANNTFOVOMLHFLKRNPNHLYKMKQIPDCEVNTKQCFPQNVK 300  
 Db 301 GYLTLRVASDGNNTSFSSEIKFTEIOAFLLPYVFNIRSDSEFHITIGAPKSGNTP 360  
 301 GYLTLRVASDGNNTSFSSEIKFTEIOAFLLPYVFNIRSDSEFHITIGAPKSGNTP 360  
 QY 301 GYLTLRVASDGNNTSFSSEIKFTEIOAFLLPYVFNIRSDSEFHITIGAPKSGNTP 360  
 Db 361 VIQDYPLY 369  
 361 VIQDYPLY 369  
 QY 361 VIQDYPLY 369

RESULT 12  
 ID R47008 standard; Protein: 17 AA.  
 AC R47008;  
 DE IFN-alpha receptor position 271-287.  
 KM Naturally-occurring immunomodulatory protein; human; therapy; class I;  
 KM major histocompatibility complex class II; allotype; type I diabetes;  
 KM autoimmune disease; rheumatoid arthritis; T-cell-mediated response;  
 KM multiple sclerosis; transplant rejection; vaccine; MHC.

OS Homo sapiens.  
 PN M09404121-A.  
 PD 03-MAR-1994.  
 PE 11-AUG-1993; U07545.  
 PR 11-AUG-1992; US-925460.  
 PK 15-JUN-1993; US-925460.  
 PA (HARD) HARVARD COLLEGE.  
 PI Chicz RM, Hedley ML, Stern LJ, Strominger JL, Urban RG;  
 PI Vignali DA;  
 DR WPI: 94-082825/10.  
 PT Novel immunomodulatory peptide(s) and nucleic acids - useful for  
 PT treatment of auto-immune diseases, transplant rejection and for  
 PT vaccination.  
 PS Disclosure; Page 48; 139pp; English.  
 CC The sequences given in R49291-505 and R46981-7038 represent peptide  
 CC fragments of naturally-occurring immunomodulatory proteins. These  
 CC fragments are between 10-30 residues in length and bind to a human  
 CC major histocompatibility complex (MHC) class II allotype. These  
 CC peptides may be used for therapy of autoimmune diseases, such as  
 CC type I diabetes, rheumatoid arthritis and multiple sclerosis, and to  
 CC reduce transplant rejection. They may also be used for vaccination  
 CC providing an exclusively T-cell mediated response, which can be  
 CC class I or class II based, or both, depending on the length and  
 CC character of the immunogenic peptides.  
 SO Sequence 17 AA;

Query Match 3.9%; Score 17; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.21e-15;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GNHLTKMKQIPDCENVK 17  
 1 GNHLTKMKQIPDCENVK 17  
 QY 271 GNHLTKMKQIPDCENVK 287

RESULT 13  
 ID R28825 standard; Protein: 153 AA.  
 AC R28825;  
 DT 23-MAR-1993 (first entry)  
 DE Alpha 3B integrin subunit CDNA.  
 KM Mouse; alpha 6A; alpha 6B; integrin; cell surface receptor; adhesion;  
 KM extracellular matrix; cytoskeleton; heterodimer; laminin receptor;  
 KW alpha 3B.  
 OS Mus musculus.  
 FH Key  
 FT domain  
 FT Location/Qualifiers  
 FT 108..112  
 FT /note="Cytoplasmic sequence CDFFR"  
 PN W09219647-A.  
 PD 12-NOV-1992.  
 PE 27-APR-1992; U03527.  
 PR 03-MAY-1991; US-695564.  
 PA (SCRI) SCRIPPS RES INST.  
 PI Quaranta V, Tamura RN;  
 DR WPI: 92-398799/48.  
 DR N-PEDB: 031192.  
 PT Integrin alpha subunit cytoplasmic domain polypeptide(s) - used  
 PT for prodn. of antibodies and in detection of integrin sub-units  
 PT in body samples  
 PS Disclosure; Page 92; 115pp; English.  
 CC The sequences given in R28823-25 are the mouse alpha 6B, 6A and  
 CC 3B integrin subunits. Integrins are a family of cell surface  
 CC receptors which serve cellular adhesion functions. These receptors  
 CC form a link between the extracellular matrix and the cytoskeleton  
 CC through their binding to various extracellular components. Each  
 CC integrin receptor is a heterodimer comprised of an alpha and a beta  
 CC subunit. Each alpha subunit tends to associate with only one type of  
 CC beta subunit but there are several exceptions to this rule. The 6A  
 CC and 6B integrin subunits correspond to the laminin receptor and the  
 CC alpha 3B subunit corresponds to the laminin, collagen and fibronectin  
 CC receptors. The cytoplasmic domain of the 6A and 6B integrins differs  
 CC from previously isolated alpha 6 integrins.  
 SO Sequence 153 AA;

Query Match 1.6%; Score 7; DB 1; Length 153;  
Best Local Similarity 100.0%; Pred. No. 2.21e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 LTVAVG 92  
11 LTVAVG 17

## RESULT 14

ID W2599 standard; protein; 258 AA.  
AC W2599;  
DT 23-MAR-1998 (first entry)  
DE Human fast twitch skeletal muscle troponin T  
KW Human; fast twitch skeletal muscle troponin; angiogenesis; inhibitor;  
KM tumour; ocular neovascularisation; arthritis; psoriasis;  
KN atherosclerotic plaque; nonunion fracture  
OS Homo sapiens  
PN W09730085-A1  
PD 21-AUG-1997; U02439  
PF 14-FEB-1997; U02439  
PR 16-FEB-1996; US-602941;  
PA (CHIL-) CHILDRENS MEDICAL CENT.  
PI Langer RS, Moses MA, Sytkowski A, Wiedersheim DG,  
PI Wu I;  
PI WPI: 97-424977/39  
PT Use of troponin subunits as angiogenesis inhibitors - used for  
PT treating e.g. tumours, ocular neovascularisation, arthritis,  
PT psoriasis, atherosclerotic plaques or nonunion fractures  
PS Claim 1; Page 9; 51pp; English.  
CC A novel pharmaceutical composition has been developed which comprises a  
CC carrier and an angiogenesis inhibiting amount of a peptide which is:  
CC (a) an inhibitor of basic fibroblast growth factor (bFGF) stimulated  
CC bovine endothelial cell proliferation having an IC50 of at least  
CC 10 mu M; (b) greater than 75 amino acids in length; and (c) greater  
CC than 80% homologous with a subunit selected from human fast-twitch  
CC troponin subunit C, subunit I or subunit T. The present sequence  
CC represents human fast-twitch troponin subunit T. The compositions can  
CC be used for inhibiting atopic angiogenesis. They can be used to treat a  
CC cancerous condition, or to prevent progression from a pre-neoplastic or  
CC non-malignant state into a neoplastic or a malignant state. They can  
CC also be used to treat ocular disorders associated with  
CC neovascularisation such as neovascular glaucoma, diabetic retinopathy,  
CC retinoblastoma, retrolental fibroplasia, uveitis, retinopathy of  
CC prematurity, macular degeneration, corneal graft neovascularisation as  
CC well as other eye inflammatory diseases, ocular tumour and diseases  
CC associated with choroidal or iris neovascularisation. They can also be  
CC used to treat other disorders e.g. haemangioma, arthritis, psoriasis,  
CC angiodysplasia, atherosclerotic plaques, delayed wound healing,  
CC granuloma, haemophilic joints, hypertrophic scars, nonunion  
CC fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma,  
CC trachoma, and vascular adhesions.  
SQ Sequence 258 AA;

Query Match 1.6%; Score 7; DB 1; Length 258;  
Best Local Similarity 100.0%; Pred. No. 2.21e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 108 RIRAEKE 114  
103 RIRAEKE 109

## RESULT 15

ID R71035 standard; protein; 337 AA.  
AC R71035;  
DT 11-OCT-1995 (first entry)  
DE Human IFN-gamma accessory factor-1  
KW Interferon-gamma; AF-1; tumour.  
OS Homo sapiens  
PN W09505847-A.  
PD 02-MAR-1995.  
PF 22-AUG-1994; U09438.

PR 20-AUG-1993; US-110119  
PA (UYNE-) UNIV NEW JERSEY  
PI Cook JR, Donnelly RJ, Emanuel S, Kotenko S, Mariano TM,  
PI Pestka S, Schwartz B, Soh J.  
PI WPI: 95-106679/14  
DR N-PSDB: 084697  
PT Suppressing tumours in mammals with accessory factor 1 (AF-1)  
PT for interferon gamma, specifically induction of class I HLA  
PT antigens, including use of AF-1 DNA in gene therapy  
PS Disclosure; Fig 21A; 114pp; English.  
CC The sequence is that of human interferon-gamma accessory factor-1.  
CC Incorporation of AF-1 into immune and tumour cells re-establishes  
CC normal function with elimination of malignant cells.  
SQ Sequence 337 AA;

Query Match 1.6%; Score 7; DB 1; Length 337;  
Best Local Similarity 100.0%; Pred. No. 2.21e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 142 PPNIEV 148  
231 PPNIEV 237

## RESULT 16

ID R75783 standard; protein; 337 AA.  
AC R75783;  
DT 13-NOV-1995 (first entry)  
DE IFN-gamma receptor beta-subunit  
KW Interferon-gamma receptor beta subunit; hUIFN.  
KM Interferon-gamma-antagonist.  
OS Homo sapiens  
PN W09516036-A.  
PD 15-JUN-1995.  
PF 07-DEC-1994; U14277.  
PR 09-DEC-1993; US-164596.  
PA (AGUE/) AGUE M.  
PA (BOEH/) BOEHNI R.  
PA (HEMM/) HEMMI S.  
PI Aguet M, Boehni R, Hemmi S;  
PI WPI: 95-224321/29.  
DR N-PSDB: 090809.  
PT Novel interferon gamma receptor beta chain polypeptide - for  
PT treatment of inflammatory bowel disease and liver damage  
PS Claim 6; Fig. 5a; 86pp; English.  
CC The IFN-gamma receptor beta-subunit encoded by a cDNA clone derived  
CC from a human cDNA library is given in R75783. Recombinant beta-subunit,  
CC pref. with the transmembrane anchoring domain deleted or  
CC inactivated and with the cytoplasmic domain deleted, may be  
CC used to treat pathological conditions associated with endogenous  
CC IFN-gamma production.  
SQ Sequence 337 AA;

Query Match 1.6%; Score 7; DB 1; Length 337;  
Best Local Similarity 100.0%; Pred. No. 2.21e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 142 PPNIEV 148  
231 PPNIEV 237

## RESULT 17

ID R77867 standard; protein; 408 AA.  
AC R77867;  
DT 13-NOV-1995 (first entry)  
DE S. clavuligerus ORF10 product.  
KW Clavulanic acid; clavulinate; antibiotic; beta-lactamase-inhibitor.  
OS Streptomyces clavuligerus.  
PN CA2108113-A.  
PD 09-APR-1995.  
PF 08-OCT-1993; 108113.  
PR 08-OCT-1993; CA-108113.

PA (UTAL-) UNIV ALBERTA;  
PI Aldoo KA, Jensen SE, Paradar AS;  
DR WPI: 95-207301/28.  
DR N-PSDB: Q91580.  
PT Clavulanic acid biosynthesis enzymes and corresp. DNA - useful for  
PT biosynthesis of the antibiotic in Streptomyces hosts which do not  
PT naturally produce clavulanate  
PS Claim 32; Fig. 19; 41pp; English.  
CC A 15 kb fragment S. clavuligerus NRRL 5741 genomic DNA (Q91580),  
CC extending downstream from pcdc, included 10 ORFs encoding the  
CC enzymes required for clavulanate biosynthesis. The ORF10  
CC product (R77867) showed high similarity to cytochrome P450-type  
CC enzymes from other Streptomyces spp.  
SQ Sequence 408 AA;

Query Match 1.6%; Score 7; DB 1; Length 408;  
Best Local Similarity 100.0%; Pred. No. 2.21e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 206 VEERIN 212  
11111111  
QY 176 VEERIN 182

RESULT 18  
ID W20402 standard; protein: 441 AA.  
AC W20402.  
DE 14-JUL-1997 (first entry)  
DT H. pylori cytoplasmic protein: 32422343.aa.  
KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;  
KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;  
KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.  
OS Helicobacter pylori.  
FN W09640893-A1.  
PD 19-DEC-1996.  
PE 06-JUN-1996; U09122.  
PR 07-JUN-1995; US-487032.  
PR 01-APR-1996; US-630405.  
PA (ASTR) ASTRA AB.  
PI Berglindh OT, Smith D, Mellgaard BL;  
DR WPI: 97-052306/05.  
DR N-PSDB: T67585.  
PT Helicobacter pylori nucleic acid sequences and related  
PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori  
PT infection, and to detect Helicobacter  
PS Claim 61; Page 582-583; 1481pp; English.  
CC The present sequence is a H. pylori cytoplasmic protein.  
CC The protein may be used in a vaccine to prevent or treat H. pylori  
CC infection or to identify H. pylori polypeptide binding compounds,  
CC useful as potential H. pylori life cycle activators or inhibitors.  
CC The genomic sequence of H. pylori (ATCC 55679) was determined from  
CC overlapping contigs generated by mechanically shearing the bacterial  
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,  
CC and the predicted coding regions defined by computer evaluation. To  
CC identify likely H. pylori antigens for vaccine development, the amino  
CC acid sequences predicted from various ORF were analysed for significant  
CC homology to other known or exported membrane proteins. Having identified  
CC and determined the sequences of interest, particular regions can be  
CC isolated from H. pylori by PCR amplification for recombinant polypeptide  
CC production, e.g. in E. coli hosts.  
SQ Sequence 441 AA;

Query Match 1.6%; Score 7; DB 1; Length 441;  
Best Local Similarity 100.0%; Pred. No. 2.21e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 406 ELPPEN 412  
11111111  
QY 228 ELPPEN 234

RESULT 19  
ID W79159 standard; protein: 553 AA.

AC W79159;  
DE 20-NOV-1998 (first entry)  
DT Zcytor7 cytokine receptor polypeptide.  
DE Zcytor7; cytokine receptor; ligand-binding polypeptide; kidney; pancreas;  
KW type 2 cytokine receptor family; CRF2; prostate tissue; nervous tissue;  
KW agonist; cell proliferation; cell differentiation; renal disease; human;  
KW neural disease; pancreatic disease.  
OS Homo sapiens.  
FH Key.  
FT Domain  
FT 30, 250  
FT /note="extracellular (ligand-binding) domain";  
FT 275, 553  
FT /note="intracellular domain".

PN W09837193-A1  
PD 27-AUG-1998.  
PE 18-FEB-1998; U03029.  
PR 02-OCT-1997; US-943087.  
PR 20-FEB-1997; US-803305.  
PA (ZYMO) ZYMOGENETICS INC.  
PI Adams RL, Farrah TM, Jellmeberg AC, Kho CJ, Lok S,  
PI Whitmore TE;  
DR WPI: 98-480796/41.  
DR N-PSDB: V57515.  
PT Novel human Zcytor7 DNA encodes a type 2 cytokine receptor - useful  
PT for treating renal, neural, pancreatic and prostatic diseases  
PS Claim 1; Pages 55-59; 72pp; English.  
CC This represents the Zcytor7 cytokine receptor. Zcytor7 is a ligand-  
CC binding receptor polypeptide and is a novel member of the type 2 cytokine  
CC receptor family (CRF). An expression vector containing the Zcytor  
CC polynucleotide, operably linked to transcription promoter, a sequence  
CC encoding a transmembrane and intracellular domain, or both, and a  
CC transcriptional terminator can be used to transform host cells for the  
CC recombinant production of the polypeptide. The sequences can be used to  
CC study the Zcytor7 gene and to isolate ligands binding to it. Zcytor7 is  
CC preferentially expressed in the kidney, pancreas, prostate or nervous  
CC tissue. Agonists of Zcytor7 can be used to stimulate proliferation and  
CC differentiation of cell in these organs. The antagonists and agonists can  
CC also be used in the treatment of renal, neural, pancreatic and prostate  
CC diseases.  
SQ Sequence 553 AA;

Query Match 1.6%; Score 7; DB 1; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.21e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 136 QIGPEV 142  
11111111  
QY 127 QIGPEV 133

RESULT 20  
ID R14118 standard; protein: 1019 AA.  
AC R14118;  
DE 10-DEC-1991 (first entry)  
DT Human GAP b3 protein.  
KW Galactoprotein b3; carcinoma; cancer; tumour.  
OS Homo sapiens.  
FH Key.  
FT modified\_site  
FT 54  
FT /label= N-glycosylation  
FT 85  
FT /label= N-glycosylation  
FT 136, 144  
FT /label= divalent cation binding site  
FT 209, 217  
FT /label= divalent cation binding site  
FT 233  
FT /label= N-glycosylation  
FT 283, 291  
FT /label= divalent cation binding site  
FT 346, 354  
FT /label= divalent cation binding site

FT binding\_site 407.415  
 FT /label- divalent cation binding site  
 FT modified\_site 468  
 FT /label- N-glycosylation  
 FT modified\_site 479  
 FT /label- N-glycosylation  
 FT modified\_site 541  
 FT /label- N-glycosylation  
 FT modified\_site 573  
 FT /label- N-glycosylation  
 FT modified\_site 624  
 FT /label- N-glycosylation  
 FT modified\_site 665  
 FT /label- N-glycosylation  
 FT modified\_site 809  
 FT /label- N-glycosylation  
 FT modified\_site 825  
 FT /label- N-glycosylation  
 FT cleavage\_site 840.841  
 FT /label- N-glycosylation  
 FT modified\_site 894  
 FT /label- N-glycosylation  
 FT modified\_site 903  
 FT /label- N-glycosylation  
 FT modified\_site 937  
 FT /label- N-glycosylation  
 FT domain 960.987  
 FT /label- transmembrane domain  
 FT WO9113983-A.  
 FT 19-SEP-1991.  
 PD 08-APR-1991; 001606.  
 PR 12-MAR-1990; US-491910.  
 PA (BION- ) BIOMEMBRANE INST.  
 PI Tsuji T, Yamamoto F, Hakomori S.  
 PI WPI: 91-295637/40.  
 DR N-PSDB: Q13822.  
 PT DNA sequences encoding galactoprotein b3 - produced using DNA  
 PT constructs also antibodies to gap b3 used to detect tumours that  
 PT result in elevated expression of protein.  
 PS Disclosure: Fig 6, 46pp; English.  
 CC The sequence was deduced from 3 overlapping clones isolated from  
 CC a human T24 cell line cDNA library. The DNA can be used to express  
 CC the gap b3 protein which is a transformation-dependent cell surface  
 CC glycoprotein. The C-terminal 32 AA segment is likely to constitute  
 CC the cytoplasmic domain with the longer 959 AA residue segment  
 CC forming a glycosylated extracellular domain. The N-terminal region  
 CC has seven homologous repeats, three of which include the putative  
 CC metal binding sequences. Each repeat consists of a long (21-28 AA)  
 CC stretch followed by a short (5 AAs) stretch. The alignment of  
 CC glycine and hydrophobic residues in each repeat shows a similar  
 CC pattern, especially the presence of XXXGAP (X- a hydrophobic AA) at  
 CC the end of most of the longer stretches (except for the 2nd and 7th  
 CC repeats. The protein may be used to produce antibodies and these,  
 CC or the DNA sequences, can be used to detect and quantify levels of  
 CC gap b3 protein or mRNA in biological samples. A high level of the  
 CC protein is indicative of certain cancers.  
 CC See also R4117.  
 SQ Sequence 1019 AA;

Query Match 1.6%; Score 7; DB 1; Length 1019;  
 Best Local Similarity 100.0%; Pred. No. 2.21e+01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 962 LVIYAVG 968  
 11111111  
 QY 11 LVIYAVG 17

RESULT 21  
 ID W54032 standard; Protein: 1051 AA.  
 AC W54032;  
 DT 31-JUL-1998 (first entry)  
 DE Human alpha3 integrin protein.  
 KW Anti-Integrin alpha3 antibody; human; anti-tumour agent;

KW chemotherapeutic drug.  
 OS Homo sapiens.  
 PN WO9809651-A1.  
 PD 12-MAR-1998.  
 PF 03-SEP-1997; 003085.  
 PR 03-SEP-1996; JP-250887.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PI Hayakawa T, Kawata H, Sekimori Y, Shimizu K, Tomimaga E;  
 DR WPI: 98-193327/17.  
 DR N-PSDB: V23920.  
 PT Anti-Integrin alpha3 antibody and chemotherapeutic drug - useful in  
 PT anti-tumour agents and diagnostic reagent compositions  
 PS Disclosure: Page 68-76; 96pp; Japanese.  
 CC This sequence is the human alpha3 integrin protein. The alpha3  
 CC integrin sequence is targeted by the anti-Integrin alpha3 antibody of the  
 CC invention. The anti-Integrin alpha3 antibody or its antigen binding  
 CC fragment are for use as anti-tumour agents, and diagnostic reagent  
 CC compositions. They can also be used in a chemotherapeutic drug.  
 SQ Sequence 1051 AA;

Query Match 1.6%; Score 7; DB 1; Length 1051;  
 Best Local Similarity 100.0%; Pred. No. 2.21e+01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 994 LVIYAVG 1000  
 11111111  
 QY 11 LVIYAVG 17

RESULT 22  
 ID R22210 standard; Protein: 2206 AA.  
 AC R22210;  
 DT 14-JUL-1992 (first entry)  
 DE True type 3 poliovirus protein from LED3.  
 KW RNA virus; error reduction.  
 OS Poliovirus.  
 PN WO9203538-A.  
 PD 05-MAR-1992.  
 PF 20-AUG-1991; 005890.  
 PR 20-AUG-1990; US-570000.  
 PA (UYNY- ) COLUMBIA UNIV NEM Y.  
 PI Racanelli V, Tatem JM, Weekslevy CL;  
 DR WPI: 92-096882/12.  
 DR N-PSDB: Q22965.  
 PT New vaccine against infectious polio-virus comprises RNA virus -  
 PT for producing RNA virus cDNA and viable RNA virus  
 PS Disclosure: Fig 6, 110pp; English.  
 CC The protein sequence was deduced from the cDNA sequence of p3  
 CC poliovirus obd as in Q22965. The cDNA sequence is that of a  
 CC true RNA virus, i.e. the cDNA directs the prodn. of a viable  
 CC RNA virus which is phenotypically similar to the source virus.  
 CC The full length cDNA in pLED3 was infectious. In vitro  
 CC transcription of pLED3 cDNA using T7 RNA Polymerase produced  
 CC RNAs which possessed several erroneous amino acids. The RNA  
 CC viruses are used in vaccines against polio. The screening method  
 CC can be used during amplification of the source virus for vaccine  
 CC prodn. to ensure maintenance of C at position 2493 in the viral  
 CC genome i.e. increasing the attenuation. The new prod. overcomes  
 CC the problem of errors introduced during replication of ss RNA,  
 CC which is much higher than for ds DNA.  
 SQ Sequence 2206 AA;

Query Match 1.6%; Score 7; DB 1; Length 2206;  
 Best Local Similarity 100.0%; Pred. No. 2.21e+01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1271 AERENTS 1277  
 11111111  
 QY 106 AERENTS 112

RESULT 23

ID W40852 standard; peptide; 9 AA.  
AC W40852;  
DT 09-JUN-1998 (first entry)  
DE Cytotoxic Epstein-Barr T-cell epitope 25.  
KW Herpes simplex virus type 4; Epstein-Barr virus; EBV; cytotoxic;  
KM T-cell epitope; nuclear antigen; human leukocyte antigen; HLA; vaccine;  
NN tetanus toxoid; diphtheria toxoid; Bordetella pertussis;  
OS Poliovirus antigen  
PN Herpes simplex virus type 4.  
MO9745444-A1.  
PD 04-DEC-1997.  
PE 23-MAY-1997; AU0328.  
PR 24-MAY-1996; AU-000073.  
PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.  
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.  
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
PA (CSIC-) CSL LTD.  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
PA (UTME-) UNIV MELBOURNE.  
PI Burrows SR, Kerr BM, Khanna R, Misko IS, Moss DJ;  
PI WPI: 98-032576/03.  
PT Cytotoxic Epstein-Barr virus T cell epitope - useful to prepare  
PS vaccine to prevent and treat infection  
PS Claim 3; Page 3; 41pp; English.  
CC This amino acid sequence is a cytotoxic Epstein-Barr virus (EBV) T-cell  
CC epitope of the EBV nuclear antigen 6 (EBNA6) which binds the human  
CC leukocyte antigen receptor B57 (HLA B57). It is used to prepare a  
CC vaccine which may include the cytotoxic EBV T-cell epitope (W40828-  
CC W40846), or a nucleic acid sequence encoding it. The vaccine produced  
CC comprises or encodes at least one antigen (W40847-W40876) to which the  
CC individual will mount an anamnestic response, e.g. a tetanus toxoid,  
CC diphtheria toxoid, Bordetella pertussis antigen, poliovirus antigen,  
CC purified protein derivative, glycoprotein 350 protein, and/or helper  
CC epitope.  
SQ Sequence 9 AA:

Query Match. 1.4%; Score 6; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 FRKAOI 6  
IIIIII  
QY 123 FRKAOI 128

RESULT 24  
ID R80024 standard; peptide; 9 AA.  
AC R80024;  
DT 24-APR-1996 (first entry)  
DE Cytotoxic Epstein-Barr virus T-cell epitope.  
KW Epitope; EBV; cytotoxic T cell; lymphocyte; vaccine; immunisation;  
KM CD8+.  
OS Epstein-Barr virus.  
PN W09524925-A1.  
PD 21-SEP-1995.  
PE 16-MAR-1995; AU0140.  
PR 16-MAR-1994; AU-004465.  
PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.  
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.  
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
PA (CSIC-) CSL LTD.  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
PA (UTME-) UNIV MELBOURNE.  
PI Burrows JM, Burrows SR, Kerr BM, Khanna R, Moss DJ;  
PI Burrows A;  
PI WPI: 95-336817/43.  
PT New cytotoxic T-cell epitope(s) of Epstein Barr virus - useful in  
PS sub-unit vaccines to induce cytotoxic T cells  
PS Claim 1; Page 15; 23pp; English.  
CC New cytotoxic T-cell epitopes of Epstein-Barr virus have been  
CC isolated and purified (R80017-R80028). Variants of these epitopes  
CC have also been identified (R80029-R80033). The epitopes are small,  
CC stable peptides whose manufacture does not involve use of any

CC Infectious material. The epitopes may be used as components of  
CC subunit vaccines to induce cytotoxic T lymphocytes in a subject.  
CC The vaccines are partic. useful against viral infections where  
CC CD8+ cytotoxic T lymphocytes are protective.  
SQ Sequence 9 AA;

Query Match. 1.4%; Score 6; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 FRKAOI 6  
IIIIII  
QY 123 FRKAOI 128

RESULT 25  
ID R84905 standard; peptide; 9 AA.  
AC R84905;  
DT 25-APR-1996 (first entry)  
DE Epstein-Barr virus derived cytotoxic T cell epitope.  
KW Cytotoxic T cell; epitope; vaccine; antigen; tetanus; toxoid;  
KM helper; poliovirus; diphtheria.  
NN Epstein-Barr virus  
OS Epstein-Barr virus  
PN W09524926-A1.  
PD 21-SEP-1995.  
PE 16-MAR-1995; AU0141.  
PR 16-MAR-1994; AU-004465.  
PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.  
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.  
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
PA (CSIC-) CSL LTD.  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
PA (UTME-) UNIV MELBOURNE.  
PI Cox JC, Elliott SL, Subbier A;  
PI WPI: 95-336818/43.  
PT Compn. for induction of cytotoxic T cells - comprising CTL epitope  
PT and at least one antigen, in a water in oil formulation  
PS Claim 6; Page 23; 35pp; English.  
CC A water in oil compn. comprising at least 1 antigen to which an  
CC cytotoxic T cell (CTL) epitope can be used to induce CD8+ CTL.  
CC cells in a vaccine, where the CTL epitope is known. The antigen is  
CC a diphtheria toxoid, a pertussis or poliovirus antigen, a helper  
CC epitope or esp. a tetanus toxoid, and the CTL epitope is 1 of the  
CC Epstein-Barr virus derived peptides R84898-910.  
SQ Sequence 9 AA:

Query Match. 1.4%; Score 6; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 FRKAOI 6  
IIIIII  
QY 123 FRKAOI 128

RESULT 26  
ID R73033 standard; peptide; 19 AA.  
AC R73033;  
DT 18-JAN-1996 (first entry)  
DE Human tyrosinase antigenic peptide.  
KW Human tyrosinase; antigenic peptide; monoclonal anti-  
NN pigment diseases; malignant melanoma; immunoassay.  
OS Homo sapiens.  
PN W09514042-A1.  
PD 26-MAY-1995.  
PE 14-OCT-1994; J01728.  
PR 16-NOV-1993; JP-286861.  
PA (POK) POLA CHEM IND INC.  
PA Masui S, Shibata K, Suzuki S, Tay  
PI WPI: 95-200348/26.  
PT Monoclonal antibody reacting with

tyrosinase-associated protein, is used as an immunoassay reagent for melanoma diagnosis.  
 Example 1: Pages 24-25, 41pp, Japanese.  
 PS R7031-R7037 are tyrosinase antigenic peptides, with low homology to the sequence of tyrosinase associated protein (TAP). The peptides were used in the prep. of an anti-tyrosinase monoclonal antibody (mab), which does not react with TAP. The mab can be used in an immunoassay for tyrosinase in biological samples, e.g. for the diagnosis of pigment associated diseases such as malignant melanoma.  
 CC Sequence 19 AA;

Query Match 1.4%; Score 6; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 7 RNPGRH 12  
 OY 268 RNPGRH 273

RESULT 27  
 ID R71509 standard; Protein: 20 AA;  
 AC R71509;  
 DT 02-NOV-1995 (first entry)  
 DE LPIR-2.1, peptide fragment of Lol PV protein allergen.  
 KW Lolium perenne; Lol PV; Dactylis glomerata; Dac GV; epitope; sensitivity; ryegrass pollen allergen.  
 OS Lolium perenne.  
 PN WO9506728-A.  
 PD 09-MAR-1995.  
 PR 05-AUG-1994; 009024.  
 PR 13-AUG-1993; US-106016.  
 PA (IMMUNO-IMMUNOLOGIC PHARM CORP.  
 PI Griffith J, Kuo M, Lugman M;  
 DR WPI; 95-115444/15.  
 PT Lolium perenne Lol PV and Dactylis glomerata Dac GV epitope(s) and DNA - for treating sensitivity to ryegrass pollen allergen or an immunologically cross-reactive allergen.  
 PS Claim 1; Fig 2; 11pp; English.  
 CC Lol PV, is a major allergen of ryegrass pollen, and is encoded by the cDNA sequence of clone 12R (Q85932), a full-length clone derived from a lambda gt11 library. Peptides (R71508-61) comprising at least one T cell-epitope derived from the Lol PV protein are claimed, and can be used to treat or diagnose sensitivity to ryegrass pollen in an individual or to pollen proteins that are immunologically related to Lol PV, such as Dac GV (see R71507).  
 CC Sequence 20 AA;

Query Match 1.4%; Score 6; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 11 AAAGK 16  
 OY 23 AAAGK 28

RESULT 28  
 ID R71510 standard; Protein: 20 AA;  
 AC R71510;  
 DT 02-NOV-1995 (first entry)  
 DE LPIR-3, peptide fragment of Lol PV protein allergen.  
 KW Lolium perenne; Lol PV; Dactylis glomerata; Dac GV; epitope; sensitivity; ryegrass pollen allergen.  
 OS Lolium perenne.  
 PN WO9506728-A.  
 PD 09-MAR-1995.  
 PR 05-AUG-1994; 009024.  
 PR 13-AUG-1993; US-106016.  
 PA (IMMUNO-IMMUNOLOGIC PHARM CORP.  
 PI Griffith J, Kuo M, Lugman M;  
 DR WPI; 95-115444/15.

Lolium perenne Lol PV and DNA - for treating se or an immunologically cro.  
 PS Claim 1; Fig 2; 11pp; Eng  
 CC Lol PV, is a major allergen cDNA sequence of clone 12R a lambda gt11 library. Pep T cell epitope derived fro CC used to treat or diagnose or to pollen proteins that Dac GV (see R71507).  
 CC Sequence 20 AA;

Query Match 1.4%;  
 Best Local Similarity 100.0%;  
 Matches 6; Conservative

DB 1 AAAGK 6  
 OY 23 AAAGK 28

RESULT 29  
 ID R15517 standard; Protein: 23  
 AC R15517;  
 DT 09-MAR-1992 (first entry)  
 DE BMP-8 peptide.  
 KW Cartilage; wound healing; tissue repair; BMP.  
 OS Bos taurus.  
 PN WO9118098-A.  
 PD 28-NOV-1991.  
 PR 15-MAY-1991; 003388.  
 PR 16-MAY-1990; US-525357.  
 PR 15-JAN-1991; US-641204.  
 PA (GENE-GENETICS INST INC.  
 PI Hewick RM, Wang JH;  
 DR WPI; 91-369252/50.  
 DR N-PSDB; Q15240, Q15242, Q15245, Q15246.  
 PT New BMP-8 protein - useful in inducing cartilage and/or bone formation to treat wounds and repair fractures and tissues, e.g. burns, incisions and ulcers.  
 PS Claim 1(d); Page 46; 50pp; English.  
 CC This sequence shares some homology (i.e. Asn-Glu-Leu-Pro) with BMP-3 (see WO88/00205 and WO89/10409).  
 CC Pharmaceutical compns. contg. BMP-8, which comprises at least one of the fragments represented in R15517 and R15522, can be used to aid bone and/or cartilage formation or wound healing and tissue repair.  
 CC The proteins are not very species specific so can be used in domestic and farm animals as well as humans.  
 CC See also Q15240-48, R15517 and R15522.  
 CC Sequence 23 AA;

Query Match 1.4%; Score 6; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 NELPP 7  
 OY 227 NELPP 232

RESULT 30  
 ID R50181 standard; Protein: 37 AA;  
 AC R50181;  
 DT 17-OCT-1994 (first entry)  
 DE Fragment of excitatory amino acid receptor.  
 KW Excitatory amino acid receptor; EA; Identification; detection; CNS; Central nervous system; therapeutic; antibody; ligand; screening.  
 KW Homo sapiens.  
 PN EP-388642-A.  
 PD 23-MAR-1994.  
 PR 16-SEP-1993; 307325.

Imoto H;  
 human tyrosinase - but not with

body;

5710126

PR 17-SEP-1992; US-945210.  
 PA (KAMB/) KAMBOJ R.  
 PA (NOT/); NOTT S L.  
 PI Elliott CE, Kamboj R, Nutt SL;  
 DR MPI: 94-094202/12.  
 PT Nucleic acid encoding human excitatory aminoacid receptors - used  
 for producing receptors and in assays for test ligands for  
 binding to human CNS receptors.  
 PS Disclosure; Figure 3; 34pp; English.  
 CC Nucleotides which encode the excitatory amino acid receptors (EAA's)  
 can be used for the production of the receptors, to identify  
 a specimen. Recombinant cells which produce the receptors, or their  
 membrane preparations, can be used for assaying a test ligand for  
 binding to a human CNS receptor to develop therapeutics. The  
 receptors can themselves be used in the production of antibodies for  
 use in detection methods. This sequence is a fragment of an EAA  
 receptor (EAA5c) which differs from EAA5a described in R50179  
 (the fragment corresponds to amino acid residues 804-840 of EAA5a).  
 CC EAA5c is composed of 840 amino acids whereas EAA5a is composed of 889  
 amino acids (mature protein).  
 SQ Sequence: 37 AA;

Query Match 1.44; Score 6; DB 1; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 VLVAVG 7  
 |||||  
 QY 12 VLVAVG 17

RESULT 31  
 ID W40091 standard; Protein; 38 AA.  
 AC W40091;  
 DT 29-MAY-1998 (first entry)  
 DE Seq ID 99 from US5703221.  
 KM Stealth virus; chronic fatigue syndrome; CFS; disease; detection;  
 KM medical diagnostic; veterinary diagnostic; agricultural diagnostic;  
 KM quality control.  
 OS Unknown.  
 PN US5703221-A.  
 PD 30-DEC-1997.  
 PE 05-JUN-1995; 463115.  
 PR 05-JUN-1995; US-463115.  
 PR 23-MAY-1991; US-704814.  
 PR 20-SEP-1991; US-763039.  
 PR 22-MAY-1992; US-887502.  
 PR 23-NOV-1993; US-157811.  
 PA (MART/) MARTIN W J.  
 PI Martin WJ;  
 DR MPI: 98-076485/07.  
 PT Stealth virus nucleic acid molecule - useful to detecting stealth  
 virus, e.g. in chronic fatigue syndrome diagnosis  
 PS Disclosure; Column 109-110; 82pp; English.  
 CC This specification outlines the isolation and analysis of nucleic acid  
 sequences obtained from a patient with a stealth virus infection, namely  
 chronic fatigue syndrome (CFS). Such nucleic acid sequences can be used  
 to detect the stealth virus in medical, veterinary and agricultural  
 diagnostics and in industrial and pharmaceutical biological quality  
 control, e.g. to diagnose a disease associated with the stealth virus.  
 CC Note: This sequence does not appear in the printed patent specification.  
 SQ Sequence 38 AA;

Query Match 1.44; Score 6; DB 1; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 3 SDAVCE 8  
 |||||  
 QY 422 SDAVCE 427

RESULT 32  
 ID W59202 standard; Protein; 38 AA.  
 AC W59202;  
 DT 14-AUG-1998 (first entry)  
 DE Seq ID 99 from US 5753486  
 KM Chronic fatigue syndrome; CFS; vaccine; cytopathic effect;  
 KM detection.  
 OS Unknown.  
 PN US5753486-A.  
 PD 19-MAY-1998.  
 PE 05-JUN-1995; 465388.  
 PR 05-JUN-1995; US-465388.  
 PR 23-MAY-1991; US-704814.  
 PR 20-SEP-1991; US-763039.  
 PR 22-MAY-1992; US-887502.  
 PR 23-NOV-1993; US-157811.  
 PA (MART/) MARTIN W J.  
 PI Martin WJ;  
 DR MPI: 98-311405/27.  
 PT Stealth virus contained in MRC-5 cell line, ATCC number VR2343 - 1s  
 useful as a vaccine against chronic fatigue syndrome  
 PS Disclosure; Column 111-112; 99pp; English.  
 CC This specification describes the amplification of stealth virus fragments  
 from patient D.W. Such fragments can be used as vaccine against chronic  
 fatigue syndrome (CFS). This illness causes unexplained fatigue lasting  
 more than 6 months and greater than 50% reduction in an infected persons  
 normal level of activity. The virus causes a cytopathic effect (CPE) to  
 fibroblast cells observed in culture, characterised by the appearance of  
 CC rounded, slightly enlarged, refractile cells in the culture.  
 CC NOTE: This sequence is given in the Seq ID listing but is not explained  
 in the body of the specification  
 SQ Sequence 38 AA;

Query Match 1.44; Score 6; DB 1; Length 38;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 3 SDAVCE 8  
 |||||  
 QY 422 SDAVCE 427

RESULT 33  
 ID W78223 standard; Protein; 42 AA.  
 AC W78223;  
 DT 13-APR-1999 (first entry)  
 DE Human secreted protein.  
 KM Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KM developmental abnormality; foetal deficiency; blood; allergy; renal;  
 KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KM inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;  
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 OS Homo sapiens.  
 FH Key location/Qualifiers  
 FT Misc-difference 42  
 PN W09856804-A1.  
 PD 17-DEC-1998.  
 PE 02-OCT-1997; US-061060.  
 PR 13-JUN-1997; US-049547.  
 PR 13-JUN-1997; US-049548.  
 PR 13-JUN-1997; US-049549.  
 PR 13-JUN-1997; US-049550.  
 PR 13-JUN-1997; US-049606.  
 PR 13-JUN-1997; US-049607.  
 PR 13-JUN-1997; US-049608.  
 PR 13-JUN-1997; US-049609.  
 PR 13-JUN-1997; US-049610.

PR 13-JUN-1997; US-049611.  
 PR 13-JUN-1997; US-050566.  
 PR 13-JUN-1997; US-050901.  
 PR 13-JUN-1997; US-052989.  
 PR 08-JUL-1997; US-051919.  
 PR 18-AUG-1997; US-055984.  
 PR 12-SEP-1997; US-058668.  
 PR 12-SEP-1997; US-058668.  
 PR 12-SEP-1997; US-058669.  
 PR 12-SEP-1997; US-058971.  
 PR 12-SEP-1997; US-058972.  
 PR 12-SEP-1997; US-058975.  
 PR 02-OCT-1997; US-060834.  
 PR 02-OCT-1997; US-060841.  
 PR 02-OCT-1997; US-060844.  
 PR 02-OCT-1997; US-060865.  
 PR 02-OCT-1997; US-061059.  
 PR (HUMA-) HUMAN GENOME SCI INC.  
 PR Brewer LA, Edner R, Ferlie AM, Feng P, Greene JM, Lafleur DW,  
 PI Moore CA, NI J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P,  
 PI Yu GL;  
 DR MPI; 99-080881/07.  
 DR N-PSDB; X04408.  
 PT New isolated human genes and the secreted polypeptides they encode -  
 PT useful for diagnosis and treatment of e.g. cancers, neurological  
 PT disorders, immune diseases, inflammation or blood disorders  
 PS Claim 11; Page 317; 380pp; English.  
 CC This sequence represents a secreted human protein encoded by the gene  
 CC clone detailed in the descriptor line. The gene can be used to generate  
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc  
 CC portion (e.g. X04302) for increasing the stability of the fused protein  
 CC as compared to the human protein only.  
 CC The invention relates to 86 novel genes and their fragments (nucleic acid  
 CC sequences: X04311-X04410; amino acid sequences W78126-W78225) which  
 CC are useful for preventing, treating or ameliorating medical conditions  
 CC e.g. by protein or gene therapy. Also, pathological conditions can be  
 CC diagnosed by determining the amount of the new polypeptides in a sample  
 CC or by determining the presence of mutations in the new polynucleotides.  
 CC Specific uses are described for each of the 86 polynucleotides, based on  
 CC which tissues they are most highly expressed in (see X04311 for described  
 CC uses).  
 SQ Sequence 42 AA;

Query Match 1.4%; Score 6; DB 1; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 14 LSNAAG 19  
 111111  
 QY 21 LSNAAG 26

RESULT 34  
 ID W33605 standard; Protein: 45 AA.  
 AC W33605;  
 DT 21-MAY-1998 (first entry)  
 DE Human secreted protein AK583 full-length sequence.  
 KW Secreted protein; AK583; cytokine; human.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..24  
 FT Protein /Label- S1g-peptide  
 FT 25..45  
 FT /Label- Mat\_protein  
 PV W09739030-A2.  
 PD 23-OCT-1997.  
 PE 16-APR-1997; 006475.  
 PR 13-JAN-1997; US-783520.  
 PR 18-APR-1996; US-634325.  
 PA (GENY) GENETICS INST INC.  
 PI Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racle LA,  
 PI Spalding V;

DR MPI; 97-526400/48.  
 DR N-PSDB; V02297.  
 PT New isolated secretory proteins AM340, AM282 and AK583 - possibly  
 PT have cytokine, cell proliferation/differentiation regulating,  
 PT immunomodulating activities, etc.  
 PS Claim 19; Page 48; 59pp; English.  
 CC This human secreted protein, designated AK583, is encoded by a  
 CC full-length cDNA clone (see V02297), deposited in ATCC 98026, that  
 CC was identified from a database search using an isolated partial  
 CC AK583 clone (see V02299). AK583 protein can be used in a claimed  
 CC method for preventing, treating or ameliorating a medical  
 CC condition. It may exhibit cytokine, cell proliferation (either  
 CC inducing or inhibiting) or cell differentiation (either inducing or  
 CC inhibiting) activity or may induce production of other cytokines in  
 CC certain cell populations. It may also exhibit e.g. immune  
 CC stimulating or suppressing activity, haematopoiesis regulating  
 CC activity, tissue growth activity, activin/inhibin activity,  
 CC chemotactic or chemokinetic activity, haemostatic or thrombolytic  
 CC activity, receptor/ligand activity, anti-inflammatory activity,  
 CC tumour inhibition activity, or other activities. No evidence of  
 CC any of these activities is given in the specification.  
 SQ Sequence 45 AA;

Query Match 1.4%; Score 6; DB 1; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 36 EKLKNS 41  
 111111  
 QY 413 EKLKNS 418

RESULT 35  
 ID W55271 standard; Protein: 60 AA.  
 AC W55271;  
 DT 02-JUL-1998 (first entry)  
 DE H. pylori ORF 056p1091orf3 protein.  
 KW Cytoplasmic; vaccine; prevention; treatment; infection; envelope;  
 KW Identificatic; binding compound; bacteria; life cycle; activator;  
 KW Inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.  
 OS Helicobacter pylori.  
 PV W097337044-A1.  
 PD 09-OCT-1997.  
 PE 27-MAR-1997; 005223.  
 PR 06-DEC-1996; US-761318.  
 PR 29-MAR-1996; US-625811.  
 PR 02-APR-1996; US-758731.  
 PR 25-OCT-1996; US-736805.  
 PR 28-OCT-1996; US-738859.  
 PA (ASTR) ASTRA AB.  
 PI Alm RA, Smith D;  
 DR MPI; 97-503122/46.  
 DR N-PSDB; V24680.  
 PT Helicobacter pylori nucleic acid sequences, and encoded  
 PT polypeptide(s) - useful in vaccines to treat or prevent H. pylori  
 PT infection and for diagnosis of H. pylori infection  
 PS Claim 14; Page 510; 1145pp; English.  
 CC This sequence is a H. pylori protein of unspecified function.  
 CC The protein may be used in a vaccine to prevent or treat H. pylori  
 CC infection or to identify H. pylori polypeptide binding compounds.  
 CC useful as potential H. pylori life cycle activators or inhibitors. The  
 CC DNA and probes derived from it may be used for the identification of  
 CC H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic  
 CC acid sequences complementary to the DNA act as antisense sequences and  
 CC can be used to prevent the translation of H. pylori mRNA. Antibodies  
 CC against the protein can be used in immunoassays to evaluate the abundance  
 CC and distribution of H. pylori-specific antigens. The genomic sequence of  
 CC H. pylori (ATCC 55679) was determined from overlapping contigs generated  
 CC by mechanically shearing the bacterial DNA. The sequences were analysed  
 CC for ORF of at least 180 nucleotides, and the predicted coding regions  
 CC defined by computer evaluation. To identify likely H. pylori antigens for  
 CC vaccine development, the amino acid sequences predicted from various ORF  
 CC were analysed for significant homology to other known or exported





e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 16 polynucleotides, based on which tissues they are most highly expressed in (see V59511 for described uses).

Sequence 76 AA:

Query Match 1.4%; Score 6; DB 1; Length 76;  
Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 FSSUKL 8  
89 FSSUKL 94

RESULT 37

ID W58848 standard; Protein; 85 AA.

AC W58848;

DT 23-JUL-1998 (first entry)

DE Human A168\_4 secreted protein.

KM Secreted protein; prevention; treatment; gene therapy.

OS Homo sapiens.

PN W09801554-A2.

PD 15-JAN-1998.

PF 07-JUL-1997; 011876.

PR 09-JUL-1996; US-677231.

PA (GENY) GENETICS INST INC.

PI Bowman M, Evans C, Jacobs K, Lavallie ER, McCoy JM,

PI Merberg D, Racle LA, Spaulding V, Treacy M,

PI WPI: 98-110230/10.

DR N-PSDB: V11431.

PT Secreted proteins and polynucleotides encoding them - useful to

PS prevent, treat and ameliorate medical conditions

PS Claim 22; Page 64; 93pp: English.

CC This sequence represents a fragment of a novel secreted protein derived

CC from clone A168\_4 which was isolated from a human adult testes cDNA

CC library. The protein can be used to prevent, treat or ameliorate a

CC medical condition, while the polynucleotides can be used for gene

CC therapy.

SO Sequence 85 AA;

Query Match 1.4%; Score 6; DB 1; Length 85;

Best Local Similarity 100.0%; Pred. No. 2.94e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 25 AFLPP 30

QY 330 AFLPP 335

RESULT 38

ID W20172 standard; Protein; 92 AA.

AC W20172;

DT 08-JUL-1997 (first entry)

DE H. pylori protein.

KM Cytoplasmic; vaccine; prevention; treatment; infection; identification;

KM binding compound; bacterium; life cycle; activator; bacteria; inhibitor;

KM duodenal ulcer disease; chronic gastritis; diagnosis; envelope;

KM outer membrane; cell envelope; transporter.

OS Helicobacter pylori.

PH Key Location/Qualifiers

FT misc difference 86

FT W09640893-A1.

PD 19-DEC-1996.

PF 06-JUN-1996; 009122.

PR 07-JUN-1995; US-487032.

PR 01-APR-1996; US-630405.

PA (ASTR) ASTRA AB.

PI Berglundh CT, Smith D, Mellgaard BL,

PI WPI: 97-052306/05.

DR N-PSDB: T67408.

PT Helicobacter pylori nucleic acid sequences and related

PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori

PT infection, and to detect Helicobacter

PS Disclosure; Pages 389; 1481pp; English.

CC The present sequence is a Helicobacter pylori protein of unknown

CC function. The protein may be used in a vaccine to prevent or treat

CC H. pylori infection or to identify H. pylori polypeptide binding

CC compounds, useful as potential H. pylori life cycle activators or

CC inhibitors. The genomic sequence of H. pylori (ATCC 55679) was

CC determined from overlapping contigs generated by mechanically shearing

CC the bacterial DNA. The sequences were analysed for ORF of at least 180

CC nucleotides, and the predicted coding regions defined by computer

CC evaluation. To identify likely H. pylori antigens for vaccine

CC development, the amino acid sequences predicted from various ORF were

CC analysed for significant homology to other known or exported membrane

CC proteins. Having identified and determined the sequences of interest,

CC particular regions can be isolated from H. pylori by PCR amplification

CC for recombinant polypeptide production, e.g. in E. coli hosts.

SO Sequence 92 AA;

Query Match 1.4%; Score 6; DB 1; Length 92;

Best Local Similarity 100.0%; Pred. No. 2.94e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 16 TTLVAV 21

QY 9 TTLVAV 14

RESULT 39

ID W29774 standard; Protein; 102 AA.

AC W29774;

DT 23-FEB-1998 (first entry)

DE Malassezia fungus ME-7 antigenic protein.

KM Malassezia; fungus; antigenic; human; IGE; immunoglobulin E;

KM antibody; allergy; antigen.

OS Malassezia sp.

PN W09721817-A1.

PD 19-JUN-1997.

PF 10-DEC-1996; J03602.

PR 05-SEP-1996; JP-257613.

PR 12-DEC-1995; JP-346627.

PR 05-SEP-1996; JP-257612.

PA (TAKI) TAKARA SHUZO CO LTD.

PI Akiyama K, Kato I, Kuroda M, Okado T, Onishi Y,

PI Takesako K, Yagihara T, Yamaguchi H, Yasuda H;

PI WPI: 97-332788/30.

DR N-PSDB: T85880.

PT Antigenic proteins from the fungus Malassezia - bind to IGE

PT antibodies present in patients with Malassezia allergies, useful for

PS diagnosis; treatment and prevention of such conditions

PS Claim 44; Page 91; 162pp; Japanese.

CC The present sequence represents a specifically claimed antigenic

CC protein isolated from the fungus Malassezia. The antigenic protein

CC can bind to IGE antibodies present in patients with allergic

CC conditions. Antigenic proteins, peptides and nucleic acids from the

CC fungus Malassezia can be used in the diagnosis, treatment and

CC prevention of allergic conditions due to Malassezia organisms (such

CC as M. furfur, M. sympodialis and M. pachydermatis).

SO Sequence 102 AA;

Query Match 1.4%; Score 6; DB 1; Length 102;

Best Local Similarity 100.0%; Pred. No. 2.94e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 DSFHY 45

QY 344 DSFHY 349

RESULT 40

ID W20533 standard; Protein; 110 AA.

AC W20533;  
 DT 15-JUN-1997 (first entry)  
 DE H. pylori cytoplasmic protein 495312.aa.  
 KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;  
 KM binding compound; bacterium; life cycle; activator; bacteria; inhibitor;  
 OS duodenal ulcer disease; chronic gastritis; diagnosis; envelope.  
 SM Helicobacter pylori.  
 FH Key Location/Qualifiers  
 FT misc\_difference 102  
 FT /note- "encoded by ASC"  
 PN M09640893-A1.  
 PD 19-DEC-1996  
 PE 06-JUN-1996; u09122.  
 PR 07-JUN-1995; US-487032.  
 PR 01-APR-1996; US-630405.  
 PA (ASTR ) ASTRA AB  
 PI Berglundh OF, Smith D, Mellgaerd BL;  
 DR WPI: 97-052306/05  
 DR N-PSDB: T67686.  
 PT Helicobacter pylori nucleic acid sequences and related  
 PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori  
 PT infection, and to detect Helicobacter  
 PS Claim 61; Page 690; 1481pp: English.  
 CC This sequence is a H. pylori cytoplasmic protein involved in  
 CC outer membrane or cell wall biosynthesis.  
 CC The protein may be used in a vaccine to prevent or treat H. pylori  
 CC infection or to identify H. pylori polypeptide binding compounds,  
 CC useful as potential H. pylori life cycle activators or inhibitors.  
 CC The genomic sequence of H. pylori (ATCC 55679) was determined from  
 CC overlapping contigs generated by mechanically shearing the bacterial  
 CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,  
 CC and the predicted coding regions defined by computer evaluation. To  
 CC identify likely H. pylori antigens for vaccine development, the amino  
 CC acid sequences predicted from various ORF were analysed for significant  
 CC homology to other known or exported membrane proteins. Having identified  
 CC and determined the sequences of interest, particular regions can be  
 CC isolated from H. pylori by PCR amplification for recombinant polypeptide  
 CC production, e.g. in E. coli hosts.  
 CC Sequence 110 AA;  
 SQ

Query Match 1.4%; Score 6; DB 1; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 98 IIDNF 103  
 111111  
 40 IIDNF 45

RESULT 41  
 ID M06050 standard; Protein; 112 AA.  
 AC M06050;  
 DT 12-OCT-1998 (first entry)  
 DE Human C-C chemokine DGMCC.  
 KW DGMCC; DNA; groin wound expressed CC chemokine; cytokine; human;  
 KM immune system; cancer; cell proliferation; therapy; diagnosis.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT peptide 1; 24  
 FT /label- Sig-peptide  
 FT Protein 25; 112  
 FT /label- Mat.protein  
 FT /note- "Claim 2"  
 PN M09823750-A2.  
 PD 04-JUN-1998.  
 PE 26-NOV-1997; U21092.  
 PR 05-DEC-1996; US-761071.  
 PR 27-NOV-1996; US-031805.  
 PA (SCHE ) SCHERING CORP.  
 PI Hedrick JA, Morales J, Vlcari A, Zlotnik A;  
 DR WPI: 98-322730/28.  
 DR N-PSDB: V38294.  
 DT Dvic-1 and DGMCC chemokines - useful for developing products for

PT treating abnormal physiology or development, e.g. cancerous or  
 PT degenerative conditions  
 PS Claim 2; Page 62; 71pp: English.  
 CC This polypeptide comprises mature human DNAx groin wound expressed  
 CC CC chemokine (DGMCC), the nature portion of which is claimed. The  
 CC DGMCC amino acid sequence was deduced from a cDNA clone (see V38294).  
 CC Also claimed is novel human DNAx VIC-1 (DVIA-1) (see W60649) mature  
 CC polypeptide, as well as expression vectors and host cells. DGMCC  
 CC and Dvic-1 play a role in the regulation or development of neuronal  
 CC or haematopoietic cells; e.g. lymphoid cells, which affect  
 CC immunological responses. They can be used in the treatment of  
 CC conditions associated with abnormal physiology or development of  
 CC including abnormal proliferation, e.g. cancerous conditions or  
 CC degenerative conditions. Abnormal proliferation, regeneration,  
 CC degeneration, and atrophy may be modulated by appropriate  
 CC therapeutic treatment using products of the invention. The products  
 CC can also be used for detection, diagnosis and drug screening.  
 CC Sequence 112 AA;  
 SQ

Query Match 1.4%; Score 6; DB 1; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 24 AFLPP 29  
 111111  
 330 AFLPP 335

Query Match 1.4%; Score 6; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 6 RSDSV 11  
 111111  
 51 RSDSV 56

RESULT 43  
 ID R26960 standard; Protein; 114 AA.  
 AC R26960;  
 DT 11-FEB-1993 (first entry)

DE Human T lymphocyte receptor V-beta w21 subfamily segment.  
 KW TCR, IGR b 02; variable region; immunomodulation;  
 KW polymerase chain reaction; T cell receptor.  
 OS Homo sapiens.  
 PN M09213950-A.  
 PD 20-AUG-1992.  
 PF 12-FEB-1992; F00130.  
 PR 12-FEB-1991; FR-001613.  
 PR 12-APR-1991; FR-004523.  
 PA (ROOS) ROUSSEL-UCIAF.  
 PI Ferradini L, Herceud T, Roman-Roman S, Tritel F;  
 DR MPI: 92-300036/36.  
 DR N-PSDB: Q28173.  
 PT Variable regions of b-chain of T-lymphocyte receptors and their  
 PT DNA: useful as immuno:modulant(s) and for diagnosing immune  
 PT disorders.  
 PS Claim 7; Page 37; 75pp; French.  
 CC RNA was isolated from peripheral lymphocytes and converted to cDNA  
 CC using a C-beta-specific primer. The cDNA was amplified by anchored  
 CC PCR using C-beta and polyC primers, then amplified again using a  
 CC different C-beta specific primer. The amplified product was SacI-  
 CC restricted, inserted into Bluescript SK+ vector and used to transform  
 CC E. coli XL-1-blue. Transformants were screened with a C-beta specific  
 CC probe and DNA from positive clones was sequenced in the C-beta  
 CC region. The sequence designated "IGR b 02" has ca. 85% homology  
 CC with the sequence H5YCRB23 (see Wilson R.K. et al., Immunogenetics  
 CC 32:406, 1990) and is a member of the Vbeta w21 subfamily. The  
 CC peptide encoded by it can be used to block T cell epitopes and in  
 CC vaccines. See also Q28174-Q28228.  
 SQ Sequence 114 AA.

Query Match 1.4%; Score 6; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 30 KIEKK 35  
 111111  
 383 KIEKK 388

RESULT 44  
 ID R25524 standard; Protein: 117 AA.  
 AC R25524.  
 DT 06-JAN-1993 (first entry)  
 KW Tobacco Ring spot Virus functional region.  
 KW Functional site; protein modification; active site; TRSV.  
 OS Tobacco Ring Spot Virus.  
 PN EP-494502-A.  
 PD 15-JUL-1992.  
 PF 29-NOV-1991; 311129.  
 PR 30-NOV-1990; JP-329895.  
 PR 15-JUL-1991; JP-173690.  
 PA (NITRA) NIPPON MINING CO.  
 PA (SAGA) SAGAMI CHEM RES CENTRE.  
 PA (TOY) TOSOH CORP.  
 PI Kidokoro S, Numao N;  
 DR MPI: 92-235588/29.  
 PT Summing functional sites in polypeptide or polynucleotide - by  
 PT comparison with sequences in polypeptide(s) whose functional  
 PT sites are known  
 PS Example 3; Page 28; 75pp; English.  
 CC The method for identifying functional sites in proteins was applied  
 CC to an RNA composed of 359 nucleotides from TRSV. It is known that  
 CC the catalytically active site exists in the 50 nucleotides between  
 CC the thymine residues at positions 175 and 224. The nucleotide  
 CC sequence was translated (the "x"s in the sequence are not defined  
 CC in the specification). A "discriminant function" was derived from  
 CC the amino acid sequences of known active sites in a range of other  
 CC polypeptides and then used to locate the putative position of the  
 CC TRSV active site.  
 SQ Sequence 117 AA;

Query Match

1.4%; Score 6; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 6 RSDSV 11  
 111111  
 51 RSDSV 56

RESULT 45  
 ID Y12709 standard; Protein: 130 AA.  
 AC Y12709.  
 DT 21-JUN-1999 (first entry)  
 DE Human 5' EST secreted protein SEQ ID NO:299.  
 KW Human; secreted protein; EST; expressed sequence tag; diagnosis;  
 KW forensic; gene therapy; chromosome mapping; signal peptide;  
 KW upstream regulatory sequence; cytokine activity; cell proliferation;  
 KW differentiation; haematopoiesis regulation; tissue growth regulation;  
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;  
 KW thrombolytic; anti-inflammatory; tumour inhibition.  
 OS Homo sapiens.  
 PN M09906549-A2.  
 PD 11-FEB-1999.  
 PF 31-JUL-1998; 1B1231.  
 PR 01-AUG-1997; US-905279.  
 PA (GEST) GENSET.  
 PI Ductert A, Dumas Milne Edwards J, Lacroix B;  
 DR MPI: 99-153779/13.  
 DR N-PSDB: X51487.  
 PT New nucleic acids encoding human secreted proteins - obtained from  
 PT cDNA libraries derived from testis, ovary, uterus and spleen tissue  
 PS Claim 34; Page 400; 522pp; English.  
 CC X51459 to X51691 represent 5' expressed sequence tags (ESTs) for human  
 CC secreted proteins, and encode the proteins given in Y12681 to Y12913,  
 CC respectively. The proteins given represent the signal peptide and an  
 CC N-terminal fragment of a secreted protein. The nucleic acid sequences  
 CC can be used for producing secreted human gene products. They can also  
 CC be used to develop products for diagnosis and therapy. The proteins  
 CC obtained may have cytokine activity, cell proliferation/differentiation  
 CC activity, haematopoiesis regulating activity, tissue growth regulating  
 CC activity, reproductive hormone regulating activity, chemotactic/  
 CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/  
 CC ligand activity, anti-inflammatory activity, tumour inhibition activity  
 CC or other activities. The products can be used in forensic, gene therapy  
 CC and chromosome mapping procedures. The sequences can also be used for  
 CC obtaining corresponding promoter sequences. The nucleic acids encoding  
 CC the signal peptide can be used for directing extracellular secretion of  
 CC a polypeptide or the insertion of a polypeptide into a membrane, or  
 CC importing a polypeptide into a cell.  
 SQ Sequence 130 AA;

Query Match 1.4%; Score 6; DB 1; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 2.94e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 19 LSDSFH 24  
 111111  
 342 LSDSFH 347

Search completed: Mon Aug 21 10:30:21 2000  
 Job time : 48 secs.

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/cgnl_7/p/odata/1/paa/US07.COMB	pep:US-07-971-834-2		340.00	747.86	4.2e-34	436	
/cgnl_7/p/odata/1/paa/US092.COMB	pep:US-09-240-675-2		340.00	747.86	4.2e-34	436	
/cgnl_7/p/odata/1/paa/PCFUS.COMB	pep:PCF-US09-11516-3		340.00	745.73	4.3e-34	557	
/cgnl_7/p/odata/1/paa/US07.COMB	pep:US-07-971-834-4		340.00	745.73	4.3e-34	557	
/cgnl_7/p/odata/1/paa/US084A.COMB	pep:US-08-453-679-2		340.00	745.73	4.3e-34	557	
/cgnl_7/p/odata/1/paa/US092.COMB	pep:US-09-240-675-4		340.00	745.73	4.3e-34	557	
/cgnl_7/p/odata/1/paa/PCFUS.COMB	pep:PCF-US09-10500-9598B-1672		334.00	731.91	2.4e-33	557	
/cgnl_7/p/odata/1/paa/US60.COMB	pep:US-60-160-202-2519		222.00	501.69	2.2e-19	42	
/cgnl_7/p/odata/1/paa/US088.COMB	pep:US-08-871-572-13		209.00	457.97	1.1e-17	224	
/cgnl_7/p/odata/1/paa/US088.COMB	pep:US-08-871-572B-13		209.00	457.97	1.1e-17	224	
/cgnl_7/p/odata/1/paa/US086.COMB	pep:US-08-860-663-22		199.00	426.38	2.3e-16	631	
/cgnl_7/p/odata/1/paa/US088.COMB	pep:US-08-888-140-22		199.00	426.38	2.3e-16	631	
/cgnl_7/p/odata/1/paa/US090.COMB	pep:US-09-056-461-22		199.00	426.38	2.3e-16	631	
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/cgnl_7/p/odata/1/paa/US088.COMB	pep:US-08-871-572B-11		198.00	433.14	2.8e-16	224	
/cgnl_7/p/odata/1/paa/US094.COMB	pep:US-09-443-060-14		186.00	407.08	8.8e-15	199	
/cgnl_7/p/odata/1/paa/US081.COMB	pep:US-60-164-763-9563		118.00	270.98	2.5e-06	27	
/cgnl_7/p/odata/1/paa/US081.COMB	pep:US-60-164-763-9563-3		117.00	251.21	4.2e-06	202	
/cgnl_7/p/odata/1/paa/US084A.COMB	pep:US-08-421-121-3		117.00	251.21	4.2e-06	202	
/cgnl_7/p/odata/1/paa/US084A.COMB	pep:US-08-421-122-3		117.00	251.21	4.2e-06	202	
/cgnl_7/p/odata/1/paa/US084A.COMB	pep:US-08-421-123-3		117.00	251.21	4.2e-06	202	
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/cgnl_7/p/odata/1/paa/US60.COMB	pep:US-60-164-763-1049		112.00	257.77	1.4e-05	26	
/cgnl_7/p/odata/1/paa/US081.COMB	pep:US-08-164-566-3		112.00	239.92	1.8e-05	202	
/cgnl_7/p/odata/1/paa/US094.COMB	pep:US-09-443-060-15		102.00	217.43	0.0003	200	
/cgnl_7/p/odata/1/paa/PCFUS.COMB	pep:PCF-US98-18782-1		75.00	139.37	0.9957	1429	
/cgnl_7/p/odata/1/paa/US094.COMB	pep:US-09-417-507-37698		68.50	136.70	6.15	35	
/cgnl_7/p/odata/1/paa/US60.COMB	pep:US-60-150-584-594		68.00	139.92	6.15	245	
/cgnl_7/p/odata/1/paa/US60.COMB	pep:US-60-173-464-8864-3		68.00	135.72	6.42	35	
/cgnl_7/p/odata/1/paa/US60.COMB	pep:US-60-191-637-37414		68.00	135.69	6.42	35	
/cgnl_7/p/odata/1/paa/US60.COMB	pep:US-60-174-325-8		67.50	131.81	7.70	487	
/cgnl_7/p/odata/1/paa/US60.COMB	pep:US-60-174-325-12		66.00	126.34	12.23	619	
/cgnl_7/p/odata/1/paa/US094.COMB	pep:US-09-417-507-30838		65.50	138.40	11.84	135	
/cgnl_7/p/odata/1/paa/US088.COMB	pep:US-08-871-572-10		64.50	131.72	16.78	226	
/cgnl_7/p/odata/1/paa/US088.COMB	pep:US-08-871-572B-10		64.50	131.72	16.78	226	
/cgnl_7/p/odata/1/paa/US094.COMB	pep:US-60-130-467-32		63.50	128.31	22.77	258	
/cgnl_7/p/odata/1/paa/US094.COMB	pep:US-60-147-507-34872		63.50	124.72	23.89	330	
/cgnl_7/p/odata/1/paa/US60.COMB	pep:US-60-150-562-571		63.50	121.72	24.87	550	

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51 CCATGGGTCTTGTCCGACGCCGAGGTGAAAAATCTAAATCTCCTC 100
|||||
17 YPTOTPVAlLeuSerAlaAlaIaGlyGlyAsnLeuLysSerProG 34
|||||
101 AAAAGTAGAGTCGACATCATATAGATGACAACTTATCCGAGGTGAAC 150
|||||
34 InYsValGluValAspIleIleAspAspAsnPhelIleuAlaGlyTPAsn 50
|||||
151 AGAGGATAGTCGTGCGGAATGTGACTTTTTCATTGATTATCAAAA 200
|||||
51 ArgSerAspIuSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
|||||
201 A 201
67 s 67

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seq\_name: /cgnl\_7/plodata/1/paa/US088\_COMB.pep:US-08-871-572B-9

seq\_documentation\_block:

Sequence 9, Application US/08871572B

GENERAL INFORMATION:

APPLICANT: Pestka, Sidney

APPLICANT: Kolenko, Serguei

APPLICANT: Soh, Jaemog

APPLICANT: Donnelly, Robert

APPLICANT: Mariano, Thomas

APPLICANT: Cook, Jeffrey

APPLICANT: Emmanuel, Stuart

APPLICANT: Schwartz, Barbara

TITLE OF INVENTION: Accessory Factor for Interferon Gamma

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Richard R. Muccino

STREET: 758 Springfield Avenue

CITY: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/871,572B

FILING DATE: 9-JUNE-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Muccino, Richard R.

REGISTRATION NUMBER: 32,538

REFERENCE/DOCKET NUMBER: UMDI-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 273-4679

TELEFAX: (908) 273-4679

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 224 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-871-572B-9

alignment\_block:  
US-09-240-675-1\_COPY\_27\_229 x US-08-871-572B-9  
Align seq 1/1 to: US-08-871-572B-9 from: 1 to: 224

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51 CCATGGGTCTTGTCCGACGCCGAGGTGAAAAATCTAAATCTCCTC 100
|||||
17 YPTOTPVAlLeuSerAlaAlaIaGlyGlyAsnLeuLysSerProG 34
|||||
101 AAAAGTAGAGTCGACATCATATAGATGACAACTTATCCGAGGTGAAC 150
|||||
34 InYsValGluValAspIleIleAspAspAsnPhelIleuAlaGlyTPAsn 50
|||||
151 AGAGGATAGTCGTGCGGAATGTGACTTTTTCATTGATTATCAAAA 200
|||||
51 ArgSerAspIuSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
|||||
201 A 201
67 s 67

```

seq\_name: /cgnl\_7/plodata/1/paa/US07\_COMB.pep:US-07-971-834-2

seq\_documentation\_block:

Sequence 2, Application US/07971834

GENERAL INFORMATION:

APPLICANT: EID, Pierre

APPLICANT: GRESSER, Ion

APPLICANT: LOTFALLA, Georges

APPLICANT: MEYER, Francois

APPLICANT: MOGENSEN, Knud E.

APPLICANT: TOVEY, Michael

APPLICANT: OZE, Gilles

TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH

TITLE OF INVENTION: AFFINITY FOR INTERFERONS ALPHA AND BETA

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/971,834

FILING DATE: 17-FEB-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR91/00318

FILING DATE: 17-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: EID-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 436 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-971-834-2

alignment\_scores:      Quality: 340.00      Length: 67  
                          Ratio: 5.075      Gaps: 0  
 Percent Similarity: 100.000      Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x US-07-971-834-2

Align seq 1/1 to: US-07-971-834-2 from: 1 to: 436

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1 ATATGTCGTCCTCCGCGCCGACACCTAGTCTGCGCCGCGG 50
|||||
1 MetetValValLeuLeuGlyAlaThrThrLeuValAlaValAlG 17
|||||
51 CCCATGGGTGTGTCGCGAGCGAGGTGGAATAAATCTACTCTC 100
|||||
17 YPOTRIPVAlLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
|||||
101 AAAAGTAGAGTCGACATCATAGATGACAACCTTATCTGAGTGAAC 150
|||||
34 IntysValGluValAlaSplletleAspAsnPhelleLeuArgTyrpsn 50
|||||
151 AGGAGCATGAGTCTGCGGAGATGACATTTCATTTCATTCACAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
|||||
201 A 201
67 s 67

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seq\_name: /cgn1\_7/ptodata/1/paa/US092\_COMB.pep:US-09-240-675-2

seq\_documentation\_block:

Sequence 2, Application US/09240675

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVEY, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSER: Foley &amp; Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/240,675

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 17283/117/GUPL

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

INFORMATION FOR SEQ. ID NO. 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 436 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-240-675-2

alignment\_scores:      Quality: 340.00      Length: 67  
                          Ratio: 5.075      Gaps: 0  
 Percent Similarity: 100.000      Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x US-09-240-675-2

Align seq 1/1 to: US-09-240-675-2 from: 1 to: 436

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1 ATATGTCGTCCTCCGCGCCGACACCTAGTCTGCGCCGCGG 50
|||||
1 MetetValValLeuLeuGlyAlaThrThrLeuValAlaValAlG 17
|||||
51 CCCATGGGTGTGTCGCGAGCGAGGTGGAATAAATCTACTCTC 100
|||||
17 YPOTRIPVAlLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProG 34
|||||
101 AAAAGTAGAGTCGACATCATAGATGACAACCTTATCTGAGTGAAC 150
|||||
34 IntysValGluValAlaSplletleAspAsnPhelleLeuArgTyrpsn 50
|||||
151 AGGAGCATGAGTCTGCGGAGATGACATTTCATTTCATTCACAAA 200
|||||
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67
|||||
201 A 201
67 s 67

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seq\_name: /cgn1\_7/ptodata/1/paa/PCTUS\_COMB.pep:PCT-US99-12156-3

seq\_documentation\_block:

Sequence 3, Application PC/TUS9912156

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc. et al.

TITLE OF INVENTION: Interferon Receptor HKAF92

FILE REFERENCE: PF465PCT

CURRENT APPLICATION NUMBER: PCT/US99/12156

CURRENT FILING DATE: 1999-06-03

EARLIER APPLICATION NUMBER: 60/088,185

EARLIER FILING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.0

SEQ. ID NO. 3

LENGTH: 557

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US99-12156-3

alignment\_scores:      Quality: 340.00      Length: 67  
                          Ratio: 5.075      Gaps: 0  
 Percent Similarity: 100.000      Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x PCT-US99-12156-3

Align seq 1/1 to: PCT-US99-12156-3 from: 1 to: 557

1 ARGANGTGCTCTCTGGGCGGACGACCCCTAGTCCTGCGCGTGGG 50  
1 MetMeValValLeuLeuGlyAlaThrThrLeuValValAlaValAl 17  
51 CCATGGGTTGTTCGGCGCGGAGTGAATAAATCAATCCGTC 100  
17 yProtpValLeuSerAlaAlaAlaGlyLysAsnLeuLysSerPro 34  
101 AAAAGTAGAGTGCATCATATGATGACAACTTATCTGAGTGAAC 150  
34 InLysValGluValAspIleIleAspAspAsnPhelleuArgTyrPasn 50  
151 AGAGCGATGAGTCTGTGCGGAATGTGACTTTTCATTCGATTATCAAA 200  
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67  
201 A 201  
67 s 67

seq\_name: /cgnl\_7/ptodata/1/paa/US07\_COMB.pep:US-07-971-834-4  
seq\_documentation\_block:  
Sequence 4, Application US/07971834

GENERAL INFORMATION:  
APPLICANT: EID, Pierre  
APPLICANT: GRESSER, Ion  
APPLICANT: LUTFALLA, Georges  
APPLICANT: MEYER, Francois  
APPLICANT: MOGENSEN, Knud E.  
APPLICANT: TOVEY, Michael  
TITLE OF INVENTION: WATER-SOLUBLE POLYPEPTIDES HAVING HIGH  
TITLE OF INVENTION: AFFINITY FOR INTERFERONS ALPHA AND BETA  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/971,834  
FILING DATE: 17-FEB-1993  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR91/00318  
FILING DATE: 17-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: EID-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-971-834-4

alignment\_scores:  
Quality: 340.00

Length: 67

Ratio: 5.075 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-240-675-1\_COPY\_27\_229 x US-07-971-834-4

Align seg 1/1 to: US-07-971-834-4 from: 1 to: 557

1 ARGANGTGCTCTCTGGGCGGACGACCCCTAGTCCTGCGCGTGGG 50  
1 MetMeValValLeuLeuGlyAlaThrThrLeuValValAlaValAl 17  
51 CCATGGGTTGTTCGGCGCGGAGTGAATAAATCAATCCGTC 100  
17 yProtpValLeuSerAlaAlaAlaGlyLysAsnLeuLysSerPro 34  
101 AAAAGTAGAGTGCATCATATGATGACAACTTATCTGAGTGAAC 150  
34 InLysValGluValAspIleIleAspAspAsnPhelleuArgTyrPasn 50  
151 AGAGCGATGAGTCTGTGCGGAATGTGACTTTTCATTCGATTATCAAA 200  
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGln 67  
201 A 201  
67 s 67

seq\_name: /cgnl\_7/ptodata/1/paa/US084A\_COMB.pep:US-08-453-090-2

seq\_documentation\_block:  
Sequence 2, Application US/08453090

GENERAL INFORMATION:  
APPLICANT: MOGENSEN, Knud E.  
APPLICANT: GRESSER, Ion  
APPLICANT: LUTFALLA, Georges  
TITLE OF INVENTION: cDNA FRAGMENT CODING FOR THE GENE FOR  
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE  
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/453,090  
FILING DATE:  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/900,642  
FILING DATE: 15-JUN-1992  
APPLICATION NUMBER: FR 89/13770  
FILING DATE: 20-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 960-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids



TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-453-090-2

alignment\_scores:  
Quality: 340.00 Length: 67  
Ratio: 5.075 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-240-675-1\_COPY\_27\_229 x US-08-453-090-2

Align seg 1/1 to: US-08-453-090-2 from: 1 to: 557

1 ATGATGTCCTCTCTGGCGCGAGACCTAGTCGTCGCGCGGG 50  
|||||  
1 MetMetValValLeuLeuValAlaThrThrLeuValLeuValAlaValAl 17  
51 CCCATGGGTGTGTCCGCGAGCCGAGGTGGAATAAATCTAATCTCTC 100  
|||||  
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34  
101 AAAAGTAGAGTCCGACATCATGATGACAACTTATCTCTGAGGTGGAAC 150  
|||||  
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50  
151 AGGAGCGATGAGTCGTGCGGAGATGACTTTTTCATTGATTCATCAAAA 200  
|||||  
51 ArgSerAspGluSerValGlyLysValThrPheSerPheAspTyrGln 67  
201 A 201  
67 s 67

seq\_name: /cgnl\_7/ptodata/1/paa/US092\_COMB.pep:US-09-240-675-4

seq\_documentation\_block:

Sequence 4, Application US/09240675

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVEY, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/240,675

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: SAYE, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 17283/117/GUPL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-240-675-4

alignment\_scores:  
Quality: 340.00 Length: 67  
Ratio: 5.075 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-240-675-1\_COPY\_27\_229 x US-09-240-675-4

Align seg 1/1 to: US-09-240-675-4 from: 1 to: 557

1 ATGATGTCCTCTCTGGCGCGAGACCTAGTCGTCGCGCGGG 50  
|||||  
1 MetMetValValLeuLeuValAlaThrThrLeuValLeuValAlaValAl 17  
51 CCCATGGGTGTGTCCGCGAGCCGAGGTGGAATAAATCTAATCTCTC 100  
|||||  
17 yProTrpValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerPro 34  
101 AAAAGTAGAGTCCGACATCATGATGACAACTTATCTCTGAGGTGGAAC 150  
|||||  
34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50  
151 AGGAGCGATGAGTCGTGCGGAGATGACTTTTTCATTGATTCATCAAAA 200  
|||||  
51 ArgSerAspGluSerValGlyLysValThrPheSerPheAspTyrGln 67  
201 A 201  
67 s 67

seq\_name: /cgnl\_7/ptodata/1/paa/PCTUS\_COMB.pep:PCT-US00-05988-1672

seq\_documentation\_block:

Sequence 1672, Application PC/TUS0005988

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruben,

TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptid

FILE REFERENCE: P4101PCT

CURRENT APPLICATION NUMBER: PCT/US00/05988

CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: 60/124,270

EARLIER FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO: 1672

LENGTH: 575

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (186)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (555)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

PCT-US00-05988-1672

## alignment\_scores:

Quality: 334.00 Length: 67  
Ratio: 4.985 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 98.507

## alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x PCT-US00-05988-1672

Align seg 1/1 to: PCT-US00-05988-1672 from: 1 to: 575

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1 ATGATGCTGCTCCTCGGCGGAGACCCCTAGTGTCTGCGCGGGG 50
19 MetMetValValLeuLeuGlyAlaThrThrLeuValValAlaValAl 35
51 CCCATGGGTGTTCGCGACCCGAGGTGAGAAAAATCTAAATCTCTC 100
35 APTPTPValLeuSerAlaAlaAlaGlyGlyAsnLeuLysSerProG 52
101 AAAAGTAGAGTCGATCATGATGATGACACCTTATCTGAGTGGAC 150
52 LnyValGluValAspIleIleAspAspAsnPhelIleuArgTyrPsn 68
151 AGAGGATAGTCTGCGGAGATGACTTTTCATTCGATTATCAAAA 200
69 ArgSerAspIleuSerValGlyAsnValThrPheserPhespyrGln 85
201 A 201
85 S 85

```

seq\_name: /cgnl\_7/ptodata/1/paa/US60\_COMB.pep:US-60-160-202-2519

## seq\_documentation\_block:

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: Sequence 2519, Application US/60160202
: GENERAL INFORMATION:
: APPLICANT: BONAZZI, VIVIAN
: TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
: FILE REFERENCE: CLO000114
: CURRENT APPLICATION NUMBER: US/60/160,202
: CURRENT FILING DATE: 1999-10-19
: NUMBER OF SEQ ID NOS: 4392
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2519
: LENGTH: 42
: TYPE: PRT
: ORGANISM: HUMAN
US-60-160-202-2519

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## alignment\_scores:

Quality: 222.00 Length: 42  
Ratio: 5.286 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x US-60-160-202-2519

Align seg 1/1 to: US-60-160-202-2519 from: 1 to: 42

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76 GGTGGAAAAATCTAAATCTCTGAAAAAGTAGAGTCGATCATGATA 125
1 GlyGlyLysAsnLeuLysSerProGlnLysValGluValAspIleIle 17
126 TGAACAATTATCTGAGTGAAGAGGAGCATGAGTGTGGGGAGT 175
17 PAspAsnPhelIleuArgTyrPsnArgSerAspGluSerValGlyAsn 34
176 TGACTTTTCATTCGATTATCAAAA 201

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34 althPheserPhespyrGlnLys 42

seq\_name: /cgnl\_7/ptodata/1/paa/US088\_COMB.pep:US-08-871-572-13

## seq\_documentation\_block:

Sequence 13, Application US/08871572

## GENERAL INFORMATION:

```

: APPLICANT: Pestka, Sidney
: APPLICANT: Kotenko, Sergei
: APPLICANT: Son, Jaemog
: APPLICANT: Donnelly, Robert
: APPLICANT: Mariano, Thomas
: APPLICANT: Cook, Jeffrey
: APPLICANT: Emanuel, Stuart
: APPLICANT: Schwartz, Barbara
: TITLE OF INVENTION: Accessory Factor for Interferon Gamma
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESS: Richard R. Muccino
: STREET: 758 Springfield Avenue
: CITY: Summit
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07901
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/871,572
: FILING DATE: 09-JUN-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/444,134
: FILING DATE: 18-MAY-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Muccino, Richard R.
: REGISTRATION NUMBER: 32,538
: REFERENCE/DOCKET NUMBER: UMD1-011
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (908) 273-4988
: TELEFAX: (908) 273-4679
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 224 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
US-08-871-572-13

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## alignment\_scores:

Quality: 209.00 Length: 65  
Ratio: 3.800 Gaps: 2  
Percent Similarity: 84.615 Percent Identity: 69.231

## alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x US-08-871-572-13

Align seg 1/1 to: US-08-871-572-13 from: 1 to: 224

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54 ATGGGTGTTCGCGACCCGAGGTGAGAAAAATCTAAATCTCTCAAA 103
16 gtrValLeuProAlaAlaSerGlyLysAlaAsnLeuLys...ProGlu 32

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Tue Aug 22 08:32:06 2000

us-09-240-675-1\_copy\_27\_229.n2p.rap

104 AAGTAGAGTCGACATCATATGACAACTTATTCGAGTGAGGAGG 153  
32 snValGluIleHisIleLeaspaspaspheLeuLysTrpAsnSer 48  
154 AGCGATGCTGTCGGGAATGACCTTTTCATTCGATTATCA 198  
49 SerSerGluSerValLysAsnValThrPheSerAlaAspTrgln 63

seq name: /cgn1\_7/ptodata/1/paa/US088\_COMB pep: US-08-871-572B-13

seq documentation block:

Sequence 13, Application US/08871572B

GENERAL INFORMATION:  
APPLICANT: Pestka, Sidney  
APPLICANT: Kolenko, Serguei  
APPLICANT: Soh, Jaemog  
APPLICANT: Donnelly, Robert  
APPLICANT: Mariano, Thomas  
APPLICANT: Cook, Jeffrey  
APPLICANT: Emmanuel, Stuart  
APPLICANT: Schwartz, Barbara  
TITLE OF INVENTION: Accessory Factor for Interferon Gamma  
TITLE OF INVENTION: and Its Receptor  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Richard R. Muccino  
STREET: 758 Springfield Avenue  
CITY: Summit  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07901

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,572B  
FILING DATE: 9-JUNE-1997  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Muccino, Richard R.  
REGISTRATION NUMBER: 32,538  
REFERENCE/DOCKET NUMBER: DMD1-011  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 273-4988  
TELEX: (908) 273-4679  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 224 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown

MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-871-572B-13

alignment\_scores:  
Quality: 209.00 Length: 65  
Ratio: 3.800 Gaps: 2  
Percent Similarity: 84.615 Percent Identity: 69.231

alignment\_block:  
US-09-240-675-1\_COPY\_27\_229 x US-08-871-572B-13  
Align seg 1/1 to: US-08-871-572B-13 from: 1 to: 224

4 ATGGTCCTCTCTGCGGCGGAGACCTTAGTGTCTGCGCGGAGGCC 53  
1 MetLeuAlaLeuLeuGluGlyAlaThrThrLeuMetLeuValAla...GlyAr 16

54 ATGGTCCTCTCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGG 103  
16 gtrValLeuProAlaIleAsnSerGlyAlaAsnLeuLys...ProGua 32  
104 AAGTAGAGTCGACATCATATGACAACTTATTCGAGTGAGGAGG 153  
32 snValGluIleHisIleLeaspaspaspheLeuLysTrpAsnSer 48  
154 AGCGATGCTGTCGGGAATGACCTTTTCATTCGATTATCA 198  
49 SerSerGluSerValLysAsnValThrPheSerAlaAspTrgln 63

seq name: /cgn1\_7/ptodata/1/paa/US086\_COMB pep: US-08-680-663-22

seq documentation block:

Sequence 22, Application US/08680663

GENERAL INFORMATION:  
APPLICANT: Chundharpal, Anon  
APPLICANT: Kim, Kyung Jin  
APPLICANT: Love, Richard B.  
APPLICANT: Lu, Ji  
TITLE OF INVENTION: Type I Interferon Receptor Antibodies  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/680,663  
FILING DATE: 16-Jul-1996  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1039  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-5530  
TELEX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 631 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear

alignment\_scores:  
Quality: 199.00 Length: 38  
Ratio: 5.237 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-240-675-1\_COPY\_27\_229 x US-08-680-663-22  
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1 LeuLysSerProGlnLysValGluValAlaAspIleLeaspaspasphe 17  
138 CCGAGGTGAGACAGAGGAGCATGAGTGTCTGCGGAATGACATTTTCAT 187  
17 eleuArGTrpAsnArSerSerAspLysSerValGlyAsnValThrPheSer 34

188 TCGATTATCAAAA 201  
|||||  
34 heaspyriginlys 38

seq\_name: /cgnl7/ptodata/1/paa/US088\_COMB.pep:US-08-888-140-22

seq\_documentation\_block:

Sequence 22, Application US/0888140

GENERAL INFORMATION:

APPLICANT: Chuntharapal, Anan

APPLICANT: Kim, Kyung Jin

APPLICANT: Love, Richard B.

APPLICANT: Lu, Ji

TITLE OF INVENTION: Monoclonal Antibodies to Type I Interferon Receptor

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/888,140

FILING DATE: 03-Jul-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/

FILING DATE: 16-Jul-1996

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1039P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 631 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-888-140-22

alignment\_scores:

Quality: 199.00

Ratio: 5.237

Percent Similarity: 100.000

Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x US-08-888-140-22

Align seg 1/1 to: US-08-888-140-22 from: 1 to: 631

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1 LeuLysSerProGlnLysValGluValAspIleIleAspAspAsnPhel 17

138 CCGAGGTGGAACAGAGCGATGAGTCGTGCGGAATGTGACTTTTCAT 187

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17 eleuAyrtrPaanArGserAspIuserValGlyAsnValThrPheserp 34

188 TCGATTATCAAAA 201

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34 heaspyriginlys 38

seq\_name: /cgnl7/ptodata/1/paa/US090\_COMB.pep:US-09-056-461-22

seq\_documentation\_block:

Sequence 22, Application US/09056461

GENERAL INFORMATION:

APPLICANT: Chuntharapal, Anon

APPLICANT: Kim, Kyung Jin

APPLICANT: Love, Richard B.

APPLICANT: Lu, Ji

APPLICANT: Stewart, Timothy A

TITLE OF INVENTION: Type I Interferon Receptor Antibodies

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,461

FILING DATE: 07-Apr-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/058212

FILING DATE: 16

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1039P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 631 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-056-461-22

alignment\_scores:

Quality: 199.00

Ratio: 5.237

Percent Similarity: 100.000

Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x US-09-056-461-22

Align seg 1/1 to: US-09-056-461-22 from: 1 to: 631

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|||||

1 LeuLysSerProGlnLysValGluValAspIleIleAspAspAsnPhel 17

138 CCGAGGTGGAACAGAGCGATGAGTCGTGCGGAATGTGACTTTTCAT 187

|||||

17 eleuAyrtrPaanArGserAspIuserValGlyAsnValThrPheserp 34

188 TCGATTATCAAAA 201

|||||

34 heaspyriginlys 38

Tue Aug 22 08:32:06 2000

us-09-240-675-1\_copy\_27\_229.n2p.rap

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|||||  
34 IntYsValGIuValAspIlelleAspAspAsnPhelIeuAgtTpsn 50  
151 AGAGGAGGAGTCTGTCGGGAGGAGTCTTTCATTGATTATCAAAA 200  
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67

201 A 201  
67 s 67

seq\_name: /cgnl\_7/ptodata/1/1aa/5B\_COMB.pep:US-08-307-588-2

seq\_documentation\_block:

Sequence 2: Application US/08307588  
Patent No. 5919453

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVER, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

TITLE OF INVENTION: INTERFERON

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: SAKI, Bernard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 17283/117/GUPL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 436 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-307-588-2

alignment\_scores:

Quality: 340.00

Ratio: 5.075

Percent Similarity: 100.000

Length: 67

Gaps: 0

Percent Identity: 100.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x US-08-307-588-2

Align seg 1/1 to: US-08-307-588-2 from: 1 to: 436

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1 MetMeValValIeuLeuGlyAlaThrPheValIleValAlaValGI 17  
51 CCCATGGGTGTTCGCCGAGCGCGGCGGAGAAATCAATCAATCCGTC 100  
17 yProtrPallIeuSerAlaAlaIleGlyIlyAsnLeuLysSerProG 34

101 AAAAGTAGAGGTGCGACATCATAGATGACACACTTATCCTGAGTGGAGC 150  
34 IntYsValGIuValAspIlelleAspAspAsnPhelIeuAgtTpsn 50

151 AGAGGAGGAGTCTGTCGGGAGGAGTCTTTCATTGATTATCAAAA 200  
51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnly 67

201 A 201  
67 s 67

seq\_name: /cgnl\_7/ptodata/1/1aa/5A\_COMB.pep:US-08-328-256-12

seq\_documentation\_block:

Sequence 12: Application US/08328256

Patent No. 5643749

GENERAL INFORMATION:

APPLICANT: REVEL, Michel

APPLICANT: ABRAMOVICH, Carolina

APPLICANT: RATOVITSKI, Edward

TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
PREPARATION AND USE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/328,256

FILING DATE: 24-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 107378

FILING DATE: 24-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: REVEL-13

REFERENCE/DOCKET NUMBER: 25,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-328-256-12

alignment\_scores:

Quality: 340.00

Ratio: 5.075

Percent Similarity: 100.000

Length: 67

Gaps: 0

Percent Identity: 100.000

alignment\_block:

**alignment\_scores:**

ADDRESSEE: NIXON & VANDERHIVE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,454  
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/900,642  
FILING DATE: 15-JUN-1992  
APPLICATION NUMBER: FR 89/13770  
FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 960-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 2:





OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,453

FILING DATE: 06-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-471-453-2

# alignment\_scores:

Quality: 340.00 Length: 67

Ratio: 5.075 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

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17 yPCTrPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProg 34

101 AAAAAGTAGAGTCGACATCATAGATGACAACTTATCTGAGGTGAGAC 150

34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50

151 AGGAGCGATGATGCTGCGGAGATGATGCTTTTCATTCGATTATCAAA 200

51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67

201 A 201

67 s 67

seq\_name: /cgml\_7/ptodata/1/laa/5B.COMB.pep:US-08-307-588-4

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Sequence 4, Application US/08307588

Patent No. 5919453

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVEY, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

TITLE OF INVENTION: INTERFERON

APPLICANT: Aguet, Michel

# NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: SAYE, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 17283/117/GUPL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 557 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-307-588-4

# alignment\_scores:

Quality: 340.00 Length: 67

Ratio: 5.075 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x US-08-307-588-4

Align seg 1/1 to: US-08-307-588-4 from: 1 to: 557

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51 CCCATGGGTGTGTCGCGAGCCGAGGTGAAAAAATCTAAATCTCTCTC 100

17 yPCTrPValLeuSerAlaAlaAlaGlyGlyLysAsnLeuLysSerProg 34

101 AAAAAGTAGAGTCGACATCATAGATGACAACTTATCTGAGGTGAGAC 150

34 InLysValGluValAspIleIleAspAspAsnPhelIleLeuArgTrpAsn 50

151 AGGAGCGATGATGCTGCGGAGATGATGCTTTTCATTCGATTATCAAA 200

51 ArgSerAspGluSerValGlyAsnValThrPheSerPheAspTyrGlnLys 67

201 A 201

67 s 67

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Sequence 3, Application PC/TUS9414277

GENERAL INFORMATION:

APPLICANT: Aguet, Michel

Page 6

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seq documentation block:
: Sequence 4, Application US/08663743
: Patent No. 5843697.
:
: GENERAL INFORMATION:
:
: APPLICANT: Pestka, Sidney
: APPLICANT: Kotenko, Sergei
: TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
: TITLE OF INVENTION: CHAIN
:
: NUMBER OF SEQUENCES: 25
:
: CORRESPONDENCE ADDRESS:
:

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seq_documentation_block:
  Sequence 7, Application US/08469412A
  Patent No. 5856125
  GENERAL INFORMATION:
  APPLICANT: Mavrothlassitis, George J.
  APPLICANT: Blair, Donald G.
  APPLICANT: Fisher, Robert J.
  APPLICANT: Beat Jr., Gregory J.
  APPLICANT: Athanasios, Meropi A.
  APPLICANT: Sgouras, Dionysios N.
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ADDRESSEE: LAHIVE & COCKFIELD

CURRENT APPLICATION DATA:

**FILING DATE:** 13-OCT-1994

CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/010,409  
 FILING DATE: 29-JAN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Quine, Jonathan A.  
 REGISTRATION NUMBER: 41,261  
 REFERENCE/DOCKET NUMBER: 015280-113100US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3135 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-323-170B-2

alignment\_scores:  
 Quality: 59.00 Length: 51  
 Ratio: 1.844 Gaps: 3  
 Percent Similarity: 62.745 Percent Identity: 37.255

alignment\_block:  
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Align seg 1/1 to: US-08-323-170B-2 from: 1 to: 3135

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||||| ||||| ||||| ||||| |||||
787 SerGlyAspIleGlyIleLeuPheProLysAsnIleLysSerThr 803
102 AAAAGTAGAGGTGACATCATGATGACAACTTATCTGAGGTGACAA 151
||||| ||||| ||||| ||||| |||||
803 rGysPheGlu..GIuMetIleProTyrAsnLysGluIleLysTyrAsn 819
152 GGAGCGATGAGTCTGTGCGGAAAT..GTGACTTTTCATTCATGATCA 198
||||| ||||| ||||| ||||| |||||
819 yGclLysnLysSerLeuGlyAsnLeuValAsnSerValValTyrAsn 835
199 AAA 201
|||
836 Lys 836

```

seq\_name: /cgnl\_7/ptodata/1/1aa/5A\_COMB.pep:US-08-252-626A-2

seq\_documentation\_block:

Sequence 2, Application US/08252626A  
 Patent No. 5585269  
 GENERAL INFORMATION:  
 APPLICANT: Baird, Henry S.  
 APPLICANT: Graham, Douglas K.  
 APPLICANT: Dawson, Thomas L.  
 APPLICANT: Mullaney, David L.  
 APPLICANT: Shodgrass, Hiram R.  
 TITLE OF INVENTION: Isolated DNA Encoding C-MER  
 TITLE OF INVENTION: Protooncogene  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Kenneth D. Sibley  
 STREET: P.O. Drawer 34009  
 CITY: Charlotte  
 STATE: No. 5585269th Carolina  
 COUNTRY: USA  
 ZIP: 28234  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/252,626A  
 FILING DATE: 02-JUN-1994  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sibley, Kenneth D.  
 REGISTRATION NUMBER: 31,665  
 REFERENCE/DOCKET NUMBER: 5470-81  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 881-3140  
 TELEFAX: (919) 881-3175  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 999 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-252-626A-2

alignment\_scores:  
 Quality: 58.00 Length: 37  
 Ratio: 2.417 Gaps: 1  
 Percent Similarity: 64.865 Percent Identity: 35.135

alignment\_block:  
 US-09-240-675-1\_COPY\_27\_229 x US-08-252-626A-2 ..

Align seg 1/1 to: US-08-252-626A-2 from: 1 to: 999

```

43 GCCGTGGCCCATGGTGTTCGCCGACCCGAGGTGAAAAATATAA 92
||||| ||||| ||||| ||||| |||||
369 AlaValSerProTyrIleLeuAsnSerThrGluGlyAlaProSerVa 385
93 ACTCTCTCAAAAGTAGAGTGCATCATGATGAT.....GACAACTTAA 136
||||| ||||| ||||| ||||| |||||
385 lAlaProLeuAsnValThrValPheLeuAsnGluSerSerAspAsnVal 402
137 TCCTGAGGTG 147
|||||
402 splLeaTyr 405

```

seq\_name: /cgnl\_7/ptodata/1/1aa/5B\_COMB.pep:US-08-505-218-4

seq\_documentation\_block:

Sequence 4, Application US/08505218

Patent No. 5914447

GENERAL INFORMATION:

APPLICANT: ARAYA, ALEJANDRO

APPLICANT: MOURAS, ARMAND

TITLE OF INVENTION: TRANSGENIC PLANTS INCLUDING A HYBRID

TITLE OF INVENTION: NUCLEIC ACID SEQUENCE, COMPRISING AN UNEDITED

TITLE OF INVENTION: MITOCHONDRIAL GENE FRAGMENT FROM HIGHER PLANTS AND PROCESS

TITLE OF INVENTION: FOR PRODUCING THEM

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER

STREET: 99 Canal Center Plaza, Suite 300

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/505,218

FILING DATE: 03-NOV-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: KRAUS, ERIC J









```

351 LeuValValLeuValValAlaLeuGlyLeuProPheLeuAlaIleGly 367
54 ATGGGTGTCCTGCGCGACCGAGTGGAAAAATCTAAATCTCTCAAA 103
104 AAGTAGAGGTC.....GACATCATGATGACAACTTATCTCTG 141
384 etlYspheValAlaAlaAlaAlaSerPheIleIlePheLeuGlyLeu 400
142 AGCGGAACAGGACGATGATCTGTCGG.....AATGT 176
401 ValPheAsnAlaSerAspArgPheGlyIleThrThrLeuProAsnI 417
177 GACTTTTCATTCGATTATTCAAAAA 201
417 etlValThr...AspTyrProlys 424
seq_name: sp_mammal:077699

```

```

seq_documentation_block:
ID 077699 PRELIMINARY; PRT: 117 AA.
AC 077699;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE TRP3 PROTEIN (FRAGMENT).
GN TRP3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RA WISSENBACH G., PHILIP S., FLOCKERZI V.;
RT Cloning and analysis of TRP channels.
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006781; CAA07246.1;
FT NON_TER 1 1
FT NON_TER 117 117
FT SEQUENCE 117 AA; 13295 MW; B9F9B808 CRC32;

```

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alignment_scores:
Quality: 62.00 Length: 75
Ratio: 1.512 Gaps: 3
Percent Similarity: 54.667 Percent Identity: 33.333

```

alignment\_block:

us-09-240-675-1\_copy\_27\_229 x 077699

Align seg 1/1 to: 077699 from: 1 to: 117

```

4 ATGGTCGTCCTGCGCGACCGAGTGGAAAAATCTAAATCTCTCTCAAA 53
104 AAGTAGAGGTC.....GACATCATGATGACAACTTATCTCTG 141
58 etlYspheValAlaAlaAlaAlaSerPheIleIlePheLeuGlyLeu 176
75 ValPheAsnAlaSerAspArgPheGlyIleThrThrLeuProAsnI 201
177 GACTTTTCATTCGATTATTCAAAAA 201
91 etlValThr...AspTyrProlys 424

```

```

seq_name: sp_human:095927
seq_documentation_block:
ID 095927 PRELIMINARY; PRT: 290 AA.
AC 095927;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE DJ465N24.2 (PUTATIVE NOVEL PROTEIN) (ISOFORM 1).
GN DJ465N24.2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA WILSON S.;
RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031432; CAB37992.1;
FT NON_TER 1 1
FT NON_TER 734 734
FT SEQUENCE 290 AA; 33613 MW; B59E0C18 CRC32;

```

```

alignment_scores:
Quality: 62.00 Length: 62
Ratio: 2.296 Gaps: 1
Percent Similarity: 43.548 Percent Identity: 29.032

```

alignment\_block:

us-09-240-675-1\_copy\_27\_229 x 095927

Align seg 1/1 to: 095927 from: 1 to: 290

```

6 GTCGTCCTGCGCGACCGAGTGGAAAAATCTAAATCTCTCTCTCAAA 55
11 GlySerProGlnGlyAspSerProSerThrSerArgSerGlyGly 27
56 GGTGTCCTGCGCGACCGCG.....AGTGGAAAAAATCT 74
27 rSerArgLeuSerArgSerArgSerArgSerArgSerArgSerArg 44
75 .....AGTGGAAAAAATCT 89
44 rSerHisSerArgValSerArgPheSerArgSerArgSerArgSer 60
90 AAAATCTCTCAAAAGTAGAGTGCACATCATAGA 125
61 LysSerArgSerArgSerArgSerArgSerArgSerArgSerArg 72

```

seq\_name: sp\_rodent:088970

seq\_documentation\_block:

us-088970 PRELIMINARY; PRT: 734 AA.

```

4 ATGGTCGTCCTGCGCGACCGAGTGGAAAAATCTAAATCTCTCTCTCAAA 53
104 AAGTAGAGGTC.....GACATCATGATGACAACTTATCTCTG 141
58 etlYspheValAlaAlaAlaAlaSerPheIleIlePheLeuGlyLeu 176
75 ValPheAsnAlaSerAspArgPheGlyIleThrThrLeuProAsnI 201
177 GACTTTTCATTCGATTATTCAAAAA 201
91 etlValThr...AspTyrProlys 424

```

```

alignment_scores:
Quality: 61.00 Length: 29
Ratio: 2.652 Gaps: 1

```



27 GACCCTAGTGTCTGTCGCCGTGGGCCCATGGGTGTGTCCGCAGCCGCAG 76

27 GACCCTAGTGCTCGTCGCCGTGGGCCCATGGGTGTGTCCGCAGCCGAG 76

```

:::|||||::: |||||
226 GIUPTGSSerValArgArg..... LysArgSerAlaG1 229
77 GTCGAAAAATCTAAATCTCTCAAAAGTAGAGTGCATCATAGAT 126
:::|||||::: |||||
239 nfhnglyAnSerGlyArgLysAnArgLysGlyArgLysHISLs. 255
127 GACAACTTATCTGAGTCGAGACAGAGCATGATCTGCGGAATGT 176
256 ..... AsnThrGluAlaGluSerAnLeuGlySerArgArgThr 267
177 GACTTTTCATT 188
|||||:::
268 AspPheTyrVal 271
seq_name: sp_prodent:060805

```

```

seq_documentation_block:
ID 060805 PRELIMINARY; PRT: 994 AA.
AC 060805;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE C-MER PROTOONCOGENE PRECURSOR (C-MER TYROSINE KINASE RECEPTOR).
GN MER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE OF 1-315 FROM N.A.
RC STRAIN-B6; TISSUE-SPLEEN;
RX MEDLINE; 95303502.
RA GRAHAM D.K., BOWMAN G.W., DAMSON T.L., STANFORD W.L., EARP H.S.,
RT "Cloning and developmental expression analysis of the murine c-met
RT tyrosine kinase."
RL Oncogene 10:2349-2359(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-B6; TISSUE-SPLEEN;
RA SNODGRASS H.R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U21301; AAA80222.1;
DR HSP; P06213; IIRK.
DR MGD; MGI:96965; Mer.
DR PFAM; PF00041; fn3; 2.
DR PFAM; PF00047; 1q; 2.
DR PFAM; PF00069; pkinase; 1.
KW Signal.
FT CHAIN 1 20 POTENTIAL.
FT SIGNAL 21 994 C-MER TYROSINE KINASE RECEPTOR.
SQ SEQUENCE 994 AA; 110156 MW; 3C2F429D CRC32;

```

```

alignment_scores:
Quality: 60.00 Length: 39
Ratio: 2.222 Gaps: 1
Percent Similarity: 69.231 Percent Identity: 33.333

```

```

alignment_block:
US-09-240-675-1_COPY_27_229 x 060805

```

```

Align seg 1/1 to: 060805 from: 1 to: 994

```

```

43 GCGGTGGGCGCATGGGTGTTCGCGAGCGCGAGGAGAAAAATCTAA 92
|||||:::|||||:::|||||
366 AlaValSerProTyrIleLeuAlaSerThrThrGluGlyAlaProSerVa 380
93 ATCTCTCAAAAGTAGAGTCAGATCATATAGACAACTTATCTCTG. 141
|||||:::|||||:::|||||
380 AlaProLeuAnSerIleThrValPheLeuAnSerIleSerAnSerIleLeuA 397
142 .....AGTGGAGACAG 153

```

```

|||||:::
397 spLleArgThrPThrIlys 402

```

```

seq_name: sp_human:09Y5L9

```

```

seq_documentation_block:
ID 09Y5L9 PRELIMINARY; PRT: 2971 AA.
AC 09Y5L9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TRANSCRIPTIONAL ACTIVATOR SRCAP.
GN SRCAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99278407.
RA JOHNSTON H., KNEER J., CHACKALAPARAMPIL I., YACIOK P., CHIRIVIA J.;
RT "Identification of a novel SNF2/SMI2 protein family member, SRCAP,
RT which interacts with CREB-binding protein."
RL J. Biol. Chem. 274:16370-16376(1999).
DR EMBL; AF143946; AAD39760.1;
SQ SEQUENCE 2971 AA; 315639 MW; 1C7B94CB CRC32;

```

```

alignment_scores:
Quality: 60.00 Length: 25
Ratio: 3.333 Gaps: 0
Percent Similarity: 72.000 Percent Identity: 52.000

```

```

alignment_block:
US-09-240-675-1_COPY_27_229/rev x 09Y5L9

```

```

Align seg 1/1 to: 09Y5L9 from: 1 to: 2971

```

```

83 TTYCCACCTGCGGTCGCGACACACCCATGGGCGCGAGCAGCAGC 34
|||||:::|||||:::|||||
942 PheProProAlaAlaAlaThrThrThrSerThrThrAlaThrAlaThr 958
33 TAGGTCGTCGCGCGCCAGAGAGCAGC 9
|||||:::|||||
958 rThrThrAlaValProAlaProThr 966

```

```

seq_name: sp_archaea:09YEB6

```

```

seq_documentation_block:
ID 09YEB6 PRELIMINARY; PRT: 108 AA.
AC 09YEB6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE 108AA LONG HYPOTHETICAL PROTEIN.
GN APE0658.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Aeropyrum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K1;
RX MEDLINE; 99310339.
RA KAWARABAYASHI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,
RA JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,
RA HOSOVAYA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAYAMA H.,
RA TAKAMIZAKI M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y.,
RA YAMAZAKI N., SAKO Y., KIKUCHI H.,
RA "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999)
DR EMBL; AP000060; BAA79630.1;
SQ SEQUENCE 108 AA; 11371 MW; BCB1E741 CRC32;

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alignment\_scores:  
Quality: 59.50 Length: 35  
Ratio: 2.705 Gaps: 1  
Percent Similarity: 62.857 Percent Identity: 42.857

alignment\_block:  
us-09-240-675-1\_copy\_27\_229 x Q9YEB6 ..

Align seg 1/1 to: Q9YEB6 from: 1 to: 108

```
12 CCCTGCGCGCGAGACCTAGTCTGCTGCGCGCGCGCCCATGGCTGT 61
   |||||:::|||||:::|||||:::|||||:::|||||
13 ProProSerArgProSerPro.....GlnArgGlyProGlnGlyVa 26
   |||||:::|||||:::|||||:::|||||:::|||||
62 TGTCGCGAGCGCGAGGTGGAATAATCTAAATCTCTCAAAAGTAGAG 111
   |||||:::|||||:::|||||:::|||||:::|||||
26 lPheGlyAlaCysArgGlyProGlnProLeuGlnSerArgSerArgG 43
   |||||:::|||||:::|||||:::|||||:::|||||
112 GTCGA 116
   |||||
43 lYarg 44
```

OM of: US-09-240-675-1\_COPY\_27\_229 to: SwissProt\_38: out\_format: pfs  
 Date: Aug 21, 2000 7:33 PM

About: Results were produced by the Gencore software, version 4.5,  
 Copyright (c) 1993-2000 Compugen Ltd.

## Command line parameters:

-MODEL-frame+g2p.model -DEV-xlp  
 -O/-gnl1/USPROT.spool/US09240675/runat\_21082000\_102213\_24165/app.query.fasta\_1.274  
 -DB-SwissProt\_38 -OFMT-fastaa -SUFFIX-n2p.rsp -GAPOP-12.000  
 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPT-0.000 -LOOEXT-0.000  
 -OGAPOP-4.500 -OGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500  
 -FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500  
 -DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62  
 -TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR\_SCORE-pct  
 -THR\_MAX-100 -THR\_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs  
 -NOR-ext -MINLEN-0 -MAXLEN-2000000000  
 -USER-US09240675\_ecgnl\_1\_26 -NCPD-6 -ICPD-3 -LONGLOG -NO\_XLPXY  
 -WAIT -THREADS-1

## Search information block:

Query: US-09-240-675-1\_COPY\_27\_229  
 Query Length: 203  
 Database: SwissProt\_38: +  
 Database sequences: 85661  
 Search time (sec): 41.190000

Sequence	Strid	Orig	ZScore	EScore	Len	Documentation
SwissProt_38:INRL_HUMAN	340.00	742.98	1.6e-34	557	1 P17181 homo sapiens (human)	
SwissProt_38:INRL_BOVIN	209.00	449.22	3.6e-18	560	1 O04790 bos taurus (bovine)	
SwissProt_38:INRL_SHEEP	204.00	438.01	1.5e-17	560	1 O28589 ovis aries (sheep)	
SwissProt_38:INRL_MOUSE	198.00	424.12	8.6e-17	590	1 P33896 mus musculus (mouse)	
SwissProt_38:INIL3_HUMAN	65.00	118.23	3.73	1475	1 P49790 homo sapiens (human)	
SwissProt_38:CONA_BPT4	62.50	132.30	6.43	141	1 O01438 bacteriophage t4, contom	
SwissProt_38:PHLC_PSEAE	62.00	127.06	8.39	730	1 P06200 pseudomonas aeruginosa	
SwissProt_38:CRF4_HUMAN	61.50	123.06	9.12	325	1 O08334 homo sapiens (human)	
SwissProt_38:ERE_MOUSE	61.00	117.52	10.96	551	1 P70459 mus musculus (mouse)	
SwissProt_38:IRK2_MOUSE	61.00	110.19	11.69	1321	1 P81122 mus musculus (mouse)	
SwissProt_38:SFRI2_CHICK	60.00	122.93	13.64	221	1 P30352 gallus gallus (chicken)	
SwissProt_38:CCAA_RABIT	60.00	102.86	16.31	2424	1 P27884 oryctolagus cuniculus	
SwissProt_38:CAPA_RABIT	59.50	109.31	17.61	982	1 P28584 anabaena sp. (strain	
SwissProt_38:SF2_HUMAN	59.00	120.69	18.19	221	1 O01130 homo sapiens (human)	
SwissProt_38:HXA_HUMAN	59.00	113.91	19.32	496	1 P31260 homo sapiens (human)	
SwissProt_38:S230_PLAFO	59.00	98.46	22.17	3135	1 O08372 plasmodium falciparum	
SwissProt_38:RPOA_STRCO	58.50	115.96	21.69	340	1 P72404 streptomyces coelicolor	
SwissProt_38:RPOA_STRGT	58.50	115.96	21.69	340	1 O9456 streptomyces griseolus	
SwissProt_38:FLBL_BACSU	58.00	122.27	23.44	140	1 P23452 bacillus subtilis, fl	
SwissProt_38:Y288_METJA	58.00	120.26	23.86	178	1 O57736 methanococcus jannaschii	
SwissProt_38:VG2_SPIR	58.00	114.91	25.03	337	1 P15893 spiroplasma virus sp	
SwissProt_38:AT6_WHEAT	57.50	112.65	29.19	386	1 P20399 triticum aestivum (wheat)	
SwissProt_38:TAP_DROME	57.50	112.39	29.26	398	1 P01687 drosophila melanogaster	
SwissProt_38:AK3_BACSU	57.50	111.29	29.55	454	1 P94417 bacillus subtilis, prod	
SwissProt_38:PERX_ERMCH	57.50	108.93	30.17	602	1 P15922 erythrina chrysanthemum	
SwissProt_38:DNLJ_ZYMO	57.50	107.30	30.61	731	1 P28719 zymomonas mobilis, d	
SwissProt_38:DEAD_KLEPN	57.00	107.05	35.08	659	1 P33960 klebsiella pneumoniae	
SwissProt_38:RPE_BACSU	56.50	115.23	37.28	217	1 O34557 bacillus subtilis, r	
SwissProt_38:VE2_HPV20	56.50	108.29	39.66	497	1 P50766 human papillomavirus t	
SwissProt_38:RRPL_RVFLZ	56.50	96.92	44.23	2149	1 P27316 rift valley fever v	
SwissProt_38:SF3_HUMAN	56.00	116.46	42.15	164	1 P23152 homo sapiens (human)	
SwissProt_38:CTL_RAT	56.00	107.25	45.75	492	1 P11671 rattus norvegicus (rat)	
SwissProt_38:SECT_MYCGA	56.00	107.15	45.80	498	1 O52251 mycoplasma gallisepti	
SwissProt_38:IRR_CAVPO	55.00	99.11	49.19	1300	1 P14617 cavia porcellus (guinea	
SwissProt_38:ET2_HUMAN	55.50	114.65	48.97	178	1 P20800 homo sapiens (human)	
SwissProt_38:AMP_NLACIC	55.50	101.06	55.00	845	1 P37897 lactococcus lactis (s	
SwissProt_38:IF2_ECOLI	55.50	101.17	55.22	890	1 P02995 escherichia coli, tr	
SwissProt_38:IF2_SATY	55.50	101.15	55.23	892	1 O9451 salmonella typhimurium	
SwissProt_38:IF2_KLEBX	55.50	101.11	55.25	896	1 O92128 klebsiella oxytoca, tr	
SwissProt_38:IF2_ENTCL	55.50	101.10	55.25	897	1 O92125 enterobacter cloacae,	

SwissProt\_38:GUNZ\_CLOSR + 55.50 100.31 55.64 986 1 P23659 clostridium sterco  
 SwissProt\_38:RHSI\_ECOLI + 55.50 97.22 57.19 1426 1 P16919 escherichia coli  
 SwissProt\_38:MOVY\_TWATO - 55.00 110.23 58.23 264 1 P03584 tobacco mosaic vir  
 SwissProt\_38:MOVY\_TOMVA - 55.00 110.23 58.23 264 1 P29799 tomato mosaic viru  
 SwissProt\_38:POOK\_RHIME + 55.00 99.97 63.80 898 1 O59754 rhizobium meliloti

seq name: SwissProt\_38:INRL\_HUMAN

seq documentation block:  
 ID INRL\_HUMAN STANDARD: PRT: 557 AA.  
 AC P17181:  
 DT 01-ANG-1990 (rel. 15, Created)  
 DT 01-ANG-1990 (rel. 15, Last sequence update)  
 DT 15-FEB-2000 (rel. 39, Last annotation update)  
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).  
 GN IFNARI OR IFNAR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 90124632.  
 RA Uze G., Lutfalla G., Gresser I.;  
 RT Genetic transfer of a functional human interferon alpha receptor  
 RT into mouse cells: cloning and expression of its cDNA.  
 RL Cell 60:225-234(1990).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92129376.  
 RA Lutfalla G., Gardiner K., Proudhon D., Vleth E., Uze G.;  
 RT The structure of the human interferon alpha/beta receptor gene.\*;  
 RL J. Biol. Chem. 267:2802-2809(1992).  
 RN (3)  
 RP PHOSPHORYLATION BY TYK2.  
 RX MEDLINE: 95059042.  
 RA Colaninich O., Yan H., Domanski P., Handa R., Smalley D.,  
 RA Mullerstein J., Witte M., Krishnan K., Krolewski J.;  
 RT Direct binding to and tyrosine phosphorylation of the alpha subunit  
 RT of the type I interferon receptor by p135tyk2 tyrosine kinase.\*;  
 RL Mol. Cell. Biol. 14:8133-8142(1994).  
 CC - FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE  
 CC I FINS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS  
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-  
 CC SUBUNITS THEMSELVES.  
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC - TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND  
 CC EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.  
 CC - PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.  
 CC - SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))  
 CC -----  
 CC EMBL: J03171; AAA52730.1; -  
 CC EMBL: X60459; CAA42992.1; -  
 CC PIR: A32694; A32694;  
 CC PIR: S17112; S17112.  
 CC MIM: 107450; -  
 CC Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;  
 CC Phosphorylation.  
 KW CHAIN 1 27  
 FT SIGNAL 1 27  
 FT CHAIN 28 557  
 FT DOMAIN 28 436  
 FT TRANSMEM 437 457  
 FT DOMAIN 458 557  
 FT DISULFID 79 87  
 FT BY SIMILARITY.







```

CC      -1- DOMAIN: CONTAINS X-E-X-F-G REPEATS.
CC      -1- SIMILARITY: THE REPEAT REGION COMPOSED OF PENTAPEPTIDE REPEATS
CC      SEPARATED BY SER/THR-RICH DOMAINS IS SIMILAR TO THAT OF YEAST
CC      NUP1, NUP1, POM 121 AND MAMMALIAN P62.
CC
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CC      or send an email to license@isb.sib.ch).
CC
DR      EMBL: Z25535; CAAB0982.1;
DR      MIM: 603948;
DR      PFM: PFM0641; zf-RanBP; 4
KW      Nuclear Protein; Transport; Repeat; Zinc-finger; DNA-binding.
FT      DOMAIN 4 14 GLY-RICH.
FT      DOMAIN 4 14 POLY-GLY.
FT      ZN_FING 443 447 C4-TYPE.
FT      ZN_FING 662 681 C4-TYPE.
FT      ZN_FING 726 745 C4-TYPE.
FT      ZN_FING 797 816 C4-TYPE.
FT      ZN_FING 855 874 C4-TYPE.
SQ      SEQUENCE 1475 AA; 153889 MW; 3CB415A6909DF80E CRC64;

```

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: M89919; AAA32485.1;  
 CC PIR: A45731; A45731.  
 CC Transcription regulation.  
 CC  
 CC SEQUENCE 141 AA; 16682 MW; 96C9EFA8C673C479 CRC64;

alignment\_scores:  
 Quality: 62.50 Length: 50  
 Ratio: 2.155 Gaps: 3  
 Percent Similarity: 58.000 Percent Identity: 34.000

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x COMA\_BPT4

Align seg 1/1 to: COMA\_BPT4 from: 1 to: 141

16 CTGGGCGGAGACCTAGTCTGCTGCGCCGCGGCGGCGGCTGTC 65  
 ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||  
 49 LcnglytrpProthrlysllemerthserlly.....Valleuly 63  
 66 CGGAGCGGCGGAGGAAAAATCTAAATCTCCCAAAAGTACAGTCG 115  
 63 shgcygslaleglyly.....A 69  
 116 ACATCATGATGACACTTATCTCTGAGTGAGACAGGAGCATGCTC 165  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 69 spleleuaspgluasnphelle.....TipleuSerThrAsnGluAla 83

seq\_name: SwissProt\_38:PHLC\_PSEAE

seq\_documentation\_block:  
 ID PHLC\_PSEAE STANDARD; PRT; 730 AA.

AC P06300:  
 DT 01-JAN-1988 (rel. 06, Created)  
 DT 01-JAN-1988 (rel. 06, Last sequence update)  
 DT 01-MAY-1991 (rel. 18, Last annotation update)  
 DE HEMOLYTIC PHOSPHOLIPASE C PRECURSOR (EC 3.1.4.3) (HEAT LABILE-  
 DE HEMOLYSIN) (PHOSPHATIDYLCHOLINE CHOLINEPHOSPHOHIDROLASE).  
 GN PLECH.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;  
 OC Pseudomonas.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 86250607.  
 RA Pritchard A.E.; Vasil M.L.;  
 RT "Nucleotide sequence and expression of a phosphate-regulated gene  
 RT encoding a secreted hemolysin of Pseudomonas aeruginosa.";  
 RL J. Bacteriol. 167:291-298(1986).  
 RN  
 RN REVISIONS.  
 RA Pritchard A.E.;  
 RL Submitted (Aug-1986) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: HYDROLYSES SPHINGOMELIN IN ADDITION TO  
 CC PHOSPHATIDYLCHOLINE.  
 CC -1- CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O -> 1,2-  
 CC DIACYLGLYCEROL + CHOLINE PHOSPHATE.  
 CC -1- SIMILARITY: 40% IDENTITY TO NON-HEMOLYTIC PHOSPHOLIPASE C.  
 CC  
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 CC  
 CC EMBL: M13047; AAA25966.1;  
 CC PIR: A26391; A26391.  
 CC Hemolysis; Toxin; Hydrolase; Signal.  
 CC  
 CC FT SIGNAL 1 38  
 CC CHAIN 39 730  
 CC SEQUENCE 730 AA; 82655 MW; F1D3695824445FBF CRC64;

alignment\_scores:  
 Quality: 62.00 Length: 69  
 Ratio: 1.824 Gaps: 4  
 Percent Similarity: 49.275 Percent Identity: 26.087

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x PHLC\_PSEAE

Align seg 1/1 to: PHLC\_PSEAE from: 1 to: 730

37 CTCTGCGCGGAGGCGCCATGGGTGTGTCGCGAGCGGAGGAAAAA 86  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 404 LeuilealalieserProtrp.....Serlysglyly..... 414  
 87 TCTAAATCTCTCTCAAAAGTAGAGTCGACATCATGATGACACTTTA 136  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 415 .....LysValSerAlaGluValPheAspHisThrSery 426  
 137 TCCTGAGG..... 144  
 426 alleuArgPheLeuGluArgArgPheGlyLeuValGluGluAsnIleSer 442  
 145 ..TGGAACGAGGAGCATGATGTGTCGGAGATGTGACTTTTCATTCGA 191  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 443 ProTrpArgArgAla.....ValCysGlyAspLeuThrSerLeuPheAs 457  
 192 TTAACAA 198  
 457 pPheGln 459

seq\_name: SwissProt\_38:CRF4\_HUMAN

seq\_documentation\_block:  
 ID CRF4\_HUMAN STANDARD; PRT; 325 AA.

AC 008334:  
 DT 01-FEB-1995 (rel. 31, Created)  
 DT 01-FEB-1995 (rel. 31, Last sequence update)  
 DT 01-OCT-1996 (rel. 34, Last annotation update)  
 DE CYTOKINE RECEPTOR CLASS-II CRF2-4 PRECURSOR.  
 GN CRF4.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE-FETAL BRAIN;  
 RC MEDLINE: 93300510.  
 RA Lutfalla G.; Gardiner K.; Uze G.;  
 RT "A new member of the cytokine receptor gene family maps on chromosome  
 RT 21 at less than 35 kb from IFNAR.";  
 RL Genomics 16:366-373(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 96054036.  
 RA Lutfalla G.; McInnis M.G.; Antonarakis S.E.; Uze G.;  
 RT "Structure of the human CRF4 gene: comparison with its IFNAR  
 RT neighbor.";  
 RL J. Mol. Evol. 41:338-344(1995).  
 CC -1- FUNCTION: IS PROBABLY INVOLVED IN THE INTERFERON SYSTEM.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC  
 CC modified and this statement is not removed. Usage by and for commercial

SECRET NO. 100-441141

Ensayos, 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 264



CCAA\_RABIT STANDARD: PRT: 2424 AA.  
 AC P27884; P27883; (Created)  
 DT 01-JUL-1993 (Rel. 26, last sequence update)  
 DT 01-JUL-1993 (Rel. 26, last sequence update)  
 DT 15-FEB-2000 (Rel. 39, last annotation update)  
 DE VOLTAGE-DEPENDENT P/O-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT (CALCIUM  
 CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 4) (BRAIN CALCIUM CHANNEL  
 DE I) (B1)  
 GN CACNA1A OR CACNA1A4 OR CACNA4 OR CACNA3  
 OS Oryctolagus cuniculus (Rabbit)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN:  
 RX MEDLINE: 91187110.  
 RA Mori Y., Friedrich T., Kim M.-S., Mikami A., Nakai J., Ruth P.,  
 RA Bosse E., Hofmann F., Flockerzi V., Furutachi T., Mikoshiba K.,  
 RA Imoto K., Tanabe T., Numa S.;  
 RT "Primary structure and functional expression from complementary DNA  
 RT of a brain calcium channel.";  
 RT Nature 350:398-402(1991).  
 RL Nature 350:398-402(1991).  
 RN BETA-SUBUNIT BINDING DOMAIN AND MUTAGENESIS.  
 RP MEDLINE: 94150724.  
 RX Pragnell M., de Waard M., Mori Y., Tanabe T., Snutch T.P.,  
 RA Campbell K.P.;  
 RT "Calcium channel beta-subunit binds to a conserved motif in the I-II  
 RT cytoplasmic linker of the alpha 1-subunit.";  
 RL Nature 368:67-70(1994).  
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE  
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1A  
 CC GIVES RISE TO P AND/OR Q-TYPE CALCIUM CURRENTS. P/O-TYPE CALCIUM  
 CC CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND  
 CC ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-ACATOXIN-  
 CC IVA (OMEGA-AGA-IVA). THEY ARE HOWEVER INSENSITIVE TO  
 CC DIHYDROPYRIDINES (DHP), AND OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-  
 CC GVIA).  
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-  
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: IN THE BRAIN, A SHORT ISOFORM BI-1/1A-1 AND  
 CC A LONG ISOFORM BI-2/1A-2 (SHOWN HERE), ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC. PURKINJE CELLS CONTAIN  
 CC PREDOMINANTLY P-TYPE VSCC, THE Q-TYPE BEING A PROMINENT CALCIUM  
 CC CURRENT IN CEREBELLAR GRANULE CELLS.  
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 CC FAMILY.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: X57477; CAA40715.1;  
 CC EMBL: X57689; CAA40872.1;

DR EMBL: X57476; CAA40714.1;  
 DR EMBL: X57688; CAA40871.1;  
 DR PDB: 1P00520; Ion trans. 4;  
 DR PRINTS: PR00157; CACNA1A;  
 DR PRINTS: PR00170; NACNA1A;  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;  
 KW Calcium-binding; Phosphorylation; Alternative splicing.  
 FT REPEAT 85 363  
 FT REPEAT 473 717  
 FT REPEAT 1240 1523  
 FT REPEAT 1560 1823  
 FT DOMAIN 1 98  
 FT TRANSMEM 99 117  
 FT DOMAIN 118 135  
 FT TRANSMEM 136 155  
 FT DOMAIN 156 167  
 FT TRANSMEM 168 185  
 FT DOMAIN 186 190  
 FT TRANSMEM 191 209  
 FT DOMAIN 210 228  
 FT TRANSMEM 229 248  
 FT DOMAIN 249 335  
 FT TRANSMEM 336 360  
 FT DOMAIN 361 487  
 FT TRANSMEM 488 506  
 FT DOMAIN 507 521  
 FT TRANSMEM 522 541  
 FT DOMAIN 542 549  
 FT TRANSMEM 550 568  
 FT DOMAIN 569 578  
 FT TRANSMEM 579 597  
 FT DOMAIN 598 616  
 FT TRANSMEM 617 636  
 FT DOMAIN 637 689  
 FT TRANSMEM 690 714  
 FT DOMAIN 715 1253  
 FT TRANSMEM 1254 1272  
 FT DOMAIN 1273 1288  
 FT TRANSMEM 1289 1308  
 FT DOMAIN 1309 1320  
 FT TRANSMEM 1321 1339  
 FT DOMAIN 1340 1350  
 FT TRANSMEM 1351 1369  
 FT DOMAIN 1370 1388  
 FT TRANSMEM 1389 1408  
 FT DOMAIN 1409 1495  
 FT TRANSMEM 1496 1520  
 FT DOMAIN 1521 1575  
 FT TRANSMEM 1576 1604  
 FT DOMAIN 1605 1609  
 FT TRANSMEM 1610 1629  
 FT DOMAIN 1630 1637  
 FT TRANSMEM 1638 1656  
 FT DOMAIN 1657 1665  
 FT TRANSMEM 1666 1684  
 FT DOMAIN 1685 1703  
 FT TRANSMEM 1704 1723  
 FT DOMAIN 1724 1795  
 FT TRANSMEM 1796 1820  
 FT DOMAIN 1821 2424  
 FT DOMAIN 13 18  
 FT TRANSMEM 727 732  
 FT DOMAIN 1004 1010  
 FT TRANSMEM 1012 1017  
 FT DOMAIN 2219 2227  
 FT TRANSMEM 2242 2246  
 FT DOMAIN 2288 2297  
 FT TRANSMEM 2298 2301  
 FT DOMAIN 2372 2377  
 FT TRANSMEM 2411 2416  
 FT DOMAIN 383 400  
 FT SITE 318 318  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S1 OF REPEAT I (POTENTIAL).  
 II. EXTRACELLULAR (POTENTIAL).  
 III. S2 OF REPEAT I (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S3 OF REPEAT I (POTENTIAL).  
 II. EXTRACELLULAR (POTENTIAL).  
 III. S4 OF REPEAT I (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S5 OF REPEAT I (POTENTIAL).  
 II. EXTRACELLULAR (POTENTIAL).  
 III. S6 OF REPEAT I (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S1 OF REPEAT II (POTENTIAL).  
 II. EXTRACELLULAR (POTENTIAL).  
 III. S2 OF REPEAT II (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S3 OF REPEAT II (POTENTIAL).  
 II. EXTRACELLULAR (POTENTIAL).  
 III. S4 OF REPEAT II (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S5 OF REPEAT II (POTENTIAL).  
 II. EXTRACELLULAR (POTENTIAL).  
 III. S6 OF REPEAT II (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S1 OF REPEAT III (POTENTIAL).  
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 III. S2 OF REPEAT III (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S3 OF REPEAT III (POTENTIAL).  
 II. EXTRACELLULAR (POTENTIAL).  
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 IV. CYTOPLASMIC (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
 III. S6 OF REPEAT III (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
 III. S2 OF REPEAT IV (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
 III. S4 OF REPEAT IV (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S5 OF REPEAT IV (POTENTIAL).  
 II. EXTRACELLULAR (POTENTIAL).  
 III. S6 OF REPEAT IV (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
 III. S2 OF REPEAT V (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S3 OF REPEAT V (POTENTIAL).  
 II. EXTRACELLULAR (POTENTIAL).  
 III. S4 OF REPEAT V (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S5 OF REPEAT V (POTENTIAL).  
 II. EXTRACELLULAR (POTENTIAL).  
 III. S6 OF REPEAT V (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
 III. S2 OF REPEAT VI (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
 I. S3 OF REPEAT VI (POTENTIAL).  
 II. EXTRACELLULAR (POTENTIAL).  
 III. S4 OF REPEAT VI (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
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 III. S6 OF REPEAT VI (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
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 I. S3 OF REPEAT VII (POTENTIAL).  
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 III. S4 OF REPEAT VII (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
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 IV. CYTOPLASMIC (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
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 III. S2 OF REPEAT X (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
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 IV. CYTOPLASMIC (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
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 IV. CYTOPLASMIC (POTENTIAL).  
 I. S1 OF REPEAT XII (POTENTIAL).  
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 III. S2 OF REPEAT XII (POTENTIAL).  
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 I. S3 OF REPEAT XII (POTENTIAL).  
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 IV. CYTOPLASMIC (POTENTIAL).  
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 III. S4 OF REPEAT XIV (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
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 III. S6 OF REPEAT XIV (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
 III. S2 OF REPEAT XVII (POTENTIAL).  
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 III. S4 OF REPEAT XX (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
 III. S6 OF REPEAT XX (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
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 IV. CYTOPLASMIC (POTENTIAL).  
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 IV. CYTOPLASMIC (POTENTIAL).  
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 IV. CYTOPLASMIC (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
 III. S2 OF REPEAT XXIII (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
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 IV. CYTOPLASMIC (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
 III. S6 OF REPEAT XXIII (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
 III. S2 OF REPEAT XXIV (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).  
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 IV. CYTOPLASMIC (POTENTIAL).  
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 II. EXTRACELLULAR (POTENTIAL).  
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 III. S6 OF REPEAT XXVII (POTENTIAL).  
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 III. S6 OF REPEAT XXXII (POTENTIAL).  
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 III. S2 OF REPEAT XLV (POTENTIAL).  
 IV. CYTOPLASMIC (POTENTIAL).<

RA  
IN  
MEDLINE, 34200648.  
Wulenburg T. A. Coleman J. B.

Fu X.-D.; Maniatis T.;

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CC      -1- PFM: EXTENSIVELY PHOSPHORYLATED ON SERINE RESIDUES IN THE RS
CC      DOMAIN.
CC      -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
CC      -1- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; M90104; AAA60306.1; -
CC      DR      EMBL; X62447; CAA44307.1; -
CC      DR      EMBL; X75755; CAA53383.1; -
CC      DR      EMBL; L03693; AAA60162.1; -
CC      DR      PIR; S17328; S17328.
CC      DR      PIR; A42634; A42634.
CC      DR      HSP; P19339; ISXL.
CC      DR      MIM; 600813; -.
CC      DR      PFM; PFO0076; rrm; 1.
CC      DR      PROSITE; PS00030; RNP_1; 1.
CC      DR      Nuclear protein; RNA-binding; mRNA splicing; Alternative splicing;
CC      Phosphorylation.
CC      FT      DOMAIN                    16      21      RNA-BINDING (RNP2) (BY SIMILARITY).
CC      FT      DOMAIN                    55      62      RNA-BINDING (RNP1) (BY SIMILARITY).
CC      FT      DOMAIN                    111     116      GLY-RICH (HINE REGION).
CC      FT      DOMAIN                    117     221      ARG/SER-RICH (RS DOMAIN).
CC      FT      CONFLICT                   38      38      R -> G (IN REF. 2 AND 3).
CC      SQ      SEQUENCE                 221 AA; 25575 MW; 9D1B76BDB65701F5 CRC64;

alignment_scores:
      Quality:      59.00      Length:      54
      Ratio:        2.185      Gaps:      2
      Percent similarity: 50.000      Percent identity: 35.185

alignment_block:
US-09-240-675-1_COPY_27_229 x SFR2_HUMAN ..

Align seg 1/1 to: SFR2_HUMAN from: 1 to: 221

      6 GGTGCTCTCTCT.....GGGCGCGAGCACCTAGTGCCTGCTGCG 43
      |||||
      93 GLYARGPROPROASPSPERHSHSSERATGARGGLYPROPROARGR 109
      |||||
      44 C.....CGTGGGCCCATGGGTGG 63
      |
      109 GYRGGLYGLYGLYTYRGLYARGARGSERARGSERPROARGARGARG 126
      |||||
      64 TCCGAGCGCCGAGGTGGAAAAATCTAAATCTCCCAAAAAAGTAGAGT 113
      |||||
      126 IGRATSERATGSRATGSRATGSRATGSRATGSRATGSRATGSRATG 142
      |||||
      114 CGACATCATAGAGA 125
      |||||
      143 AGTYISERATG 146

seq_name: SwissProt_38:HXAA_HUMAN

seq_documentation_block:
ID      HXAA_HUMAN      STANDARD;          PRT;      496 AA.
AC      P31260; 015949;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      15-FEB-2000 (Rel. 39, Last annotation update)
DE      HOMEOBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL).
GN      HOXA10 OR HOX1H.
OS      Homo sapiens (Human).
CC      Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC      [1]

```

RP SEQUENCE FROM N.A.  
RX MEDLINE: 91288229.  
RA Lowney P., Corral J.C., Detmer K., Lebeau M.M., Deaven L.,  
RT "A human HOX 1 homeobox gene exhibits myeloid-specific expression of  
RT alternative transcripts in human hematopoietic cells.";  
RL Nucleic Acids Res. 19:3443-3449(1991).  
RN [2]  
RP SEQUENCE OF 404-486 FROM N.A.  
RX MEDLINE: 90046832.  
RA Shen W.-F., Largman C., Lowney P., Corral J.C., Detmer K.,  
RA Hausen C.A., Simionich T.A., Hack F.M., Lawrence H.J.;  
RT "tissue-restricted expression of homeobox-containing genes in human  
RT hematopoietic cell lines.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).  
RN [3]  
RP SEQUENCE OF 422-487 FROM N.A.  
RX MEDLINE: 90098876.  
RA Acampora D., D'Esposito M., Fatella A., Pannese M., Migliaccio E.,  
RA Morelli F., Stornaiuolo A., Nigro V., Simeone A., Boncinelli E.;  
RT "The human HOX gene family.";  
RL Nucleic Acids Res. 17:10385-10402(1989).  
RN [4]  
RP SEQUENCE OF 435-473 FROM N.A.  
RX MEDLINE: 94145486.  
RA Castonovo V., Kusaka M., Chariot A., Gielen J., Sobel M.;  
RT "Homeobox genes: potential candidates for the transcriptional control  
RT of the transformed and invasive phenotype.";  
RL Blochem. Pharmacol. 47:137-143(1994).  
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
CC BINDS TO THE DNA SEQUENCE 5'-AATATTTTATATAC-3'.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS: HOX-A10-1/PL1 (SHOWN HERE) AND  
CC HOX-A10-2/PL2. ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- SIMILARITY: BELONGS TO THE ADB-B FAMILY OF HOMEOBOX PROTEINS.  
CC  
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CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
DR EMBL: X58430; -; NOT\_ANNOTATED\_CDS.  
DR EMBL: M30599; AAA36006.1; -;  
DR EMBL: S69027; AAD14030.1; -;  
DR EMBL: S69029; AAD14031.1; -;  
DR PIR: S14930; S14930.  
DR PIR: S26402; S26402.  
DR PIR: A34425; A34425.  
DR HSSP: P02833; 1SAN.  
DR TRANSFAC: T01713; -;  
DR MIM: 142957; -;  
DR PFAM: PF00046; homeobox; 1.  
DR PRINTS: PR00024; HOMEOBOX.  
DR PROSITE: PS00027; HOMEOBOX\_1; 1.  
DR PROSITE: PS00071; HOMEOBOX\_2; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
KW Transcription regulation; Alternative splicing.  
FT DOMAIN 181 192 POLY-GLY.  
FT DOMAIN 219 223 POLY-PRO.  
FT DOMAIN 227 236 POLY-PRO.  
FT DOMAIN 366 371 POLY-ALA.  
FT DNA\_BIND 422 481 HOMEOBOX.  
FT VAAPSPIC 1 402 MISSING (IN ISOFORM HOX-A10-2).  
FT VAAPSPIC 403 405 DSL -> MCQ (IN ISOFORM HOX-A10-2).  
FT CONFLICT 435 435 L -> S (IN REF. 2).  
FT CONFLICT 437 437 L -> F (IN REF. 2).  
FT CONFLICT 473 473 R -> P (IN REF. 2).  
SQ SEQUENCE 496 AA; 5473 MW; 77C6F675916552F0 CRC64;

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alignment_scores:
    quality: 59.00
    ratio: 3.105
    percent_similarity: 79.167
    percent_identity: 58.333

alignment_block:
    US-09-240-675-1_COPY_27_229 x HXAA_HUMAN ..

Align seg 1/1 to: HXAA_HUMAN from: 1 to: 496

15 CCTGGCGCCGACGACCTAGTCGTCGCGCCGCGGCCCATGGGTGTTGT 64
|||||.....:||||| ||| |||
350 ProGlyAArgserGluProSerIleArgNrgsArgProIaArgTrp.LeuA 366
65 CCGGACCGCGAGGTGGAAA 84
:::|||||.....:
366 IaAlaAlaIaGlaGlyAlaArg 372

```



Tue Aug 22 08:32:08 2000

us-09-240-675-1\_copy\_27\_229.n2p.rsp

OM of: US-09-240-675-1\_COPY\_27\_229 to: PIR\_64: \* out\_format : pfs

Date: Aug 21, 2000 7:27 PM

About: Results were produced by the GenCore software, Version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL-frame.n2p.model -DEV-rlp  
-Q/cgml\_1/USPTO.spool/US09240675/runat\_21082000.102212.24099/app\_query.fasta\_1.274  
-DB-PIR\_64 -OFMT-fastan -SUFFIX-n2p.rpr -GAPOP-12.000  
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPEXT-0.000 -LOOPEXT-0.000  
-GAPOP-4.500 -GAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500  
-FEAPOP-6.000 -FEAPEXT-7.000 -TGAPOP-10.000 -TGAPEXT-0.500  
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-biosun62  
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR-SCORE-pct  
-THR\_MAX-100 -THR\_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs  
-NORMEXT -MINLEN-0 -MAXLEN-200000000  
-USER-US09240675.ecgml\_1\_53 -NCPU-6 -ICPD-3 -LONGLOG -NO\_XLPHY  
-WAIT -THREADS-1

Search information block:

Query: US-09-240-675-1\_COPY\_27\_229  
Query length: 203  
Database: PIR\_64: \*  
Database sequences: 178050  
Database length: 61884766  
Search time (sec): 47.930000

Sequence	Strd Orig	ZScore	EScore	len	Documentation
PIR2:A32694	+	340.00	768.91	1.1e-35	557   Interferon alpha/beta receptor
PIR2:S27387	+	209.00	466.39	1.0e-18	560   Interferon alpha/beta receptor type
PIR2:A45283	+	198.00	438.39	2.7e-17	504   Interferon alpha/beta receptor
PIR2:T03857	+	71.00	148.74	0.72230	304   hypothetical protein F23K16.40
PIR2:JC8307	+	71.00	140.39	0.7742	628   trypsin protein - rat
PIR2:T26391	+	68.50	146.67	1.48	1194   hypothetical protein Y105C5B.0
PIR2:J00405	+	67.00	128.69	2.60	1106   hypothetical 119.5K protein (c
PIR2:T43286	+	66.00	135.60	3.25	365   cet-1 protein - Caenorhabditis
PIR2:S42718	+	65.00	124.64	4.82	1475   nuclear pore complex protein r
PIR2:T08930	+	63.00	124.90	8.19	571   hypothetical protein F15N24.90
PIR2:A45731	+	62.50	133.38	8.64	141   comc-alpha protein - phage T4
PIR2:I54418	+	62.50	127.55	9.22	361   MHC class I histocompatibility
PIR2:A26391	+	62.50	120.53	11.23	730   phospholipase C (EC 3.1.4.3) -
PIR2:G01418	+	61.50	127.56	12.18	273   cytokine receptor family II, me
PIR2:A47003	+	61.50	126.10	12.33	325   cytokine receptor family class
PIR2:T25677	+	60.50	123.40	16.66	340   hypothetical protein F08D12.9
PIR2:B42701	+	60.00	124.16	19.04	270   probable cytochrome P450 monoo
PIR2:T02955	+	60.00	121.34	19.49	379   hypothetical protein T25F10.2
PIR2:T29518	+	60.00	113.31	20.81	994   c-met tyrosine kinase receptor
PIR2:I46276	+	60.00	111.42	21.14	1247   hypothetical protein F24M12.16
PIR2:T45743	+	60.00	105.88	22.12	2424   calcium channel Bi-2 - rabbit
PIR2:I46479	+	60.00	105.88	22.12	2424   calcium channel Bi-2 - rabbit
PIR2:I46479	+	59.50	130.63	20.76	108   hypothetical protein APF0658 -
PIR2:F72653	+	59.50	121.08	22.45	340   class I histocompatibility anti
PIR2:S11143	+	59.50	121.24	24.14	982   phosphoenolpyruvate carboxylase
PIR2:A48311	+	59.00	123.51	25.30	221   PR264/SC35 protein - human
PIR2:A4701	+	59.00	123.51	25.30	221   PR264/SC35 protein - human
PIR2:A46534	+	59.00	123.51	25.30	221   PR264/SC35 protein - human
PIR2:S24169	+	59.00	117.68	26.54	445   self-incompatibility locus ii pr
PIR2:J01733	+	59.00	117.68	26.54	445   self-incompatibility locus ii pr
PIR2:S42281	+	59.00	116.77	26.74	496   homeotic protein Hox A10 - huma
PIR2:SC6402	+	59.00	116.27	26.85	527   hypothetical protein T22H2.2
PIR2:T25131	+	59.00	116.27	26.85	527   hypothetical protein T22H2.2
PIR2:DB1225	+	59.00	116.27	26.85	527   hypothetical protein T22H2.2
PIR2:A4584	+	59.00	110.41	30.33	3135   DNA gyrase chain B NMB0212 (Im
PIR2:T33558	+	58.50	118.76	30.25	340   DNA-directed RNA polymerase al
PIR2:A38845	+	58.00	122.98	33.04	140   flagellar protein required for
PIR2:A64336	+	58.00	122.98	33.59	178   hypothetical protein Mj0288 - M
PIR2:S08459	+	58.00	117.67	35.09	337   hypothetical protein 2 - spirog
PIR2:T14516	+	58.00	114.48	36.02	494   S-locus-specific glycoprotein S

seq\_name: PIR2:A32694  
seq\_documentation\_block:  
Interferon alpha/beta receptor precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 22-Oct-1999  
C:Accession: A32694, S17112  
R:0ze, G.: Luffalla, G.: Gresser, I.  
Cell 60, 225-234, 1990  
A:Title: Genetic transfer of a functional human interferon alpha receptor into mo  
A:Reference number: A32694; MUID:90124632  
A:Accession: A32694  
A:Molecule type: mRNA  
A:Residues: 1-557 <UZE>  
A:Cross-references: GB:J03171; NID:G184645; PIDN:AAA52730.1; PID:G306914  
R:Luffalla, G.  
submitted to the EMBL Data Library, July 1991  
A:Description: The structure of the human interferon alpha/beta receptor gene.  
A:Reference number: S17112  
A:Accession: S17112  
A:Molecule type: DNA  
A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>  
A:Cross-references: EMBL:X60459; NID:932671  
C:Genetics:  
A:Gene: GDB:IFNAR1; IFNAR: IFRC  
A:Cross-references: GDB:120078; OMIM:107450  
A:Map position: 21q22.1-21q22.1  
A:Intons: 26/1; 67/1; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3  
C:Keywords: cytokine receptor; glycoprotein; transmembrane protein  
F:1-21/Domain: transmembrane #status predicted <TRN1>  
F:437-455/Domain: transmembrane #status predicted <TRN2>  
F:50,58,81,88,110,117,254,313,314,376,416,433,507,518,537/Binding site: carboxydr

#### alignment\_scores:

Quality: 340.00 Length: 67  
Ratio: 5.075 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

#### alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x A32694  
Align seg 1/1 to: A32694 from: 1 to: 557

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1 ATGATGTCGTCCTCTGCGCGCGACGACCTAGTCGTCGCGCGG 50
|||||
1 MetMetValValLeuLeuValAlaThrThrLeuValLeuValAlaValAla 17
51 CCATGCGTGTGTCGCGCGCGACGCGAGGGAATAATCTAATCTCTC 100
|||||
17 GTCATGTCGTCCTCTGCGCGCGACGCGAGGGAATAATCTAATCTCTC 34
101 AAAAGTAAAGTCGATCATCATGATGACACTTATCTCTGAGGAGAC 150
|||||
34 InlyValAlaInlyValAlaPheIleLeuPhePhePheLeuValGyrPhe 50
51 AGGATGTCGTCCTCTGCGCGCGACGATGATCTTCTTCTGATTCACAA 200
|||||
201 AATGTCGTCCTCTGCGCGCGACGATGATCTTCTTCTGATTCACAA 200
67 s 67

```

seq\_name: PIR2:S27387

seq\_documentation\_block:

## Interferon alpha receptor type 1 precursor - bovine

C:Species: Bos primigenius taurus (cattle)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
 C:Accession: S27387; S33770  
 R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.  
 FEBS Lett. 313, 255-259, 1992  
 A:Title: Specific antiviral activities of the human alpha interferons are determined at  
 A:Reference number: S27387; MID:93076908  
 A:Accession: S27387  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-560 <MOU>  
 A:Cross-references: EMBL:X68443; NID:g431; PIDN:CAA48484.1; PID:g432  
 A:Experimental source: MDBK cells  
 R:Lim, J.K.; Langer, J.A.  
 Blochim. Biophys. Acta 1173, 314-319, 1993  
 A:Title: Cloning and characterization of a bovine alpha interferon receptor.  
 A:Reference number: S33770; MID:93305725  
 A:Accession: S33770  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-421, 'V', 423-560 <LIN>  
 A:Cross-references: EMBL:L06320; NID:g163187; PIDN:AAA02571.1; PID:g163188  
 A:Experimental source: Lung  
 C:Keywords: antiviral; cytokine receptor; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-560/Product: Interferon alpha receptor type 1 #status predicted <MAT>

## alignment\_scores:

Quality:	209.00	Length:	65
Ratio:	3.800	Gaps:	2
Percent Similarity:	84.615	Percent Identity:	69.231

## alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x S27387

Align seg 1/1 to: S27387 from: 1 to: 560

```

4 ATGGTCGCTCTCTGCGCGGCGACGACCTAGTCTGTCGCGCGGCGCC 53
|||||
1 MetLeuAlaValValGlyAlaValThrThrMetLeuValAla...GlyAr 16
54 ATGGGCTGTTCGCGACCGCAGGTGTAATAAATCTCTCTCAAA 103
|||||
16 GTPValLeuProAlaAlaSerGlyAlaAlaAsnLeuLys...ProGluA 32
104 AAGGATGAGCTGTCTGCGGAATGTGCTTTTCATTCGATTATCA 153
|||||
32 snValGluLeuHisIleLeuAspAsnPhenLeuLysTrpAsnSer 48
154 AGCGATGAGCTGTCTGCGGAATGTGCTTTTCATTCGATTATCA 198
|||||
49 SerSerGluSerValLysAsnValThrPheSerAlaAspTyrGln 63

```

seq\_name: p1r2:A45283

## seq\_documentation\_block:

Interferon alpha/beta receptor - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 25-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429  
 R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proud'homme, D.; Mogensen, K.E.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992  
 A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homospo  
 A:Reference number: A45283; MID:92262522  
 A:Accession: A45283  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-590 <UZE>  
 A:Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; PID:g194112  
 A:Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIP:102357)  
 R:Lutfalla, G.; Uze, G.

## Gene 148, 343-346, 1994

A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: h1c  
 A:Reference number: I48423; MID:95047447  
 A:Accession: I48423  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 118-125 <RES>  
 A:Cross-references: EMBL:U06237; NID:g497103; PIDN:AAA65003.1; PID:g755810  
 A:Accession: I48424  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 127-224 <RE2>  
 A:Cross-references: EMBL:U06238; NID:g497104; PIDN:AAAC01749.1; PID:g755811  
 A:Accession: I48425  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 243-264 <RE3>  
 A:Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261  
 A:Accession: I48426  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 265-375 <RE4>  
 A:Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262  
 A:Accession: I48427  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 397-424 <RE5>  
 A:Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g55812  
 A:Accession: I48428  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 426-445 <RE6>  
 A:Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g55813  
 A:Accession: I48429  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 473-590 <RE7>  
 A:Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265  
 C:Genetics:  
 A:Gene: IFNAR  
 A:Introns: 177/3; 331/1  
 C:Keywords: cytokine receptor; transmembrane protein

## alignment\_scores:

Quality:	198.00	Length:	65
Ratio: <td>3.536</td> <td>Gaps: <td>0</td> </td>	3.536	Gaps: <td>0</td>	0
Percent Similarity: <td>86.154</td> <td>Percent Identity: <td>55.385</td> </td>	86.154	Percent Identity: <td>55.385</td>	55.385

## alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x A45283

Align seg 1/1 to: A45283 from: 1 to: 590

```

4 ATGGTCGCTCTCTGCGCGGCGACGACCTAGTCTGTCGCGCGGCGCC 53
|||||
1 MetLeuAlaValValGlyAlaValThrThrMetLeuValAlaGlyAlaPr 17
54 ATGGGCTGTTCGCGACCGCAGGTGTAATAAATCTCTCTCAAA 103
|||||
17 GTPValLeuProSerAlaAlaSerGlyAlaAlaAsnLeuLysTrpAsnSer 34
104 AAGGATGAGCTGTCTGCGGAATGTGCTTTTCATTCGATTATCA 153
|||||
34 snLeuAspValTyrIleLeuAspAsnTyrThrLeuLysTrpAsnSer 50
154 AGCGATGAGCTGTCTGCGGAATGTGCTTTTCATTCGATTATCA 198
|||||
51 HisGlyGluSerMetGlySerValThrPheSerAlaGluTyrGln 65

```

seq\_name: p1r2:109357

## seq\_documentation\_block:



## seq\_documentation\_block:

hypothetical 119.5k protein (uvra region) - Micrococcus luteus  
M:Alternate names: ORF 1 protein

C:Species: Micrococcus luteus, Micrococcus lysodeikticus

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 04-Feb-2000

C:Accession: J00405

R:Shiota, S.; Nakayama, H.

Mol. Gen. Genet. 217, 332-340, 1989

A:Title: Micrococcus luteus homolog of the Escherichia coli uvra gene: identification of

A:Reference number: S04781; MUID:89364717

A:Accession: J00405

A:Molecule type: DNA

A:Residues: 1-1106 <SH1>

A:Cross-references: EMBL:X15867

A>Note: this reading frame extends between two stop codons and does not begin with a sta

A>Note: the gene encoding this protein overlaps uvra gene

C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

## alignment\_scores:

Quality: 67.00 Length: 65  
Ratio: 2.233 Gaps: 2  
Percent Similarity: 46.154 Percent Identity: 32.308

## alignment\_block:

US-09-240-675-1\_COPY\_27\_229/rev x J00405

Align seg 1/1 to: J00405 from: 1 to: 1106

```

178 TCACATCCGACGACATCGCTCCTGTCACCTCAGATTAAGTTG 129
    |||  ::  ::::|  |||||
36 SerProthrglycylthrProvalSerCysPro..... 46
128 TCATCATGATGTCGACCTCTACTTTTGAGGATTTGATTTTCC 79
    |||  |||||  ::  ::  ::::|  |||||
47 .....CysProProleucCysTrpProArglaInglnleuH 60
78 ACCTCGCGCTG.....CGACAAACCCATGGGC 50
    ||  |||||
60 lshlstrgleuleuArgArgglyProArgtrgArgProArgleuArg 76
49 CCAGCGCGGACGACACTAGGTCGCGCCGCCGACGAGACGACCA 5
    |||||
77 ProArgArgArgAlaLeuGlYArgAlaGlyProHlshlstrgArgPro 91

```

seq\_name: p1r2:T43286

## seq\_documentation\_block:

cet-1 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 18-Feb-2000

C:Accession: T43286

R:Morita, K.; Chow, K.L.; Ueno, N.

Development 126, 1337-1347, 1999

A:Title: Regulation of body length and male tail ray pattern formation of Caenorhabditis

A:Reference number: 222393; MUID:99146896

A:Accession: T43286

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-365 <MOR>

A:Cross-references: EMBL:AF074395; PIDN:AAC26791.1

C:Genetics:

A:Gene: cet-1

A:Map position: 5

C:Superfamily: Inhibin

## alignment\_scores:

Quality: 66.00 Length: 54  
Ratio: 1.941 Gaps: 2  
Percent Similarity: 62.963 Percent Identity: 31.481

## alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x T43286

Align seg 1/1 to: T43286 from: 1 to: 365

```

27 GACCCATAGGCTCGTCGCGCGCCGACCATAGGCTGTGCCGACGCCGAC 76
    ::::|  |||||
228 GluProSerSerValArgArg.....LysArgSerArgG1 239
77 GCGCAAAATCTAAATCTCCGCAAAAGTAGAGTCGACATCATAGAT 126
    ::::|  |||||
239 nrlhglAsnSerGluArgLysAsnArgLysGlyArgLysHlshls. 255
127 GACCACTTATCCCTGAGGTGAGACAGACGATGACTCTGCGGAAATGT 176
    ::::|  |||||
256 .....AsnThrGluAlaGluSerAsnLeuGlyArgArgThr 267
177 GACTTTTCAT 188
    |||||
268 AspPheTyrVal 271

```

seq\_name: p1r2:S42718

## seq\_documentation\_block:

nuclear pore complex protein nup153 - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999

C:Accession: S42718; S37477

R:McMorrow, I.; Bastos, R.; Horton, H.; Burke, B.

Biochim. Biophys. Acta 1217, 219-223, 1994

A:Title: Sequence analysis of a cDNA encoding a human nuclear pore complex protei

A:Reference number: S42718; MUID:94154002

A:Accession: S42718

A:Molecule type: mRNA

A:Cross-references: EMBL:Z25535; MUID:9406224; PIDN:CAA80982.1; PID:9406225

## alignment\_scores:

Quality: 65.00 Length: 51  
Ratio: 2.167 Gaps: 1  
Percent Similarity: 58.824 Percent Identity: 39.216

## alignment\_block:

US-09-240-675-1\_COPY\_27\_229/rev x S42718

Align seg 1/1 to: S42718 from: 1 to: 1475

```

167 ACAGACTATGCGCTCCTGTCACCTCAGATTAAGTGTCTATCATGAT 118
    ||:::|  |||||
1248 ThrSerGlnSerLeuLeuPheSerGlnAspSerLysLeuAlaThrThrSe 1264
117 GTTCGACCTCTACTTTTGAGGATTTAGATTTTTCACCTCGCGCTG 68
    ::::|  |||||
1264 rSerThrGlyThrAlaValThrProPheValPheGlyProGlyAlaSerS 1281
67 CGGACAAACAC.....CATGGCCCGACGGCGACGACG 36
    ::::|  |||||
1281 eAsnAsnThrThrThrSerGlyPheGlyPheGlyAlaThrThrThrser 1297
35 ACT 33
1298 Ser 1298

```

seq\_name: p1r2:T08930

## seq\_documentation\_block:

hypothetical protein T15N24\_90 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 22-Oct-1999

C:Accession: T08930

R:Bevan, M.; Zimmermann, W.; Gruenelsen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.I

submitted to the Protein Sequence Database, May 1999



A/Cross-references: GB:M13047; NID:g151492; PIDN:AAA25966.1; PID:g151493  
C/Keywords: phosphoric diester hydrolase

alignment\_scores:  
Quality: 62.00 Length: 69  
Ratio: 1.824 Gaps: 4  
Percent Similarity: 49.275 Percent Identity: 26.087

alignment\_block:  
US-09-240-675-1\_COPY\_27\_229 x A26391 ..

Align seg 1/1 to: A26391 from: 1 to: 730

```

37 CTGCTGCGCGTGGCCGATGGTGTTCGCCGACGAGTGCAAAAA 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
404 Leu11Ala11IleSerProTrp.....SerLysGlyGly..... 414
87 TCTAAATATCTCCCAAAAGTAGAGGTCGACATCATAGATGACACTT 136
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
415 .....LysValSerAlaGluValPheAspHisThrSerV 426
137 TCCTGAGG..... 144
426 alleuArgPheLeuGluArgArgPheGlyLeuValGluGluAsnIleSer 442
145 ...TGGACACGAGCGCATGAGTCTGCGGCAATGACATTTTCATTCGA 191
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
443 ProTrpArgArgAla.....ValCysGlyAspLeuThrSerLeuPheAs 457
192 TTATCAA 198
457 PheGln 459

```

seq\_name: p1r2:G01418

seq\_documentation\_block:

Cytokine receptor family II, member 4 - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 17-Jul-1998  
C/Accession: G01418  
R:Luftalla, G.  
Submitted to the EMBL Data Library, April 1994  
A/Reference number: G06935  
A/Accession: G01418  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-273 <LUT>  
A/Cross-references: EMBL:U08988; NID:g571295; PID:g571296  
C/Genetics:  
A/Gene: GDB:CRFB4; CRF2-4  
A/Cross-references: GDB:138168; OMIM:123889  
A/Map position: 21q22.1-21q22.2  
A/Introns: 17/1; 58/2; 111/1; 166/3; 216/1

alignment\_scores:

Quality: 61.50 Length: 54  
Ratio: 1.922 Gaps: 1  
Percent Similarity: 59.259 Percent Identity: 29.630

alignment\_block:

US-09-240-675-1\_COPY\_27\_229 x G01418

Align seg 1/1 to: G01418 from: 1 to: 273

```

55 TGGGTGTGTCGCGACCGCGAGTGAATAATCTAAATCT..... 96
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
3 TrpSerLeuGlySerTrpLeuGlyCysLeuLeuValSerAlaLeuG1 19
97 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
19 yMetValProProGluAsnValArgMetAsnSerValAsnPheIysA 36

```

```

134 TTATCTGAGTGGAAACAGACGATGACTCTGCGGAATGACTTT 183
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
184 TCATTCGATTA 195
53 ThrAlaGlnTrp 56

```

seq\_name: p1r2:A47003

seq\_documentation\_block:

Cytokine receptor family class II protein CRF2-4 precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 10-Sep-1997  
C/Accession: A47003  
R:Luftalla, G.; Gardiner, R.; Uze, G.  
Genomics 16, 366-373, 1993  
A/Title: A new member of the cytokine receptor gene family maps on chromosome 21  
A/Reference number: A47003; MUID:93300510  
A/Accession: A47003  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-325 <LUT>  
A/Cross-references: GB:217227; NID:g393378; PID:g393379  
C/Genetics:  
A/Map position: 21q  
C/Keywords: transmembrane protein

alignment\_scores:  
Quality: 61.50 Length: 54  
Ratio: 1.922 Gaps: 1  
Percent Similarity: 59.259 Percent Identity: 29.630

alignment\_block:  
US-09-240-675-1\_COPY\_27\_229 x A47003

Align seg 1/1 to: A47003 from: 1 to: 325

```

55 TGGGTGTGTCGCGACCGCGAGTGAATAATCTAAATCT..... 96
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
3 TrpSerLeuGlySerTrpLeuGlyCysLeuLeuValSerAlaLeuG1 19
97 .....CCTCAAAAAGTAGAGGTCGACATCATAGATGACAACT 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
19 yMetValProProGluAsnValArgMetAsnSerValAsnPheIysA 36
134 TTATCTGAGTGGAAACAGACGATGACTCTGCGGAATGACTTT 183
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
36 snIleLeuGlnTrpGluSerProAlaPheAlaLysGlyAsnLeuThrPhe 52
184 TCATTCGATTA 195
53 ThrAlaGlnTrp 56

```







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Msearch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 21 10:34:37 2000; MasPar time 9.36 Seconds  
713,960 Million cell updates/sec

Tabular output not generated.

Title: >US-09-240-675-2  
Description: (1-436) from US09240675.pep  
Perfect Score: 436  
Sequence: 1 MMVVLGATTLVAVGPV.....KSYFSDAVCEKTKPGNTSK 436

Scoring table: TABLE uniprottable  
Gap 60

Searched: 152433 seqs, 15329240 residues

Post-processing: Minimum Match 0%  
Listing first 1000 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:6\_COMB 4:PCT\_COMB 5:backfile1

Statistics: Mean 2.820; Variance 0.722; scale 3.904

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	436	100.0	436	2	US-08-307-Sequence 2, Applicatio	0.00e+00
2	436	100.0	557	1	US-08-471-Sequence 2, Applicatio	0.00e+00
3	436	100.0	557	2	US-08-466-Sequence 2, Applicatio	0.00e+00
4	436	100.0	557	2	US-08-471-Sequence 2, Applicatio	0.00e+00
5	436	100.0	557	2	US-08-328-Sequence 10, Applicati	0.00e+00
6	436	100.0	557	2	US-08-307-Sequence 4, Applicatio	0.00e+00
7	427	97.9	434	1	US-08-328-Sequence 11, Applicati	0.00e+00
8	413	94.7	496	1	US-08-488-Sequence 12, Applicati	0.00e+00
9	413	94.7	496	1	US-08-488-Sequence 243, Applicat	1.24e-12
10	399	91.7	496	1	PCT-US93-0-Sequence 243, Applicat	1.24e-12
11	399	91.7	496	1	US-08-480-Sequence 243, Applicat	1.24e-12
12	399	91.7	496	1	US-08-328-Sequence 9, Applicatio	3.39e-11
13	399	91.7	496	1	PCT-US94-1-Sequence 4, Applicatio	2.61e-04
14	399	91.7	496	1	US-08-328-Sequence 4, Applicatio	2.03e+01
15	399	91.7	496	1	US-08-241-Sequence 9, Applicatio	2.03e+01
16	399	91.7	496	1	US-07-695-Sequence 9, Applicatio	2.03e+01
17	399	91.7	496	1	PCT-US94-1-Sequence 9, Applicatio	2.03e+01
18	399	91.7	496	1	US-08-943-Sequence 50, Applicati	2.03e+01
19	399	91.7	496	1	US-08-943-Sequence 54, Applicati	2.03e+01
20	399	91.7	496	1	US-08-943-Sequence 58, Applicati	2.03e+01
21	399	91.7	496	1	US-08-943-Sequence 56, Applicati	2.03e+01
22	399	91.7	496	1	US-08-943-Sequence 56, Applicati	2.03e+01
23	399	91.7	496	1	US-08-961-Sequence 3, Applicatio	2.03e+01

97	6	1.4	250	5	5223425-4	atent No. 5223425	2.35e+02	170	6	1.4	607	3	US-08-685-	Sequence 6, Applicatio	2.35e+02
98	6	1.4	253	5	5223425-8	atent No. 5223425	2.35e+02	171	6	1.4	607	1	US-08-409-	Sequence 6, Applicatio	2.35e+02
99	6	1.4	259	5	5223425-2	atent No. 5223425	2.35e+02	172	6	1.4	608	1	US-08-766-	Sequence 3, Applicatio	2.35e+02
100	6	1.4	260	5	5223425-10	atent No. 5223425	2.35e+02	173	6	1.4	638	2	US-08-681-	Sequence 3, Applicatio	2.35e+02
101	6	1.4	269	4	US-08-118-	Sequence 64, Applicati	2.35e+02	174	6	1.4	648	3	US-08-286-	Sequence 4, Applicatio	2.35e+02
102	6	1.4	269	4	PCR-US93-0	Sequence 64, Applicati	2.35e+02	175	6	1.4	654	1	US-08-083-	Sequence 16, Applicati	2.35e+02
103	6	1.4	274	4	PCR-US93-0	Sequence 69, Applicati	2.35e+02	176	6	1.4	654	2	US-08-446-	Sequence 35, Applicati	2.35e+02
104	6	1.4	274	1	US-08-118-	Sequence 69, Applicati	2.35e+02	177	6	1.4	657	3	US-08-508-	Sequence 35, Applicati	2.35e+02
105	6	1.4	284	1	US-08-118-	Sequence 67, Applicati	2.35e+02	178	6	1.4	664	5	5240838-5	atent No. 5240838	2.35e+02
106	6	1.4	284	4	PCR-US93-0	Sequence 67, Applicati	2.35e+02	179	6	1.4	670	2	US-08-473-	Sequence 11, Applicati	2.35e+02
107	6	1.4	285	1	US-08-149-	Sequence 24, Applicati	2.35e+02	180	6	1.4	670	2	US-08-477-	Sequence 11, Applicati	2.35e+02
108	6	1.4	286	4	PCR-US96-0	Sequence 9, Applicatio	2.35e+02	181	6	1.4	693	2	US-08-380-	Sequence 2, Applicatio	2.35e+02
109	6	1.4	286	2	US-08-628-	Sequence 9, Applicatio	2.35e+02	182	6	1.4	693	2	US-08-895-	Sequence 5, Applicatio	2.35e+02
110	6	1.4	286	1	US-08-467-	Sequence 9, Applicatio	2.35e+02	183	6	1.4	693	2	US-08-895-	Sequence 5, Applicatio	2.35e+02
111	6	1.4	301	2	US-08-433-	Sequence 2, Applicatio	2.35e+02	184	6	1.4	693	2	US-08-895-	Sequence 5, Applicatio	2.35e+02
112	6	1.4	301	1	US-08-174-	Sequence 2, Applicatio	2.35e+02	185	6	1.4	719	3	US-08-286-	Sequence 8, Applicatio	2.35e+02
113	6	1.4	301	1	US-08-440-	Sequence 2, Applicatio	2.35e+02	186	6	1.4	719	3	US-09-003-	Sequence 2, Applicatio	2.35e+02
114	6	1.4	301	2	US-08-195-	Sequence 2, Applicatio	2.35e+02	187	6	1.4	742	1	US-07-921-	Sequence 2, Applicatio	2.35e+02
115	6	1.4	301	1	US-08-433-	Sequence 2, Applicatio	2.35e+02	188	6	1.4	742	1	US-08-441-	Sequence 2, Applicatio	2.35e+02
116	6	1.4	301	2	US-08-433-	Sequence 2, Applicatio	2.35e+02	189	6	1.4	760	1	US-08-195-	Sequence 2, Applicatio	2.35e+02
117	6	1.4	313	2	US-08-284-	Sequence 5, Applicatio	2.35e+02	190	6	1.4	830	3	US-08-804-	Sequence 20, Applicati	2.35e+02
118	6	1.4	322	1	US-08-136-	Sequence 2, Applicatio	2.35e+02	191	6	1.4	830	3	US-08-720-	Sequence 20, Applicati	2.35e+02
119	6	1.4	324	3	US-08-508-	Sequence 31, Applicati	2.35e+02	192	6	1.4	831	2	US-09-047-	Sequence 4, Applicatio	2.35e+02
120	6	1.4	337	2	US-08-784-	Sequence 8, Applicatio	2.35e+02	193	6	1.4	855	2	US-08-619-	Sequence 6, Applicatio	2.35e+02
121	6	1.4	338	2	US-08-784-	Sequence 6, Applicatio	2.35e+02	194	6	1.4	864	2	US-08-209-	Sequence 29, Applicati	2.35e+02
122	6	1.4	338	2	US-08-784-	Sequence 10, Applicati	2.35e+02	195	6	1.4	872	1	US-08-766-	Sequence 2, Applicatio	2.35e+02
123	6	1.4	341	1	US-08-118-	Sequence 48, Applicati	2.35e+02	196	6	1.4	909	3	US-08-936-	Sequence 8, Applicatio	2.35e+02
124	6	1.4	341	4	PCR-US93-0	Sequence 48, Applicati	2.35e+02	197	6	1.4	909	3	US-08-936-	Sequence 10, Applicati	2.35e+02
125	6	1.4	341	2	US-08-209-	Sequence 11, Applicati	2.35e+02	198	6	1.4	909	3	US-08-936-	Sequence 18, Applicati	2.35e+02
126	6	1.4	351	1	US-08-700-	Sequence 2, Applicatio	2.35e+02	199	6	1.4	914	3	US-08-936-	Sequence 12, Applicati	2.35e+02
127	6	1.4	351	1	US-08-402-	Sequence 2, Applicatio	2.35e+02	200	6	1.4	921	1	US-08-481-	Sequence 14, Applicati	2.35e+02
128	6	1.4	351	1	US-08-993-	Sequence 2, Applicatio	2.35e+02	201	6	1.4	921	1	US-08-486-	Sequence 14, Applicati	2.35e+02
129	6	1.4	359	1	US-07-937-	Sequence 19, Applicati	2.35e+02	202	6	1.4	921	1	US-07-718-	Sequence 14, Applicati	2.35e+02
130	6	1.4	384	2	US-08-103-	Sequence 19, Applicati	2.35e+02	203	6	1.4	925	1	US-08-252-	Sequence 4, Applicatio	2.35e+02
131	6	1.4	387	1	US-08-196-	Sequence 14, Applicati	2.35e+02	204	6	1.4	925	2	US-08-834-	Sequence 4, Applicatio	2.35e+02
132	6	1.4	387	2	US-08-760-	Sequence 14, Applicati	2.35e+02	205	6	1.4	926	3	US-08-936-	Sequence 11, Applicati	2.35e+02
133	6	1.4	390	1	US-08-568-	Sequence 2, Applicatio	2.35e+02	206	6	1.4	926	3	US-08-936-	Sequence 20, Applicati	2.35e+02
134	6	1.4	412	1	US-08-208-	Sequence 12, Applicati	2.35e+02	207	6	1.4	931	3	US-08-936-	Sequence 16, Applicati	2.35e+02
135	6	1.4	415	1	US-08-602-	Sequence 10, Applicati	2.35e+02	208	6	1.4	956	1	US-08-185-	Sequence 2, Applicatio	2.35e+02
136	6	1.4	415	1	US-08-680-	Sequence 10, Applicati	2.35e+02	209	6	1.4	956	1	US-08-416-	Sequence 2, Applicatio	2.35e+02
137	6	1.4	433	1	US-08-700-	Sequence 20, Applicati	2.35e+02	210	6	1.4	956	3	US-08-789-	Sequence 2, Applicatio	2.35e+02
138	6	1.4	437	2	US-08-473-	Sequence 9, Applicatio	2.35e+02	211	6	1.4	971	2	US-09-066-	Sequence 19, Applicati	2.35e+02
139	6	1.4	437	2	US-08-477-	Sequence 6, Applicatio	2.35e+02	212	6	1.4	971	2	US-08-805-	Sequence 19, Applicati	2.35e+02
140	6	1.4	437	2	US-08-477-	Sequence 9, Applicatio	2.35e+02	213	6	1.4	971	1	US-08-446-	Sequence 19, Applicati	2.35e+02
141	6	1.4	438	1	US-08-440-	Sequence 5, Applicatio	2.35e+02	214	6	1.4	971	2	US-08-064-	Sequence 19, Applicati	2.35e+02
142	6	1.4	438	1	US-08-439-	Sequence 2, Applicatio	2.35e+02	215	6	1.4	971	1	US-08-446-	Sequence 19, Applicati	2.35e+02
143	6	1.4	459	1	US-08-403-	Sequence 5, Applicatio	2.35e+02	216	6	1.4	993	1	US-08-446-	Sequence 19, Applicati	2.35e+02
144	6	1.4	465	1	US-08-447-	Sequence 2, Applicatio	2.35e+02	217	6	1.4	1026	2	US-08-614-	Sequence 7, Applicatio	2.35e+02
145	6	1.4	473	1	US-08-439-	Sequence 4, Applicatio	2.35e+02	218	6	1.4	1026	1	US-08-194-	Sequence 7, Applicatio	2.35e+02
146	6	1.4	473	1	US-08-440-	Sequence 4, Applicatio	2.35e+02	219	6	1.4	1064	1	US-08-537-	Sequence 3, Applicatio	2.35e+02
147	6	1.4	483	3	US-09-027-	Sequence 7, Applicatio	2.35e+02	220	6	1.4	1088	2	US-08-742-	Sequence 23, Applicati	2.35e+02
148	6	1.4	483	3	US-09-027-	Sequence 9, Applicatio	2.35e+02	221	6	1.4	1088	2	US-08-742-	Sequence 23, Applicati	2.35e+02
149	6	1.4	488	1	US-08-448-	Sequence 10, Applicati	2.35e+02	222	6	1.4	1132	2	US-08-567-	Sequence 2, Applicatio	2.35e+02
150	6	1.4	495	2	US-08-749-	Sequence 3, Applicatio	2.35e+02	223	6	1.4	1132	2	US-09-196-	Sequence 2, Applicatio	2.35e+02
151	6	1.4	508	2	US-08-861-	Sequence 10, Applicati	2.35e+02	224	6	1.4	1138	1	US-08-404-	Sequence 4, Applicatio	2.35e+02
152	6	1.4	508	1	US-07-891-	Sequence 10, Applicati	2.35e+02	225	6	1.4	1358	1	US-08-404-	Sequence 4, Applicatio	2.35e+02
153	6	1.4	508	2	US-08-396-	Sequence 10, Applicati	2.35e+02	226	6	1.4	1358	1	US-08-404-	Sequence 4, Applicatio	2.35e+02
154	6	1.4	529	2	US-08-504-	Sequence 8, Applicatio	2.35e+02	227	6	1.4	1390	1	US-08-770-	Sequence 9, Applicatio	2.35e+02
155	6	1.4	529	1	US-07-891-	Sequence 8, Applicatio	2.35e+02	228	6	1.4	1398	2	US-08-750-	Sequence 9, Applicatio	2.35e+02
156	6	1.4	535	3	US-08-370-	Sequence 19, Applicati	2.35e+02	229	6	1.4	1437	3	US-09-061-	Sequence 2, Applicatio	2.35e+02
157	6	1.4	535	3	US-08-286-	Sequence 8, Applicatio	2.35e+02	230	6	1.4	1437	3	US-09-061-	Sequence 2, Applicatio	2.35e+02
158	6	1.4	539	1	US-08-173-	Sequence 8, Applicatio	2.35e+02	231	6	1.4	1453	2	US-09-001-	Sequence 2, Applicatio	2.35e+02
159	6	1.4	539	2	US-08-265-	Sequence 8, Applicatio	2.35e+02	232	6	1.4	1548	1	US-08-463-	Sequence 7, Applicatio	2.35e+02
160	6	1.4	548	2	US-08-452-	Sequence 8, Applicatio	2.35e+02	233	6	1.4	1891	2	US-08-804-	Sequence 12, Applicati	2.35e+02
161	6	1.4	552	1	US-08-588-	Sequence 2, Applicatio	2.35e+02	234	6	1.4	1891	2	US-08-804-	Sequence 6, Applicatio	2.35e+02
162	6	1.4	552	2	US-09-005-	Sequence 2, Applicatio	2.35e+02	235	6	1.4	1912	3	US-08-683-	Sequence 6, Applicatio	2.35e+02
163	6	1.4	552	3	US-08-701-	Sequence 14, Applicati	2.35e+02	236	6	1.4	1912	1	US-08-409-	Sequence 4, Applicatio	2.35e+02
164	6	1.4	552	2	US-08-915-	Sequence 2, Applicatio	2.35e+02	237	6	1.4	2366	1	US-08-480-	Sequence 10, Applicati	2.35e+02
165	6	1.4	560	1	US-07-891-	Sequence 5, Applicatio	2.35e+02	238	6	1.4	2366	1	US-08-480-	Sequence 10, Applicati	2.35e+02
166	6	1.4	563	1	US-08-442-	Sequence 4, Applicatio	2.35e+02	239	6	1.4	2523	1	US-08-185-	Sequence 18, Applicati	2.35e+02
167	6	1.4	578	1	US-08-766-	Sequence 4, Applicatio	2.35e+02	240	6	1.4	3491	2	US-07-642-	Sequence 2, Applicati	2.35e+02
168	6	1.4	602	4	PCR-US93-0	Sequence 2, Applicatio	2.35e+02	241	5	1.1	7	2	US-08-442-	Sequence 3, Applicati	2.13e+03
169	6	1.4	602	1	US-08-295-	Sequence 2, Applicatio	2.35e+02	242	5	1.1	7	3	US-08-944-	Sequence 9, Applicatio	2.13e+03

243	5	1.1	11	5	5177060-27	atent No. 5177060	2.13e+03	316	5	1.1	73	4	PCT-US94-0	Sequence 3, Applicatio	2.13e+03
244	5	1.1	11	5	5178861-16	atent No. 5178861	2.13e+03	317	5	1.1	73	4	PCT-US94-0	Sequence 2, Applicatio	2.13e+03
245	5	1.1	11	4	PCT-US96-0	Sequence 8, Applicatio	2.13e+03	318	5	1.1	73	1	US-08-330	Sequence 2, Applicatio	2.13e+03
246	5	1.1	12	4	PCT-US96-1	Sequence 46, Applicatio	2.13e+03	319	5	1.1	73	1	US-08-340	Sequence 19, Applicatio	2.13e+03
247	5	1.1	13	2	US-08-195	Sequence 1, Applicatio	2.13e+03	320	5	1.1	76	2	US-08-722	Sequence 7, Applicatio	2.13e+03
248	5	1.1	13	2	US-08-542	Sequence 19, Applicatio	2.13e+03	321	5	1.1	77	5	5466783-4	atent No. 5466783	2.13e+03
249	5	1.1	15	1	US-08-156	Sequence 15, Applicatio	2.13e+03	322	5	1.1	77	4	PCT-US95-1	Sequence 7, Applicatio	2.13e+03
250	5	1.1	15	2	US-08-332	Sequence 70, Applicatio	2.13e+03	323	5	1.1	77	4	PCT-US92-0	Sequence 5, Applicatio	2.13e+03
251	5	1.1	17	4	PCT-US95-1	Sequence 15, Applicatio	2.13e+03	324	5	1.1	77	2	US-08-460	Sequence 10, Applicatio	2.13e+03
252	5	1.1	18	3	US-08-788	Sequence 11, Applicatio	2.13e+03	325	5	1.1	81	2	US-08-468	Sequence 10, Applicatio	2.13e+03
253	5	1.1	18	3	US-08-920	Sequence 44, Applicatio	2.13e+03	326	5	1.1	82	5	5498694-2	atent No. 5498694	2.13e+03
254	5	1.1	19	3	US-08-871	Sequence 3, Applicatio	2.13e+03	327	5	1.1	85	2	US-08-468	Sequence 9, Applicatio	2.13e+03
255	5	1.1	19	3	US-08-788	Sequence 6, Applicatio	2.13e+03	328	5	1.1	86	5	5179196-2	atent No. 5179196	2.13e+03
256	5	1.1	19	2	US-08-719	Sequence 1, Applicatio	2.13e+03	329	5	1.1	86	5	5164304-2	atent No. 5164304	2.13e+03
257	5	1.1	20	5	5225193-7	atent No. 5225193	2.13e+03	330	5	1.1	86	1	5514582-41	Sequence 20, Applicatio	2.13e+03
258	5	1.1	20	5	5225193-2	atent No. 5225193	2.13e+03	331	5	1.1	88	1	US-08-469	Sequence 21, Applicatio	2.13e+03
259	5	1.1	20	1	US-08-179	Sequence 18, Applicatio	2.13e+03	332	5	1.1	88	1	US-08-203	Sequence 21, Applicatio	2.13e+03
260	5	1.1	23	4	PCT-US93-1	Sequence 15, Applicatio	2.13e+03	333	5	1.1	93	2	US-08-467	Sequence 36, Applicatio	2.13e+03
261	5	1.1	23	1	US-08-086	Sequence 18, Applicatio	2.13e+03	334	5	1.1	96	2	US-08-482	Sequence 21, Applicatio	2.13e+03
262	5	1.1	23	3	US-08-484	Sequence 19, Applicatio	2.13e+03	335	5	1.1	96	2	US-08-485	Sequence 53, Applicatio	2.13e+03
263	5	1.1	23	2	US-08-332	Sequence 2, Applicatio	2.13e+03	336	5	1.1	96	2	US-08-464	Sequence 18, Applicatio	2.13e+03
264	5	1.1	24	2	US-08-470	Sequence 2, Applicatio	2.13e+03	337	5	1.1	97	4	PCT-US94-0	Sequence 29, Applicatio	2.13e+03
265	5	1.1	24	2	US-08-761	Sequence 17, Applicatio	2.13e+03	338	5	1.1	99	2	US-08-838	Sequence 11, Applicatio	2.13e+03
266	5	1.1	25	4	PCT-US95-1	Sequence 17, Applicatio	2.13e+03	339	5	1.1	100	2	US-08-474	Sequence 11, Applicatio	2.13e+03
267	5	1.1	25	4	PCT-US95-0	Sequence 38, Applicatio	2.13e+03	340	5	1.1	101	2	US-08-468	Sequence 2, Applicatio	2.13e+03
268	5	1.1	25	1	US-08-425	Sequence 2, Applicatio	2.13e+03	341	5	1.1	105	3	US-09-120	Sequence 14, Applicatio	2.13e+03
269	5	1.1	26	1	US-07-879	Sequence 47, Applicatio	2.13e+03	342	5	1.1	105	2	US-08-466	Sequence 63, Applicatio	2.13e+03
270	5	1.1	27	2	US-08-317	Sequence 59, Applicatio	2.13e+03	343	5	1.1	105	3	US-09-115	Sequence 14, Applicatio	2.13e+03
271	5	1.1	27	1	US-08-425	Sequence 43, Applicatio	2.13e+03	344	5	1.1	106	4	PCT-US95-1	Sequence 5, Applicatio	2.13e+03
272	5	1.1	28	2	US-08-317	Sequence 48, Applicatio	2.13e+03	345	5	1.1	106	3	US-09-203	Sequence 7, Applicatio	2.13e+03
273	5	1.1	30	2	US-08-317	Sequence 60, Applicatio	2.13e+03	346	5	1.1	106	2	US-08-468	Sequence 7, Applicatio	2.13e+03
274	5	1.1	30	2	US-08-317	Sequence 61, Applicatio	2.13e+03	347	5	1.1	107	4	PCT-US95-1	Sequence 7, Applicatio	2.13e+03
275	5	1.1	30	2	US-08-317	Sequence 10, Applicatio	2.13e+03	348	5	1.1	107	4	PCT-US95-1	Sequence 4, Applicatio	2.13e+03
276	5	1.1	31	2	US-08-317	Sequence 46, Applicatio	2.13e+03	349	5	1.1	107	2	US-08-446	Sequence 4, Applicatio	2.13e+03
277	5	1.1	31	2	US-08-317	Sequence 46, Applicatio	2.13e+03	350	5	1.1	107	1	US-08-015	Sequence 4, Applicatio	2.13e+03
278	5	1.1	34	5	5200327-16	atent No. 5200327	2.13e+03	351	5	1.1	107	2	US-08-662	Sequence 7, Applicatio	2.13e+03
279	5	1.1	34	1	US-08-318	Sequence 5, Applicatio	2.13e+03	352	5	1.1	107	2	US-08-470	Sequence 2, Applicatio	2.13e+03
280	5	1.1	38	5	5185441-1	atent No. 5185441	2.13e+03	353	5	1.1	108	2	US-08-378	Sequence 28, Applicatio	2.13e+03
281	5	1.1	39	2	US-08-488	Sequence 58, Applicatio	2.13e+03	354	5	1.1	113	2	US-08-850	Sequence 15, Applicatio	2.13e+03
282	5	1.1	39	2	US-08-612	Sequence 26, Applicatio	2.13e+03	355	5	1.1	116	1	US-08-459	Sequence 38, Applicatio	2.13e+03
283	5	1.1	39	1	US-08-446	Sequence 64, Applicatio	2.13e+03	356	5	1.1	121	4	PCT-US96-0	Sequence 32, Applicatio	2.13e+03
284	5	1.1	41	5	5200327-15	atent No. 5200327	2.13e+03	357	5	1.1	121	2	US-08-588	Sequence 32, Applicatio	2.13e+03
285	5	1.1	41	1	US-08-318	Sequence 4, Applicatio	2.13e+03	358	5	1.1	122	1	US-08-476	Sequence 14, Applicatio	2.13e+03
286	5	1.1	42	4	PCT-US93-0	Sequence 33, Applicatio	2.13e+03	359	5	1.1	122	1	US-08-485	Sequence 14, Applicatio	2.13e+03
287	5	1.1	42	4	PCT-US93-0	Sequence 33, Applicatio	2.13e+03	360	5	1.1	123	2	US-08-476	Sequence 2, Applicatio	2.13e+03
288	5	1.1	43	1	US-08-453	Sequence 73, Applicatio	2.13e+03	361	5	1.1	123	2	US-08-337	Sequence 1, Applicatio	2.13e+03
289	5	1.1	43	1	US-08-453	Sequence 73, Applicatio	2.13e+03	362	5	1.1	123	2	US-08-553	Sequence 55, Applicatio	2.13e+03
290	5	1.1	43	4	PCT-US95-0	Sequence 85, Applicatio	2.13e+03	363	5	1.1	125	2	US-08-553	Sequence 57, Applicatio	2.13e+03
291	5	1.1	43	4	PCT-US95-1	Sequence 85, Applicatio	2.13e+03	364	5	1.1	131	2	US-08-820	Sequence 15, Applicatio	2.13e+03
292	5	1.1	43	1	US-07-998	Sequence 73, Applicatio	2.13e+03	365	5	1.1	135	5	5179196-7	atent No. 5179196	2.13e+03
293	5	1.1	43	3	US-08-488	Sequence 60, Applicatio	2.13e+03	366	5	1.1	135	5	5164304-7	atent No. 5164304	2.13e+03
294	5	1.1	43	3	US-09-273	Sequence 60, Applicatio	2.13e+03	367	5	1.1	135	5	5219996-19	atent No. 5219996	2.13e+03
295	5	1.1	44	1	US-08-479	Sequence 2, Applicatio	2.13e+03	368	5	1.1	138	4	PCT-US95-1	Sequence 4, Applicatio	2.13e+03
296	5	1.1	44	4	PCT-US93-0	Sequence 6, Applicatio	2.13e+03	369	5	1.1	138	1	US-08-698	Sequence 4, Applicatio	2.13e+03
297	5	1.1	45	1	US-08-407	Sequence 1, Applicatio	2.13e+03	370	5	1.1	138	2	US-08-649	Sequence 4, Applicatio	2.13e+03
298	5	1.1	48	4	PCT-US95-1	Sequence 23, Applicatio	2.13e+03	371	5	1.1	142	2	US-08-476	Sequence 12, Applicatio	2.13e+03
299	5	1.1	48	4	US-07-876	Sequence 13, Applicatio	2.13e+03	372	5	1.1	142	1	US-08-470	Sequence 31, Applicatio	2.13e+03
300	5	1.1	49	2	US-08-488	Sequence 36, Applicatio	2.13e+03	373	5	1.1	142	5	5180813-2	atent No. 5180813	2.13e+03
301	5	1.1	50	1	US-07-940	Sequence 2, Applicatio	2.13e+03	374	5	1.1	148	2	US-08-645	Sequence 13, Applicatio	2.13e+03
302	5	1.1	50	1	US-08-459	Sequence 2, Applicatio	2.13e+03	375	5	1.1	148	2	US-08-645	Sequence 36, Applicatio	2.13e+03
303	5	1.1	52	2	US-08-874	Sequence 9, Applicatio	2.13e+03	376	5	1.1	150	1	US-08-378	Sequence 6, Applicatio	2.13e+03
304	5	1.1	54	2	US-08-164	Sequence 6, Applicatio	2.13e+03	377	5	1.1	152	1	5187153-4	atent No. 5187153	2.13e+03
305	5	1.1	54	1	US-08-209	Sequence 11, Applicatio	2.13e+03	378	5	1.1	152	1	US-08-471	Sequence 22, Applicatio	2.13e+03
306	5	1.1	60	1	US-08-197	Sequence 11, Applicatio	2.13e+03	379	5	1.1	156	4	PCT-US95-0	Sequence 2, Applicatio	2.13e+03
307	5	1.1	60	1	US-08-459	Sequence 11, Applicatio	2.13e+03	380	5	1.1	156	2	US-08-508	Sequence 2, Applicatio	2.13e+03
308	5	1.1	63	3	US-08-871	Sequence 18, Applicatio	2.13e+03	381	5	1.1	156	3	US-08-581	Sequence 2, Applicatio	2.13e+03
309	5	1.1	63	3	US-09-061	Sequence 10, Applicatio	2.13e+03	382	5	1.1	157	4	PCT-US96-0	Sequence 5, Applicatio	2.13e+03
310	5	1.1	70	2	US-08-468	Sequence 11, Applicatio	2.13e+03	383	5	1.1	158	2	US-08-403	Sequence 29, Applicatio	2.13e+03
311	5	1.1	70	1	US-08-329	Sequence 2, Applicatio	2.13e+03	384	5	1.1	162	5	5220013-4	atent No. 5220013	2.13e+03
312	5	1.1	70	1	US-08-340	Sequence 17, Applicatio	2.13e+03	385	5	1.1	162	5	5224883-4	atent No. 5224883	2.13e+03
313	5	1.1	71	3	US-08-943	Sequence 2, Applicatio	2.13e+03	386	5	1.1	166	2	US-08-483	Sequence 3, Applicatio	2.13e+03
314	5	1.1	71	3	US-08-943	Sequence 2, Applicatio	2.13e+03	387	5	1.1	166	2	US-07-965	Sequence 3, Applicatio	2.13e+03
315	5	1.1	73	2	US-08-637	Sequence 406, Applicatio	2.13e+03	388	5	1.1	166	2	US-07-965	Sequence 3, Applicatio	2.13e+03

389	5	1.1	167	2	US-08-993-	Sequence 8, Applicatio	2.13e+03	462	5	1.1	280	4	PCT-US92-0	Sequence 3, Applicatio	2.13e+03
390	5	1.1	170	3	US-09-186-	Sequence 8, Applicatio	2.13e+03	463	5	1.1	284	2	US-08-767-	Sequence 3, Applicatio	2.13e+03
391	5	1.1	172	1	US-08-471-	Sequence 16, Applicati	2.13e+03	464	5	1.1	287	5	5198342-2	Sequence 3, Applicatio	2.13e+03
392	5	1.1	172	3	US-09-113-	Sequence 3, Applicatio	2.13e+03	465	5	1.1	288	1	US-08-781-	Sequence 3, Applicatio	2.13e+03
393	5	1.1	174	2	US-08-709-	Sequence 2, Applicatio	2.13e+03	466	5	1.1	289	2	US-08-472-	Sequence 4, Applicatio	2.13e+03
394	5	1.1	177	2	US-08-737-	Sequence 2, Applicatio	2.13e+03	467	5	1.1	290	1	US-08-457-	Sequence 4, Applicatio	2.13e+03
395	5	1.1	178	1	US-08-271-	Sequence 7, Applicatio	2.13e+03	468	5	1.1	292	2	US-08-688-	Sequence 7, Applicatio	2.13e+03
396	5	1.1	185	2	US-08-463-	Sequence 3, Applicatio	2.13e+03	469	5	1.1	293	3	US-08-688-	Sequence 7, Applicatio	2.13e+03
397	5	1.1	190	4	PCT-US95-0	Sequence 29, Applicati	2.13e+03	470	5	1.1	293	2	5210025-4	Sequence 7, Applicatio	2.13e+03
398	5	1.1	192	2	US-08-468-	Sequence 29, Applicati	2.13e+03	471	5	1.1	295	4	US-08-701-	Sequence 20, Applicati	2.13e+03
399	5	1.1	192	2	5242821-18	Sequence 93, Applicati	2.13e+03	472	5	1.1	296	4	PCT-US95-0	Sequence 20, Applicati	2.13e+03
400	5	1.1	192	1	US-08-086-	Sequence 94, Applicati	2.13e+03	473	5	1.1	298	2	US-09-006-	Sequence 3, Applicatio	2.13e+03
401	5	1.1	192	2	US-08-468-	Sequence 102, Applicat	2.13e+03	474	5	1.1	303	1	US-07-917-	Sequence 3, Applicatio	2.13e+03
402	5	1.1	192	2	US-08-290-	Sequence 95, Applicati	2.13e+03	475	5	1.1	303	1	US-07-917-	Sequence 3, Applicatio	2.13e+03
403	5	1.1	196	4	PCT-US93-0	Sequence 7, Applicatio	2.13e+03	481	5	1.1	303	2	US-08-294-	Sequence 6, Applicatio	2.13e+03
404	5	1.1	201	5	5489533-3	Sequence 7, Applicatio	2.13e+03	482	5	1.1	303	2	US-08-294-	Sequence 6, Applicatio	2.13e+03
405	5	1.1	201	2	US-08-801-	Sequence 7, Applicatio	2.13e+03	483	5	1.1	304	2	US-08-294-	Sequence 5, Applicatio	2.13e+03
406	5	1.1	202	1	US-08-274-	Sequence 2, Applicatio	2.13e+03	484	5	1.1	306	1	US-08-328-	Sequence 2, Applicatio	2.13e+03
407	5	1.1	202	2	US-08-462-	Sequence 2, Applicatio	2.13e+03	485	5	1.1	308	1	US-08-093-	Sequence 6, Applicatio	2.13e+03
408	5	1.1	206	1	US-08-494-	Sequence 7, Applicatio	2.13e+03	486	5	1.1	308	2	US-08-468-	Sequence 16, Applicati	2.13e+03
409	5	1.1	206	1	US-08-097-	Sequence 7, Applicatio	2.13e+03	487	5	1.1	309	4	PCT-US95-1	Sequence 2, Applicatio	2.13e+03
410	5	1.1	210	3	US-08-471-	Sequence 22, Applicati	2.13e+03	488	5	1.1	310	2	US-08-705-	Sequence 3, Applicatio	2.13e+03
411	5	1.1	212	2	US-08-924-	Sequence 14, Applicati	2.13e+03	489	5	1.1	312	2	US-08-510-	Sequence 11, Applicati	2.13e+03
412	5	1.1	213	3	US-09-186-	Sequence 6, Applicatio	2.13e+03	490	5	1.1	312	2	US-08-420-	Sequence 11, Applicati	2.13e+03
413	5	1.1	219	1	US-08-461-	Sequence 13, Applicati	2.13e+03	491	5	1.1	312	1	US-08-809-	Sequence 2, Applicatio	2.13e+03
414	5	1.1	221	3	US-08-484-	Sequence 96, Applicati	2.13e+03	492	5	1.1	313	2	US-08-605-	Sequence 12, Applicati	2.13e+03
415	5	1.1	221	1	US-08-360-	Sequence 106, Applicat	2.13e+03	493	5	1.1	317	3	US-08-605-	Sequence 12, Applicati	2.13e+03
416	5	1.1	222	3	US-08-328-	Sequence 8, Applicatio	2.13e+03	494	5	1.1	318	2	US-08-695-	Sequence 17, Applicati	2.13e+03
417	5	1.1	222	2	US-08-756-	Sequence 1, Applicatio	2.13e+03	495	5	1.1	319	3	US-09-100-	Sequence 10, Applicati	2.13e+03
418	5	1.1	223	2	US-08-615-	Sequence 13, Applicati	2.13e+03	496	5	1.1	320	2	US-09-053-	Sequence 2, Applicatio	2.13e+03
419	5	1.1	223	1	US-08-472-	Sequence 13, Applicati	2.13e+03	497	5	1.1	320	1	US-08-465-	Sequence 2, Applicatio	2.13e+03
420	5	1.1	227	5	5498499-2	Sequence 13, Applicati	2.13e+03	498	5	1.1	321	2	US-08-813-	Sequence 2, Applicatio	2.13e+03
421	5	1.1	233	5	5422425-2	Sequence 10, Applicati	2.13e+03	499	5	1.1	323	4	5260223-4	Sequence 18, Applicati	2.13e+03
422	5	1.1	233	4	PCT-US95-1	Sequence 10, Applicati	2.13e+03	500	5	1.1	323	4	PCT-US93-0	Sequence 1, Applicatio	2.13e+03
423	5	1.1	233	1	US-08-607-	Sequence 6, Applicatio	2.13e+03	501	5	1.1	324	1	US-08-746-	Sequence 10, Applicati	2.13e+03
424	5	1.1	233	1	US-08-081-	Sequence 24, Applicati	2.13e+03	502	5	1.1	324	2	US-08-671-	Sequence 11, Applicati	2.13e+03
425	5	1.1	233	4	PCT-US95-0	Sequence 14, Applicati	2.13e+03	503	5	1.1	324	2	PCT-US95-1	Sequence 13, Applicati	2.13e+03
426	5	1.1	233	1	US-08-471-	Sequence 24, Applicati	2.13e+03	504	5	1.1	327	4	PCT-US95-1	Sequence 15, Applicati	2.13e+03
427	5	1.1	240	5	5223394-6	Sequence 14, Applicati	2.13e+03	505	5	1.1	327	4	PCT-US93-0	Sequence 18, Applicati	2.13e+03
428	5	1.1	240	5	5223394-4	Sequence 10, Applicati	2.13e+03	506	5	1.1	329	2	US-08-606-	Sequence 2, Applicatio	2.13e+03
429	5	1.1	240	5	5185441-36	Sequence 10, Applicati	2.13e+03	507	5	1.1	329	2	US-08-827-	Sequence 2, Applicatio	2.13e+03
430	5	1.1	241	5	5213972-7	Sequence 48, Applicati	2.13e+03	508	5	1.1	330	4	PCT-US95-1	Sequence 2, Applicatio	2.13e+03
431	5	1.1	245	2	US-09-912-	Sequence 48, Applicati	2.13e+03	509	5	1.1	331	1	US-08-319-	Sequence 3, Applicatio	2.13e+03
432	5	1.1	249	2	US-08-989-	Sequence 5, Applicatio	2.13e+03	510	5	1.1	331	1	US-08-356-	Sequence 3, Applicatio	2.13e+03
433	5	1.1	250	5	5223394-1	Sequence 5, Applicatio	2.13e+03	511	5	1.1	331	1	US-08-356-	Sequence 3, Applicatio	2.13e+03
434	5	1.1	250	4	PCT-US92-0	Sequence 10, Applicati	2.13e+03	512	5	1.1	331	1	US-08-630-	Sequence 3, Applicatio	2.13e+03
435	5	1.1	250	4	US-08-646-	Sequence 8, Applicatio	2.13e+03	513	5	1.1	332	1	US-08-442-	Sequence 7, Applicatio	2.13e+03
436	5	1.1	250	2	5185441-38	Sequence 8, Applicatio	2.13e+03	514	5	1.1	332	1	US-08-530-	Sequence 7, Applicatio	2.13e+03
437	5	1.1	251	5	US-08-468-	Sequence 15, Applicati	2.13e+03	515	5	1.1	334	1	US-08-474-	Sequence 8, Applicatio	2.13e+03
438	5	1.1	253	2	US-09-193-	Sequence 15, Applicati	2.13e+03	516	5	1.1	336	2	US-08-784-	Sequence 2, Applicatio	2.13e+03
439	5	1.1	254	2	US-08-468-	Sequence 15, Applicati	2.13e+03	517	5	1.1	336	2	US-09-032-	Sequence 2, Applicatio	2.13e+03
440	5	1.1	255	4	PCT-US96-0	Sequence 9, Applicatio	2.13e+03	518	5	1.1	337	3	US-08-442-	Sequence 17, Applicati	2.13e+03
441	5	1.1	255	4	US-08-816-	Sequence 9, Applicatio	2.13e+03	519	5	1.1	338	1	US-08-606-	Sequence 17, Applicati	2.13e+03
442	5	1.1	255	2	US-08-152-	Sequence 36, Applicati	2.13e+03	520	5	1.1	338	1	5210183-2	Sequence 10, Applicati	2.13e+03
443	5	1.1	255	4	PCT-US96-0	Sequence 36, Applicati	2.13e+03	521	5	1.1	344	5	US-08-031-	Sequence 10, Applicati	2.13e+03
444	5	1.1	256	4	US-09-097-	Sequence 6, Applicatio	2.13e+03	522	5	1.1	345	1	US-08-446-	Sequence 58, Applicati	2.13e+03
445	5	1.1	259	3	US-08-245-	Sequence 4, Applicatio	2.13e+03	523	5	1.1	347	1	US-08-630-	Sequence 2, Applicatio	2.13e+03
446	5	1.1	263	1	US-08-441-	Sequence 4, Applicatio	2.13e+03	524	5	1.1	347	1	US-08-446-	Sequence 2, Applicatio	2.13e+03
447	5	1.1	263	1	PCT-US96-1	Sequence 6, Applicatio	2.13e+03	525	5	1.1	350	3	US-09-211-	Sequence 2, Applicatio	2.13e+03
448	5	1.1	264	4	US-08-605-	Sequence 93, Applicati	2.13e+03	526	5	1.1	351	2	US-08-468-	Sequence 46, Applicati	2.13e+03
449	5	1.1	264	1	US-07-990-	Sequence 5, Applicatio	2.13e+03	527	5	1.1	355	2	US-08-846-	Sequence 93, Applicati	2.13e+03
450	5	1.1	264	1	US-08-155-	Sequence 5, Applicatio	2.13e+03	528	5	1.1	355	1	US-08-602-	Sequence 12, Applicati	2.13e+03
451	5	1.1	265	1	US-08-446-	Sequence 2, Applicatio	2.13e+03	529	5	1.1	357	1	US-08-356-	Sequence 29, Applicati	2.13e+03
452	5	1.1	274	5	5512660-2	Sequence 2, Applicatio	2.13e+03	530	5	1.1	364	1	US-08-459-	Sequence 29, Applicati	2.13e+03
453	5	1.1	274	5	5489533-2	Sequence 16, Applicati	2.13e+03	531	5	1.1	364	1	US-08-860-	Sequence 20, Applicati	2.13e+03
454	5	1.1	278	1	US-08-201-	Sequence 16, Applicati	2.13e+03	532	5	1.1	366	3	US-08-630-	Sequence 19, Applicati	2.13e+03
455	5	1.1	280	1	US-08-477-	Sequence 128, Applicati	2.13e+03	533	5	1.1	367	3	US-09-150-	Sequence 1, Applicatio	2.13e+03
460	5	1.1	280	2	US-08-646-	Sequence 128, Applicati	2.13e+03	534	5	1.1	370	3			

535	1.1	370	3	US-09-150-	Sequence 3, Applicatio	2.13e+03	608	5	1.1	439	1	US-08-694-	Sequence 10, Applicati	2.13e+03	
536	1.1	371	5	5168050-3	Sequence 2, Applicatio	2.13e+03	609	5	1.1	455	2	US-08-912-	Sequence 25, Applicati	2.13e+03	
537	1.1	372	3	US-08-685-	Sequence 2, Applicatio	2.13e+03	610	5	1.1	455	4	US-08-406-	Sequence 25, Applicati	2.13e+03	
538	1.1	373	2	US-08-555-	Sequence 2, Applicatio	2.13e+03	611	5	1.1	455	4	PCT-US93-0	Sequence 25, Applicati	2.13e+03	
539	1.1	375	5	US-08-542-	Sequence 5, Applicatio	2.13e+03	612	5	1.1	455	4	PCT-US93-0	Sequence 25, Applicati	2.13e+03	
540	1.1	375	4	PCT-US94-1	Sequence 28, Applicati	2.13e+03	613	5	1.1	455	3	US-09-038-	Sequence 18, Applicati	2.13e+03	
541	1.1	376	5	5180810-1	Sequence 4, Applicatio	2.13e+03	614	5	1.1	455	1	US-08-462-	Sequence 25, Applicati	2.13e+03	
542	1.1	376	5	US-08-385-	Sequence 6, Applicatio	2.13e+03	615	5	1.1	455	5	US-08-278-	Sequence 25, Applicati	2.13e+03	
543	1.1	376	2	US-08-737-	Sequence 6, Applicatio	2.13e+03	616	5	1.1	456	5	5432081-7	Sequence 6, Applicatio	2.13e+03	
544	1.1	376	4	PCT-US95-0	Sequence 8, Applicatio	2.13e+03	617	5	1.1	457	2	US-08-882-	Sequence 22, Applicati	2.13e+03	
545	1.1	380	1	US-08-073-	Sequence 18, Applicati	2.13e+03	618	5	1.1	457	2	US-07-951-	Sequence 22, Applicati	2.13e+03	
546	1.1	380	1	US-08-120-	Sequence 51, Applicati	2.13e+03	619	5	1.1	464	1	US-08-459-	Sequence 22, Applicati	2.13e+03	
547	1.1	384	2	US-08-474-	Sequence 40, Applicati	2.13e+03	620	5	1.1	464	3	US-08-788-	Sequence 2, Applicatio	2.13e+03	
548	1.1	385	1	US-08-329-	Sequence 4, Applicatio	2.13e+03	621	5	1.1	467	1	US-08-146-	Sequence 30, Applicati	2.13e+03	
549	1.1	385	1	US-08-539-	Sequence 4, Applicatio	2.13e+03	622	5	1.1	467	1	US-08-151-	Sequence 32, Applicati	2.13e+03	
550	1.1	388	1	US-08-261-	Sequence 4, Applicatio	2.13e+03	623	5	1.1	467	2	US-07-923-	Sequence 8, Applicatio	2.13e+03	
551	1.1	396	5	5349058-2	Sequence 5, Applicatio	2.13e+03	624	5	1.1	467	2	US-08-374-	Sequence 2, Applicatio	2.13e+03	
552	1.1	396	5	5166058-4	Sequence 5, Applicatio	2.13e+03	625	5	1.1	474	3	US-08-022-	Sequence 2, Applicatio	2.13e+03	
553	1.1	396	2	US-08-449-	Sequence 14, Applicati	2.13e+03	626	5	1.1	475	2	US-08-861-	Sequence 3, Applicatio	2.13e+03	
554	1.1	396	2	US-08-939-	Sequence 10, Applicati	2.13e+03	627	5	1.1	477	2	US-08-700-	Sequence 3, Applicatio	2.13e+03	
555	1.1	396	2	US-08-459-	Sequence 2, Applicatio	2.13e+03	628	5	1.1	480	3	US-08-306-	Sequence 4, Applicatio	2.13e+03	
556	1.1	397	1	US-07-956-	Sequence 5, Applicatio	2.13e+03	629	5	1.1	480	3	US-08-445-	Sequence 24, Applicati	2.13e+03	
557	1.1	397	1	5168050-5	Sequence 10, Applicati	2.13e+03	630	5	1.1	489	5	5221789-1	Sequence 2, Applicatio	2.13e+03	
558	1.1	400	5	PCT-US91-0	Sequence 4, Applicatio	2.13e+03	631	5	1.1	489	1	US-08-124-	Sequence 18, Applicati	2.13e+03	
559	1.1	400	4	US-08-483-	Sequence 8, Applicatio	2.13e+03	632	5	1.1	489	2	US-09-020-	Sequence 12, Applicati	2.13e+03	
560	1.1	405	2	US-08-393-	Sequence 5, Applicatio	2.13e+03	633	5	1.1	489	2	US-09-020-	Sequence 16, Applicati	2.13e+03	
561	1.1	405	2	US-09-203-	Sequence 6, Applicatio	2.13e+03	634	5	1.1	489	2	US-09-020-	Sequence 8, Applicatio	2.13e+03	
562	1.1	406	2	US-08-765-	Sequence 6, Applicatio	2.13e+03	635	5	1.1	489	2	US-09-020-	Sequence 22, Applicati	2.13e+03	
563	1.1	407	3	US-08-795-	Sequence 6, Applicatio	2.13e+03	636	5	1.1	489	2	US-09-020-	Sequence 2, Applicatio	2.13e+03	
564	1.1	407	3	US-08-487-	Sequence 2, Applicatio	2.13e+03	637	5	1.1	489	2	US-09-020-	Sequence 2, Applicatio	2.13e+03	
565	1.1	407	3	US-08-487-	Sequence 2, Applicatio	2.13e+03	638	5	1.1	489	2	US-09-020-	Sequence 2, Applicatio	2.13e+03	
566	1.1	407	3	US-08-487-	Sequence 2, Applicatio	2.13e+03	639	5	1.1	489	2	US-09-020-	Sequence 2, Applicatio	2.13e+03	
567	1.1	407	3	US-08-487-	Sequence 2, Applicatio	2.13e+03	640	5	1.1	489	2	US-09-020-	Sequence 2, Applicatio	2.13e+03	
568	1.1	408	5	5166058-6	Sequence 11, Applicati	2.13e+03	641	5	1.1	489	2	US-09-020-	Sequence 2, Applicatio	2.13e+03	
569	1.1	408	3	US-08-459-	Sequence 21, Applicati	2.13e+03	642	5	1.1	490	2	US-08-201-	Sequence 5, Applicatio	2.13e+03	
570	1.1	408	3	US-08-743-	Sequence 17, Applicati	2.13e+03	643	5	1.1	490	2	US-08-912-	Sequence 5, Applicatio	2.13e+03	
571	1.1	410	3	US-08-630-	Sequence 2, Applicatio	2.13e+03	644	5	1.1	495	5	5258283-9	Sequence 20, Applicati	2.13e+03	
572	1.1	410	3	US-09-083-	Sequence 2, Applicatio	2.13e+03	645	5	1.1	495	5	5171684-2	Sequence 20, Applicati	2.13e+03	
573	1.1	412	5	5262319-2	Sequence 3, Applicatio	2.13e+03	646	5	1.1	497	4	US-08-454-	Sequence 15, Applicati	2.13e+03	
574	1.1	412	2	US-08-395-	Sequence 6, Applicatio	2.13e+03	647	5	1.1	500	1	US-08-307-	Sequence 20, Applicati	2.13e+03	
575	1.1	412	2	US-08-878-	Sequence 6, Applicatio	2.13e+03	648	5	1.1	502	2	US-08-700-	Sequence 8, Applicatio	2.13e+03	
576	1.1	413	2	US-08-605-	Sequence 10, Applicati	2.13e+03	649	5	1.1	502	3	US-08-464-	Sequence 7, Applicatio	2.13e+03	
577	1.1	413	2	US-08-943-	Sequence 10, Applicati	2.13e+03	650	5	1.1	503	3	US-08-359-	Sequence 8, Applicatio	2.13e+03	
578	1.1	413	2	US-08-295-	Sequence 2, Applicatio	2.13e+03	651	5	1.1	503	3	US-08-700-	Sequence 8, Applicatio	2.13e+03	
579	1.1	415	1	US-07-757-	Sequence 5, Applicatio	2.13e+03	652	5	1.1	507	1	US-08-484-	Sequence 12, Applicati	2.13e+03	
580	1.1	416	1	US-08-117-	Sequence 61, Applicati	2.13e+03	653	5	1.1	508	1	51870765-6	Sequence 6, Applicatio	2.13e+03	
581	1.1	420	2	US-08-845-	Sequence 8, Applicatio	2.13e+03	654	5	1.1	513	5	US-07-989-	Sequence 8, Applicatio	2.13e+03	
582	1.1	420	4	PCT-US96-0	Sequence 4, Applicatio	2.13e+03	655	5	1.1	513	3	US-08-889-	Sequence 19, Applicati	2.13e+03	
583	1.1	420	1	US-07-847-	Sequence 29, Applicati	2.13e+03	656	5	1.1	513	2	US-08-459-	Sequence 41, Applicati	2.13e+03	
584	1.1	423	4	PCT-US96-1	Sequence 14, Applicati	2.13e+03	657	5	1.1	516	1	US-08-638-	Sequence 4, Applicatio	2.13e+03	
585	1.1	423	3	US-08-494-	Sequence 14, Applicati	2.13e+03	658	5	1.1	516	1	US-08-577-	Sequence 4, Applicatio	2.13e+03	
586	1.1	425	3	US-08-105-	Sequence 2, Applicatio	2.13e+03	659	5	1.1	516	2	US-08-676-	Sequence 7, Applicatio	2.13e+03	
587	1.1	425	3	5268463-8	Sequence 63, Applicati	2.13e+03	660	5	1.1	520	4	PCT-US95-0	Sequence 5, Applicatio	2.13e+03	
588	1.1	426	1	US-08-833-	Sequence 63, Applicati	2.13e+03	661	5	1.1	525	4	PCT-US95-1	Sequence 27, Applicati	2.13e+03	
589	1.1	426	1	US-08-459-	Sequence 41, Applicati	2.13e+03	662	5	1.1	525	4	US-08-681-	Sequence 2, Applicatio	2.13e+03	
590	1.1	428	5	5432081-9	Sequence 12, Applicati	2.13e+03	663	5	1.1	528	1	US-08-368-	Sequence 13, Applicati	2.13e+03	
591	1.1	428	1	US-08-816-	Sequence 12, Applicati	2.13e+03	664	5	1.1	528	4	PCT-US93-0	Sequence 13, Applicati	2.13e+03	
592	1.1	428	1	US-08-417-	Sequence 12, Applicati	2.13e+03	665	5	1.1	531	2	US-08-789-	Sequence 3, Applicatio	2.13e+03	
593	1.1	428	1	US-08-301-	Sequence 18, Applicati	2.13e+03	666	5	1.1	531	4	PCT-US95-0	Sequence 3, Applicatio	2.13e+03	
594	1.1	429	5	5182195-13	Sequence 18, Applicati	2.13e+03	667	5	1.1	532	3	5284931-2	Sequence 3, Applicatio	2.13e+03	
595	1.1	430	1	US-08-535-	Sequence 8, Applicatio	2.13e+03	668	5	1.1	532	3	US-08-933-	Sequence 13, Applicati	2.13e+03	
596	1.1	430	2	US-08-677-	Sequence 7, Applicatio	2.13e+03	669	5	1.1	533	1	US-08-484-	Sequence 13, Applicati	2.13e+03	
597	1.1	433	1	US-08-522-	Sequence 18, Applicati	2.13e+03	670	5	1.1	533	1	US-08-220-	Sequence 15, Applicati	2.13e+03	
598	1.1	437	1	US-08-484-	Sequence 1, Applicatio	2.13e+03	671	5	1.1	540	4	PCT-US95-1	Sequence 25, Applicati	2.13e+03	
599	1.1	438	1	US-08-764-	Sequence 11, Applicati	2.13e+03	672	5	1.1						
600	1.1	438	1	US-08-494-	Sequence 11, Applicati	2.13e+03	673	5	1.1						
601	1.1	438	1	US-08-494-	Sequence 11, Applicati	2.13e+03	674	5	1.1						
602	1.1	438	1	US-08-494-	Sequence 11, Applicati	2.13e+03	675	5	1.1						
603	1.1	438	1	US-08-494-	Sequence 11, Applicati	2.13e+03	676	5	1.1						
604	1.1	438	1	US-08-494-	Sequence 11, Applicati	2.13e+03	677	5	1.1						
605	1.1	438	1	US-08-494-	Sequence 11, Applicati	2.13e+03	678	5	1.1						
606	1.1	438	1	US-08-494-	Sequence 11, Applicati	2.13e+03	679	5	1.1						
607	1.1	438	1	US-08-494-	Sequence 11, Applicati	2.13e+03	680	5	1.1						

681	5	1.1	540.	4	PCR-US95-1	Sequence 26, Applicant	2.13e+03	754	5	1.1	694	2	US-08-689-	Sequence 5, Applicant	2.13e+03
682	5	1.1	541	1	US-08-604-	Sequence 2, Applicant	2.13e+03	755	5	1.1	695	5	5218100-2	Sequence 5, Applicant	2.13e+03
683	5	1.1	543	3	US-08-808-	Sequence 12, Applicant	2.13e+03	756	5	1.1	695	2	US-08-104-	Sequence 1, Applicant	2.13e+03
684	5	1.1	543	2	US-08-808-	Sequence 1, Applicant	2.13e+03	757	5	1.1	696	3	US-08-906-	Sequence 4, Applicant	2.13e+03
685	5	1.1	548	2	US-08-676-	Sequence 50, Applicant	2.13e+03	758	5	1.1	705	2	US-08-770-	Sequence 7, Applicant	2.13e+03
686	5	1.1	548	2	US-08-782-	Sequence 2, Applicant	2.13e+03	759	5	1.1	713	3	US-08-149-	Sequence 2, Applicant	2.13e+03
687	5	1.1	548	3	US-08-111-	Sequence 14, Applicant	2.13e+03	760	5	1.1	714	4	PCR-US93-0	Sequence 2, Applicant	2.13e+03
688	5	1.1	548	3	US-08-463-	Sequence 2, Applicant	2.13e+03	761	5	1.1	718	1	US-08-425-	Sequence 2, Applicant	2.13e+03
689	5	1.1	549	4	PCR-US95-1	Sequence 16, Applicant	2.13e+03	762	5	1.1	722	1	US-08-158-	Sequence 5, Applicant	2.13e+03
690	5	1.1	549	4	PCR-US95-1	Sequence 15, Applicant	2.13e+03	763	5	1.1	724	1	US-08-121-	Sequence 6, Applicant	2.13e+03
691	5	1.1	549	2	US-08-676-	Sequence 59, Applicant	2.13e+03	764	5	1.1	724	1	US-08-835-	Sequence 62, Applicant	2.13e+03
692	5	1.1	552	3	US-09-111-	Sequence 10, Applicant	2.13e+03	765	5	1.1	729	2	US-08-459-	Sequence 14, Applicant	2.13e+03
693	5	1.1	553	3	US-09-082-	Sequence 2, Applicant	2.13e+03	766	5	1.1	732	2	PCR-US95-1	Sequence 2, Applicant	2.13e+03
694	5	1.1	555	4	PCR-US96-0	Sequence 2, Applicant	2.13e+03	767	5	1.1	732	2	US-08-456-	Sequence 9, Applicant	2.13e+03
695	5	1.1	559	1	US-08-458-	Sequence 12, Applicant	2.13e+03	768	5	1.1	732	1	US-08-456-	Sequence 9, Applicant	2.13e+03
696	5	1.1	562	4	PCR-US95-0	Sequence 16, Applicant	2.13e+03	769	5	1.1	738	5	5264554-2	Sequence 9, Applicant	2.13e+03
697	5	1.1	572	1	US-08-191-	Sequence 81, Applicant	2.13e+03	770	5	1.1	745	2	US-08-484-	Sequence 43, Applicant	2.13e+03
698	5	1.1	576	4	PCR-US96-0	Sequence 4, Applicant	2.13e+03	771	5	1.1	745	2	US-08-862-	Sequence 5, Applicant	2.13e+03
699	5	1.1	582	1	US-08-261-	Sequence 6, Applicant	2.13e+03	772	5	1.1	745	2	US-08-484-	Sequence 43, Applicant	2.13e+03
700	5	1.1	583	2	US-08-616-	Sequence 4, Applicant	2.13e+03	773	5	1.1	746	2	US-08-838-	Sequence 6, Applicant	2.13e+03
701	5	1.1	585	2	US-08-869-	Sequence 6, Applicant	2.13e+03	774	5	1.1	751	5	5187153-2	Sequence 6, Applicant	2.13e+03
702	5	1.1	587	4	PCR-US93-0	Sequence 4, Applicant	2.13e+03	775	5	1.1	751	5	5223482-2	Sequence 6, Applicant	2.13e+03
703	5	1.1	591	2	US-08-179-	Sequence 5, Applicant	2.13e+03	776	5	1.1	751	5	5220013-2	Sequence 4, Applicant	2.13e+03
704	5	1.1	591	2	US-08-628-	Sequence 10, Applicant	2.13e+03	777	5	1.1	751	1	US-08-123-	Sequence 4, Applicant	2.13e+03
705	5	1.1	595	3	US-08-628-	Sequence 3, Applicant	2.13e+03	778	5	1.1	751	2	US-08-104-	Sequence 2, Applicant	2.13e+03
706	5	1.1	595	3	PCR-US93-0	Sequence 16, Applicant	2.13e+03	779	5	1.1	751	2	US-08-422-	Sequence 2, Applicant	2.13e+03
707	5	1.1	603	2	US-08-687-	Sequence 8, Applicant	2.13e+03	780	5	1.1	761	1	US-08-192-	Sequence 4, Applicant	2.13e+03
708	5	1.1	604	4	PCR-US96-1	Sequence 4, Applicant	2.13e+03	781	5	1.1	764	4	PCR-US95-1	Sequence 4, Applicant	2.13e+03
709	5	1.1	604	4	PCR-US96-1	Sequence 12, Applicant	2.13e+03	782	5	1.1	764	3	US-09-177-	Sequence 4, Applicant	2.13e+03
710	5	1.1	607	1	US-07-879-	Sequence 1, Applicant	2.13e+03	783	5	1.1	765	2	US-08-825-	Sequence 19, Applicant	2.13e+03
711	5	1.1	610	1	US-08-410-	Sequence 1, Applicant	2.13e+03	784	5	1.1	769	4	PCR-US96-0	Sequence 45, Applicant	2.13e+03
712	5	1.1	610	3	US-08-970-	Sequence 2, Applicant	2.13e+03	785	5	1.1	769	2	US-08-789-	Sequence 1, Applicant	2.13e+03
713	5	1.1	610	3	US-08-455-	Sequence 2, Applicant	2.13e+03	786	5	1.1	769	2	US-08-752-	Sequence 1, Applicant	2.13e+03
714	5	1.1	612	4	PCR-US96-1	Sequence 14, Applicant	2.13e+03	787	5	1.1	770	2	US-08-104-	Sequence 3, Applicant	2.13e+03
715	5	1.1	617	4	US-08-240-	Sequence 35, Applicant	2.13e+03	788	5	1.1	787	4	PCR-US95-0	Sequence 10, Applicant	2.13e+03
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717	5	1.1	619	4	US-08-770-	Sequence 6, Applicant	2.13e+03	790	5	1.1	788	2	US-07-728-	Sequence 3, Applicant	2.13e+03
718	5	1.1	619	4	PCR-US93-0	Sequence 2, Applicant	2.13e+03	791	5	1.1	789	2	US-08-838-	Sequence 4, Applicant	2.13e+03
719	5	1.1	620	4	PCR-US95-0	Sequence 2, Applicant	2.13e+03	792	5	1.1	789	2	US-08-469-	Sequence 29, Applicant	2.13e+03
720	5	1.1	621	1	US-08-462-	Sequence 9, Applicant	2.13e+03	793	5	1.1	794	2	US-08-359-	Sequence 9, Applicant	2.13e+03
721	5	1.1	624	2	US-08-756-	Sequence 14, Applicant	2.13e+03	794	5	1.1	794	1	US-07-885-	Sequence 2, Applicant	2.13e+03
722	5	1.1	626	2	US-08-596-	Sequence 9, Applicant	2.13e+03	795	5	1.1	797	2	US-08-453-	Sequence 112, Applicant	2.13e+03
723	5	1.1	636	2	US-08-460-	Sequence 36, Applicant	2.13e+03	796	5	1.1	797	2	US-08-453-	Sequence 112, Applicant	2.13e+03
724	5	1.1	638	1	US-07-688-	Sequence 22, Applicant	2.13e+03	797	5	1.1	800	5	5183745-3	Sequence 4, Applicant	2.13e+03
725	5	1.1	649	4	PCR-US96-0	Sequence 2, Applicant	2.13e+03	798	5	1.1	800	4	PCR-US96-0	Sequence 2, Applicant	2.13e+03
726	5	1.1	649	4	PCR-US96-0	Sequence 2, Applicant	2.13e+03	799	5	1.1	807	2	US-08-935-	Sequence 45, Applicant	2.13e+03
727	5	1.1	649	2	US-08-472-	Sequence 20, Applicant	2.13e+03	800	5	1.1	821	1	US-07-928-	Sequence 2, Applicant	2.13e+03
728	5	1.1	659	1	PCR-US95-1	Sequence 14, Applicant	2.13e+03	801	5	1.1	821	1	US-08-261-	Sequence 5, Applicant	2.13e+03
729	5	1.1	660	4	PCR-US95-1	Sequence 19, Applicant	2.13e+03	802	5	1.1	831	1	US-08-405-	Sequence 5, Applicant	2.13e+03
730	5	1.1	660	4	PCR-US95-1	Sequence 19, Applicant	2.13e+03	803	5	1.1	832	1	US-08-254-	Sequence 1, Applicant	2.13e+03
731	5	1.1	660	4	PCR-US95-1	Sequence 2, Applicant	2.13e+03	804	5	1.1	836	1	US-07-998-	Sequence 105, Applicant	2.13e+03
732	5	1.1	660	4	PCR-US95-1	Sequence 2, Applicant	2.13e+03	805	5	1.1	836	1	US-08-453-	Sequence 105, Applicant	2.13e+03
733	5	1.1	660	4	PCR-US95-1	Sequence 2, Applicant	2.13e+03	806	5	1.1	836	1	US-08-453-	Sequence 105, Applicant	2.13e+03
734	5	1.1	660	4	PCR-US95-1	Sequence 2, Applicant	2.13e+03	807	5	1.1	836	1	US-08-453-	Sequence 105, Applicant	2.13e+03
735	5	1.1	660	4	PCR-US95-1	Sequence 2, Applicant	2.13e+03	808	5	1.1	836	1	US-08-453-	Sequence 105, Applicant	2.13e+03
736	5	1.1	660	4	PCR-US95-1	Sequence 2, Applicant	2.13e+03	809	5	1.1	836	1	US-08-453-	Sequence 105, Applicant	2.13e+03
737	5	1.1	661	2	US-08-770-	Sequence 2, Applicant	2.13e+03	810	5	1.1	837	1	US-07-923-	Sequence 15, Applicant	2.13e+03
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739	5	1.1	667	2	US-09-300-	Sequence 8, Applicant	2.13e+03	812	5	1.1	844	3	US-07-646-	Sequence 2, Applicant	2.13e+03
740	5	1.1	669	2	US-08-456-	Sequence 8, Applicant	2.13e+03	813	5	1.1	845	3	US-08-804-	Sequence 94, Applicant	2.13e+03
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742	5	1.1	669	4	PCR-US92-0	Sequence 8, Applicant	2.13e+03	815	5	1.1	846	1	US-08-451-	Sequence 94, Applicant	2.13e+03
743	5	1.1	669	4	PCR-US92-0	Sequence 8, Applicant	2.13e+03	816	5	1.1	846	1	US-08-451-	Sequence 94, Applicant	2.13e+03
744	5	1.1	675	4	PCR-US96-0	Sequence 10, Applicant	2.13e+03	817	5	1.1	857	3	US-08-804-	Sequence 103, Applicant	2.13e+03
745	5	1.1	680	4	US-08-436-	Sequence 2, Applicant	2.13e+03	818	5	1.1	857	3	US-08-804-	Sequence 103, Applicant	2.13e+03
746	5	1.1	681	4	PCR-US96-0	Sequence 4, Applicant	2.13e+03	819	5	1.1	858	1	US-08-251-	Sequence 113, Applicant	2.13e+03
747	5	1.1	681	3	US-09-183-	Sequence 4, Applicant	2.13e+03	820	5	1.1	868	1	US-08-413-	Sequence 7, Applicant	2.13e+03
748	5	1.1	682	1	US-08-453-	Sequence 107, Applicant	2.13e+03	821	5	1.1	873	3	US-09-187-	Sequence 6, Applicant	2.13e+03
749	5	1.1	682	1	US-07-998-	Sequence 107, Applicant	2.13e+03	822	5	1.1	880	1	US-08-445-	Sequence 10, Applicant	2.13e+03
750	5	1.1	682	4	PCR-US95-0	Sequence 107, Applicant	2.13e+03	823	5	1.1	883	2	US-08-596-	Sequence 2, Applicant	2.13e+03
751	5	1.1	682	4	US-08-453-	Sequence 107, Applicant	2.13e+03	824	5	1.1	884	5	5208144-8	Sequence 2, Applicant	2.13e+03
752	5	1.1	683	5	5210183-3	Sequence 107, Applicant	2.13e+03	825	5	1.1	884	2	US-08-471-	Sequence 5, Applicant	2.13e+03
753	5	1.1	689	1	US-08-454-	Sequence 18, Applicant	2.13e+03	826	5	1.1	886	2	US-08-474-	Sequence 65, Applicant	2.13e+03



827	5	1.1	880	US-08-445-	Sequence 35, Applicant	2.13e+03	500	5	1.1	1184	2	US-08-639-	Sequence 32, Applicant
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829	5	1.1	898	US-08-036-	Sequence 22, Applicant	2.13e+03	902	5	1.1	1189	5	5188960-6	Sequence 32, Applicant
830	5	1.1	904	US-08-453-	Sequence 97, Applicant	2.13e+03	903	5	1.1	1189	2	US-08-980-	Sequence 8, Applicant
831	5	1.1	904	US-08-453-	Sequence 97, Applicant	2.13e+03	904	5	1.1	1189	2	US-08-980-	Sequence 8, Applicant
832	5	1.1	912	US-08-425-	Sequence 19, Applicant	2.13e+03	905	5	1.1	1189	2	US-08-980-	Sequence 6, Applicant
833	5	1.1	912	US-08-425-	Sequence 19, Applicant	2.13e+03	906	5	1.1	1189	2	US-08-980-	Sequence 6, Applicant
834	5	1.1	915	US-08-328-	Sequence 5, Applicant	2.13e+03	907	5	1.1	1189	2	US-08-980-	Sequence 59, Applicant
835	5	1.1	917	US-08-723-	Sequence 2, Applicant	2.13e+03	908	5	1.1	1189	2	US-08-980-	Sequence 61, Applicant
836	5	1.1	917	US-08-588-	Sequence 16, Applicant	2.13e+03	909	5	1.1	1189	3	US-09-314-	Sequence 6, Applicant
837	5	1.1	948	US-08-839-	Sequence 14, Applicant	2.13e+03	910	5	1.1	1189	2	US-08-757-	Sequence 2, Applicant
838	5	1.1	948	US-08-839-	Sequence 14, Applicant	2.13e+03	911	5	1.1	1189	2	US-08-980-	Sequence 12, Applicant
839	5	1.1	951	US-08-162-	Sequence 2, Applicant	2.13e+03	912	5	1.1	1190	1	US-08-239-	Sequence 12, Applicant
840	5	1.1	969	US-08-162-	Sequence 2, Applicant	2.13e+03	913	5	1.1	1190	1	US-08-317-	Sequence 13, Applicant
841	5	1.1	970	US-08-752-	Sequence 7, Applicant	2.13e+03	914	5	1.1	1202	2	US-08-825-	Sequence 22, Applicant
842	5	1.1	976	US-08-449-	Sequence 16, Applicant	2.13e+03	915	5	1.1	1205	2	US-08-937-	Sequence 10, Applicant
843	5	1.1	979	US-08-449-	Sequence 16, Applicant	2.13e+03	916	5	1.1	1213	2	US-08-937-	Sequence 2, Applicant
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847	5	1.1	990	US-08-904-	Sequence 2, Applicant	2.13e+03	920	5	1.1	1245	2	US-08-801-	Sequence 6, Applicant
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983 5 1.1 2620 2 US-08-384- Sequence 32, Applicatio 2.13e+03
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## ALIGNMENTS

RESULT 1 STANDARD: PRT: 436 AA.

Sequence 2, Application US/08307588

Sequence 2, Application US/08307588  
Patent No. 5919453

GENERAL INFORMATION:

APPLICANT: BENOIT, Patrick

APPLICANT: MEYER, Francois

APPLICANT: MAGUIRE, Deborah

APPLICANT: PLAVEC, Ivan

APPLICANT: TOVER, Michael G.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON

TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE I

TITLE OF INVENTION: INTERFERON

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patenting Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,588

FILING DATE: 05-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00770

FILING DATE: 30-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92400902.0

FILING DATE: 31-MAR-1992

ATTORNEY/AGENT INFORMATION:  
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REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 11283/117/GUPL  
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TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 436 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE 436 AA: 49723 MW, 1061275 CN;

Query Match 100.0%; Score 436; DB 2; Length 436;

Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2 STANDARD: PRT: 557 AA.

Sequence 2, Application US/08471454

Sequence 2, Application US/08471454

Patent No. 5731169

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LOTFALA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

Sequence 2, Application US/08471454

Patent No. 5731169

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: UZE, Gilles

APPLICANT: LOTFALA, Georges

APPLICANT: GRESSER, Ion

CC ADDRESSEE: NIXON & VANDERHAYE P.C.  
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CC CITY: ARLINGTON  
CC STATE: VIRGINIA  
CC COUNTRY: U.S.A.  
CC ZIP: 22201-4714  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/471,454  
CC FILING DATE: 06-JUN-1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/900,642  
CC FILING DATE: 15-JUN-1992  
CC APPLICATION NUMBER: FR 89/13770  
CC FILING DATE: 20-OCT-1989  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: BYRNE, THOMAS E.  
CC REGISTRATION NUMBER: 32,205  
CC REFERENCE/DOCKET NUMBER: 960-7  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (703) 816-4000  
CC TELEFAX: (703) 816-4100  
CC TELETYPE: 200797 NIXN UR  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 557 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE: 557 AA; 63525 MW; 1717510 CN;

Query Match 100.0%; Score 436; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MAAVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFTLWNSDESIGNVT 60  
OY 1 MAAVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFTLWNSDESIGNVT 60  
Db 61 FSPDYOKTGMNWKLSGCCNTSTKCNFSSSLKLVYEIKLRIRAKENTSSWYEDSF 120  
OY 61 FSPDYOKTGMNWKLSGCCNTSTKCNFSSSLKLVYEIKLRIRAKENTSSWYEDSF 120  
Db 121 TPFRAOIGPPEVHLAEADKAIVIHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180  
OY 121 TPFRAOIGPPEVHLAEADKAIVIHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180  
Db 181 ENIYSRHHIYKLSPEYTCVAKVALLTSMKIGVSPVHCITTVENELPPENIEVSQ 240  
OY 181 ENIYSRHHIYKLSPEYTCVAKVALLTSMKIGVSPVHCITTVENELPPENIEVSQ 240  
Db 241 ENIYSRHHIYKLSPEYTCVAKVALLTSMKIGVSPVHCITTVENELPPENIEVSQ 240  
OY 241 ENIYSRHHIYKLSPEYTCVAKVALLTSMKIGVSPVHCITTVENELPPENIEVSQ 240  
Db 241 NONVYLKADYTYANNTPOVOMLHAFKLRNPGNHLTKMKOIPDCENVTTCQCFPONTYOK 300  
OY 241 NONVYLKADYTYANNTPOVOMLHAFKLRNPGNHLTKMKOIPDCENVTTCQCFPONTYOK 300  
Db 301 GIYLLRVASDGNNTSFSESEIKFETEOAFLPPVFNIRSLDSDFHIYIGAPKOSGMP 360  
OY 301 GIYLLRVASDGNNTSFSESEIKFETEOAFLPPVFNIRSLDSDFHIYIGAPKOSGMP 360  
Db 361 VIODPLLYEITFEMENISNAEKITTEKTDVTPVPLKPLTYCYAARAHYDDEKLNKSSV 420  
OY 361 VIODPLLYEITFEMENISNAEKITTEKTDVTPVPLKPLTYCYAARAHYDDEKLNKSSV 420  
Db 421 FSDAVCEKTKPGNTSK 436  
OY 421 FSDAVCEKTKPGNTSK 436  
OY 421 FSDAVCEKTKPGNTSK 436

RESULT 3  
ID US-08-466-974-2 STANDARD; PRT: 557 AA.  
XX  
XX  
AC xxxxxx  
XX  
XX  
DT  
XX  
DE Sequence 2; Application US/08466974  
XX  
XX Sequence 2; Application US/08466974  
CC Patent No. 5861258  
CC  
CC GENERAL INFORMATION:  
CC APPLICANT: MOGENSEN, Knud E.  
CC APPLICANT: UZE, Gilles  
CC APPLICANT: LUTFALLA, Georges  
CC APPLICANT: GRESSER, Ion  
CC TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR  
CC TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE  
CC PREPARATION OF THE CORRESPONDING PROTEIN  
CC NUMBER OF SEQUENCES: 2  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: NIXON & VANDERHAYE P.C.  
CC STREET: 1100 NORTH GLEBE ROAD  
CC CITY: ARLINGTON  
CC STATE: VIRGINIA  
CC COUNTRY: U.S.A.  
CC ZIP: 22201-4714  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/466,974  
CC FILING DATE: 06-JUN-1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/900,642  
CC FILING DATE: 15-JUN-1992  
CC APPLICATION NUMBER: FR 89/13770  
CC FILING DATE: 20-OCT-1989  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: BYRNE, THOMAS E.  
CC REGISTRATION NUMBER: 32,205  
CC REFERENCE/DOCKET NUMBER: 960-7  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (703) 816-4000  
CC TELEFAX: (703) 816-4100  
CC TELETYPE: 200797 NIXN UR  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 557 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE: 557 AA; 63525 MW; 1717510 CN;

Query Match 100.0%; Score 436; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MAAVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFTLWNSDESIGNVT 60  
OY 1 MAAVLLGATTLVAVGPMVLSAAGGNLKSPOKVEVDIIDNFTLWNSDESIGNVT 60  
Db 61 FSPDYOKTGMNWKLSGCCNTSTKCNFSSSLKLVYEIKLRIRAKENTSSWYEDSF 120  
OY 61 FSPDYOKTGMNWKLSGCCNTSTKCNFSSSLKLVYEIKLRIRAKENTSSWYEDSF 120  
Db 121 TPFRAOIGPPEVHLAEADKAIVIHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180  
OY 121 TPFRAOIGPPEVHLAEADKAIVIHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180

OY 121 TPFRKAQIGPEVHLEAEADKAIVIHISPGTRDSVMAALDGLSFTYSILLINKNSGVEERI 180  
DB 181 ENIYSRRIKIKLSPETTYCLKAKAALLTSMKIGYSPVHCIKTTVENELPPENIEVSQ 240  
OY 181 ENIYSRRIKIKLSPETTYCLKAKAALLTSMKIGYSPVHCIKTTVENELPPENIEVSQ 240  
DB 241 NONVFLKMDTYANMTFOVOMLHAFKRNPNHLYKMKOIPDCENVTTTCVFPQNVFOR 300  
OY 241 NONVFLKMDTYANMTFOVOMLHAFKRNPNHLYKMKOIPDCENVTTTCVFPQNVFOR 300  
DB 301 GYLLARVQASDGNNTSPWSEIKFDEIOAFLLPPVNIKSLSDSFHIIYGAPQSGNTP 360  
OY 301 GYLLARVQASDGNNTSPWSEIKFDEIOAFLLPPVNIKSLSDSFHIIYGAPQSGNTP 360  
DB 361 VIQDYPILYEIIFWENTSNMERKIIKKTDTVPNKLPLVYCYKAAHMTDEKLNSV 420  
OY 361 VIQDYPILYEIIFWENTSNMERKIIKKTDTVPNKLPLVYCYKAAHMTDEKLNSV 420  
DB 421 FSDAVCEKTRPGNTSK 436  
OY 421 FSDAVCEKTRPGNTSK 436

## RESULT

4 US-08-471-453-2 STANDARD: PRT: 557 AA.

AC xxxxxx

Sequence 2, Application US/08471453

Patent No. 5886153

GENERAL INFORMATION:

APPLICANT: MOGENSEN, Knud E.

APPLICANT: LOTFALLA, Georges

APPLICANT: GRESSER, Ion

TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR

TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P. C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,453

FILING DATE: 06-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/900,642

FILING DATE: 15-JUN-1992

APPLICATION NUMBER: FR 89/13770

FILING DATE: 20-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 960-7

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

TELEX: 200797 NIKN UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE 557 AA; 63525 MW; 1717510 CN;  
Query Match 100.0%; Score 436; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMYVLLGATTLVLYAVGPWVLSAAGKRNLSKPKYVEVDIIDDFFILRRNRSDSVGNVT 60  
OY 1 MMYVLLGATTLVLYAVGPWVLSAAGKRNLSKPKYVEVDIIDDFFILRRNRSDSVGNVT 60  
DB 61 FSPDYQGTGMDNMTKISGCONITSTKCNFSSLKNTVEEIKLRRAKENTSSMYEVSF 120  
OY 61 FSPDYQGTGMDNMTKISGCONITSTKCNFSSLKNTVEEIKLRRAKENTSSMYEVSF 120  
DB 121 TPFRKAQIGPEVHLEAEADKAIVIHISPGTRDSVMAALDGLSFTYSILLINKNSGVEERI 180  
OY 121 TPFRKAQIGPEVHLEAEADKAIVIHISPGTRDSVMAALDGLSFTYSILLINKNSGVEERI 180  
DB 181 ENIYSRRIKIKLSPETTYCLKAKAALLTSMKIGYSPVHCIKTTVENELPPENIEVSQ 240  
OY 181 ENIYSRRIKIKLSPETTYCLKAKAALLTSMKIGYSPVHCIKTTVENELPPENIEVSQ 240  
DB 241 NONVFLKMDTYANMTFOVOMLHAFKRNPNHLYKMKOIPDCENVTTTCVFPQNVFOR 300  
OY 241 NONVFLKMDTYANMTFOVOMLHAFKRNPNHLYKMKOIPDCENVTTTCVFPQNVFOR 300  
DB 301 GYLLARVQASDGNNTSPWSEIKFDEIOAFLLPPVNIKSLSDSFHIIYGAPQSGNTP 360  
OY 301 GYLLARVQASDGNNTSPWSEIKFDEIOAFLLPPVNIKSLSDSFHIIYGAPQSGNTP 360  
DB 361 VIQDYPILYEIIFWENTSNMERKIIKKTDTVPNKLPLVYCYKAAHMTDEKLNSV 420  
OY 361 VIQDYPILYEIIFWENTSNMERKIIKKTDTVPNKLPLVYCYKAAHMTDEKLNSV 420  
DB 421 FSDAVCEKTRPGNTSK 436  
OY 421 FSDAVCEKTRPGNTSK 436

## RESULT

5 US-08-328-256-10 STANDARD: PRT: 557 AA.

AC xxxxxx

Sequence 10, Application US/08328256

Patent No. 5643749

GENERAL INFORMATION:

APPLICANT: REVEL, Michel

APPLICANT: ABRAMOVICH, Carolina

TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NETMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/328,256  
FILING DATE: 24-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: II, 107378  
FILING DATE: 24-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: REVEL-13  
REFERENCE/DOCKET NUMBER: 25,618  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE: 557 AA; 63525 MW; 1718021 CN;

Query Match 100.0%; Score 436; DB 1; Length 557;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVVLGATTLVAVGVWVLSAAGGKRLKSPQVEVDIIDNFIILRNRSDESVGNT 60  
QY 1 MMVVLGATTLVAVGVWVLSAAGGKRLKSPQVEVDIIDNFIILRNRSDESVGNT 60  
DB 61 FSDYOKTGMWIKLSGCONITSTKCNFSSKLNVYEIRIKIRAEKENTSSWYEVDSF 120  
QY 61 FSDYOKTGMWIKLSGCONITSTKCNFSSKLNVYEIRIKIRAEKENTSSWYEVDSF 120  
DB 121 TPFRKQIGPPEVHLAEADKALVIHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180  
QY 121 TPFRKQIGPPEVHLAEADKALVIHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180  
DB 181 ENIYSRHKIYKLSPEPTYCLAKYKALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240  
QY 181 ENIYSRHKIYKLSPEPTYCLAKYKALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240  
DB 241 NONVYLKWDYTYANNTFOVOMLHAFKRNPGNHLTKMKOIPDCENVKTTQCFPQNVFQK 300  
QY 241 NONVYLKWDYTYANNTFOVOMLHAFKRNPGNHLTKMKOIPDCENVKTTQCFPQNVFQK 300  
DB 301 GIYLLRVOASDGNNTSFWSSEIKFDTEIOAFLPPVFNIRSLSDSFHIYIGAPKOSGNT 360  
QY 301 GIYLLRVOASDGNNTSFWSSEIKFDTEIOAFLPPVFNIRSLSDSFHIYIGAPKOSGNT 360  
DB 361 VIQDPLLYEIIFFWENTSNAEKRIIEKTDVYVNLKPLTYCVARAHTEDEKLNKSSV 420  
QY 361 VIQDPLLYEIIFFWENTSNAEKRIIEKTDVYVNLKPLTYCVARAHTEDEKLNKSSV 420  
DB 421 FSDAVCEKTKPGNTSK 436  
QY 421 FSDAVCEKTKPGNTSK 436

RESULT 6  
ID US-08-307-588-4 STANDARD; PRT: 557 AA.  
AC xxxxxx  
DE Sequence 4, Application US/08307588  
CC Sequence 4, Application US/08307588  
CC Patent No. 5919453

GENERAL INFORMATION:  
APPLICANT: BENOIT, Patrick  
APPLICANT: MEYER, Francois  
APPLICANT: MAGUIRE, Deborah  
APPLICANT: PLAVEC, Ivan  
APPLICANT: TOVEY, Michael G.  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST THE INTERFERON  
TITLE OF INVENTION: RECEPTOR, WITH NEUTRALIZING ACTIVITY AGAINST TYPE 1  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/307,588  
FILING DATE: 05-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00770  
FILING DATE: 30-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92400902.0  
FILING DATE: 31-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 17283/117/GUPL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE: 557 AA; 63525 MW; 1717510 CN;

Query Match 100.0%; Score 436; DB 2; Length 557;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVVLGATTLVAVGVWVLSAAGGKRLKSPQVEVDIIDNFIILRNRSDESVGNT 60  
QY 1 MMVVLGATTLVAVGVWVLSAAGGKRLKSPQVEVDIIDNFIILRNRSDESVGNT 60  
DB 61 FSDYOKTGMWIKLSGCONITSTKCNFSSKLNVYEIRIKIRAEKENTSSWYEVDSF 120  
QY 61 FSDYOKTGMWIKLSGCONITSTKCNFSSKLNVYEIRIKIRAEKENTSSWYEVDSF 120  
DB 121 TPFRKQIGPPEVHLAEADKALVIHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180  
QY 121 TPFRKQIGPPEVHLAEADKALVIHISPTKDSVMALDGLSFTYSLIMKNSGVEERI 180  
DB 181 ENIYSRHKIYKLSPEPTYCLAKYKALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240  
QY 181 ENIYSRHKIYKLSPEPTYCLAKYKALLTSWKIGVSPVHCITTYENELPPENIEVSQ 240  
DB 241 NONVYLKWDYTYANNTFOVOMLHAFKRNPGNHLTKMKOIPDCENVKTTQCFPQNVFQK 300  
QY 241 NONVYLKWDYTYANNTFOVOMLHAFKRNPGNHLTKMKOIPDCENVKTTQCFPQNVFQK 300  
DB 301 GIYLLRVOASDGNNTSFWSSEIKFDTEIOAFLPPVFNIRSLSDSFHIYIGAPKOSGNT 360  
QY 301 GIYLLRVOASDGNNTSFWSSEIKFDTEIOAFLPPVFNIRSLSDSFHIYIGAPKOSGNT 360

Db 361 VIODYPLIYEIIEWENTSNARKIIEKTDVTPNKLPLTYCYKARAHMDEKLNSSV 420  
 OY 361 VIODYPLIYEIIEWENTSNARKIIEKTDVTPNKLPLTYCYKARAHMDEKLNSSV 420  
 Db 421 FSDAVCEKTRKGNJSK 436  
 OY 421 FSDAVCEKTRKGNJSK 436

RESULT 7  
 ID US-08-328-256-11 STANDARD: PRT: 434 AA.  
 XX xxxxxx

Sequence 11, Application US/08328256

CC Sequence 11, Application US/08328256  
 CC Patent No. 5643749  
 CC GENERAL INFORMATION:  
 CC APPLICANT: REVEL, Michel  
 CC APPLICANT: ABRAMOVICH, Carolina  
 CC APPLICANT: RATOVIJSKI, Edward  
 CC TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
 CC TITLE OF INVENTION: PREPARATION AND USE  
 CC NUMBER OF SEQUENCES: 12  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: BROMDY AND NEIMARK  
 CC STREET: 419 Seventh Street, N.W., Suite 300  
 CC CITY: Washington  
 CC STATE: D.C.  
 CC COUNTRY: USA  
 CC ZIP: 20004  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patentin Release #1.0, Version #1.30  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/328,256  
 CC FILING DATE: 24-OCT-1994  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: IL 107378  
 CC FILING DATE: 24-OCT-1993  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: BROMDY, Roger L.  
 CC REGISTRATION NUMBER: REVEL-13  
 CC REFERENCE/DOCKET NUMBER: 25,618  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 202-628-5197  
 CC TELEFAX: 202-737-3528  
 CC TELEX: 248633  
 CC INFORMATION FOR SEQ ID NO: 11:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 434 amino acids  
 CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 434 AA: 49546 MW: 1042221 CN:

Query Match 97.9%; Score 427; DB 1; Length 434;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 427; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMYVLGATLVLYVANGPWLTSAAGGKNLSPQKVEVDIIDNFILRNRSDESNGVNT 60  
 OY 1 MMYVLGATLVLYVANGPWLTSAAGGKNLSPQKVEVDIIDNFILRNRSDESNGVNT 60  
 Db 61 FSDYOKTGDNNIKLSCGONITSTKCNFSLKLVYEEIKLRRAKENTSSMYEDSF 120  
 OY 61 FSDYOKTGDNNIKLSCGONITSTKCNFSLKLVYEEIKLRRAKENTSSMYEDSF 120

Db 121 TPFKRAOIGPPEVHLEEDAAIVIHISPGKDSYMAALDGLSPYSLIMKNSGVEERI 180  
 OY 121 TPFKRAOIGPPEVHLEEDAAIVIHISPGKDSYMAALDGLSPYSLIMKNSGVEERI 180  
 Db 181 ENIYSRKIKYLSPEYTYCCKVKAALLTSMKIGVYSPVHCITKTVENELPPENIEVSQ 240  
 OY 181 ENIYSRKIKYLSPEYTYCCKVKAALLTSMKIGVYSPVHCITKTVENELPPENIEVSQ 240  
 Db 241 NONYVLKMDYTNAMTFVOYOMLHAFILKRNNGNHLKXKQIPDCENVYTCQVPONFQK 300  
 OY 241 NONYVLKMDYTNAMTFVOYOMLHAFILKRNNGNHLKXKQIPDCENVYTCQVPONFQK 300  
 Db 301 GYLLRVQASDGNNSTFSWESEIKFDEIQAFLLPVPNIRSLSDSFHIIYGAPQSGNTP 360  
 OY 301 GYLLRVQASDGNNSTFSWESEIKFDEIQAFLLPVPNIRSLSDSFHIIYGAPQSGNTP 360  
 Db 361 VIODYPLIYEIIEWENTSNARKIIEKTDVTPNKLPLTYCYKARAHMDEKLNSSV 420  
 OY 361 VIODYPLIYEIIEWENTSNARKIIEKTDVTPNKLPLTYCYKARAHMDEKLNSSV 420  
 Db 421 FSDAVCE 427  
 OY 421 FSDAVCE 427

RESULT 8  
 ID US-08-328-256-12 STANDARD: PRT: 496 AA.  
 XX xxxxxx

Sequence 12, Application US/08328256

CC Sequence 12, Application US/08328256  
 CC Patent No. 5643749  
 CC GENERAL INFORMATION:  
 CC APPLICANT: REVEL, Michel  
 CC APPLICANT: ABRAMOVICH, Carolina  
 CC APPLICANT: RATOVIJSKI, Edward  
 CC TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
 CC TITLE OF INVENTION: PREPARATION AND USE  
 CC NUMBER OF SEQUENCES: 12  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: BROMDY AND NEIMARK  
 CC STREET: 419 Seventh Street, N.W., Suite 300  
 CC CITY: Washington  
 CC STATE: D.C.  
 CC COUNTRY: USA  
 CC ZIP: 20004  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: Patentin Release #1.0, Version #1.30  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/328,256  
 CC FILING DATE: 24-OCT-1994  
 CC PRIORITY APPLICATION DATA:  
 CC APPLICATION NUMBER: IL 107378  
 CC FILING DATE: 24-OCT-1993  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: BROMDY, Roger L.  
 CC REGISTRATION NUMBER: REVEL-13  
 CC REFERENCE/DOCKET NUMBER: 25,618  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 202-628-5197  
 CC TELEFAX: 202-737-3528  
 CC TELEX: 248633  
 CC INFORMATION FOR SEQ ID NO: 12:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 496 amino acids

CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 496 AA; 56718 MM; 1344690 CN;  
 SO  
 Query Match 94.7%; Score 413; DB 1; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MMVLLGATLVLYAVGPMVLSAAGKRLKSPQKVEVDIIDNFILRMNRSDESVGNT 60  
 |||||||  
 QY 1 MMVLLGATLVLYAVGPMVLSAAGKRLKSPQKVEVDIIDNFILRMNRSDESVGNT 60  
 |||||||  
 DB 61 FSDYQFTGMDNWKISGCONITSTKCNFSSLKLVYEEIKRLIRAKENKTSWYEVDSF 120  
 |||||||  
 QY 61 FSDYQFTGMDNWKISGCONITSTKCNFSSLKLVYEEIKRLIRAKENKTSWYEVDSF 120  
 |||||||  
 DB 121 TPRKQIGPPEVHLEDAIYHISPGKRDYMMALDGLSTFYSLIKNNSGVEERI 180  
 |||||||  
 QY 121 TPRKQIGPPEVHLEDAIYHISPGKRDYMMALDGLSTFYSLIKNNSGVEERI 180  
 |||||||  
 DB 181 ENIYSRHKIKLSPETTYCKLVKRALITSMKIGVSPVHCIKTVENELPPEKIEVSQ 240  
 |||||||  
 QY 181 ENIYSRHKIKLSPETTYCKLVKRALITSMKIGVSPVHCIKTVENELPPEKIEVSQ 240  
 |||||||  
 DB 241 NQNVYLMQDYTYANMTFOYOMLHAFKRNPNHLYKMKQIPDCENVTTQCVFQNVFOK 300  
 |||||||  
 QY 241 NQNVYLMQDYTYANMTFOYOMLHAFKRNPNHLYKMKQIPDCENVTTQCVFQNVFOK 300  
 |||||||  
 DB 301 GYLLRVQASDGNNTSWSEIKFDTEIOAFLLPVPVNISSLSPHIYIGAPKQSGNTP 360  
 |||||||  
 QY 301 GYLLRVQASDGNNTSWSEIKFDTEIOAFLLPVPVNISSLSPHIYIGAPKQSGNTP 360  
 |||||||  
 DB 361 VIQDYPLIYIIIFEMENTSNAERKIIIEKTDVTPNKLPLVYCVKARAHMTDE 413  
 |||||||  
 QY 361 VIQDYPLIYIIIFEMENTSNAERKIIIEKTDVTPNKLPLVYCVKARAHMTDE 413  
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RESULT 9  
 ID US-08-488-379-243 STANDARD; PRT; 17 AA.  
 XX xxxxxx  
 DT  
 XX  
 XX  
 DE Sequence 243, Application US/08488379  
 CC  
 CC Sequence 243, Application US/08488379  
 CC Patent No. 5580103  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Robert G. Urban  
 CC APPLICANT: Roman M. Chicz  
 CC APPLICANT: Dario A. A. Vignali  
 CC APPLICANT: Mary L. Hedley  
 CC APPLICANT: Lawrence J. Stern  
 CC APPLICANT: Jack L. Strominger  
 CC TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
 CC NUMBER OF SEQUENCES: 274  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Fish & Richardson  
 CC STREET: 225 Franklin Street  
 CC CITY: Boston  
 CC STATE: Massachusetts  
 CC COUNTRY: U.S.A.  
 CC ZIP: 02110-2804  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 CC COMPUTER: IBM PS/2 Model 502 or 55SX  
 CC OPERATING SYSTEM: MS-DOS (Version 5.0)  
 CC SOFTWARE: WordPerfect (Version 5.1)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/488-379

CC FILING DATE: 514  
 CC CLASSIFICATION: 514  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: 08/077,255  
 CC FILING DATE: June 15, 1993  
 CC APPLICATION NUMBER: 07/925,460  
 CC FILING DATE: August 11, 1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Clark, Paul T.  
 CC REGISTRATION NUMBER: 30,162  
 CC REFERENCE/DOCKET NUMBER: 00246/168001  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (617) 542-5070  
 CC TELEFAX: (617) 542-8906  
 CC TELEX: 200154  
 CC INFORMATION FOR SEQ ID NO: 243:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 17  
 CC TYPE: amino acid  
 CC STRANDEDNESS:  
 CC TOPOLOGY: linear  
 SO SEQUENCE 17 AA; 2072 MM; 1573 CN;  
 Query Match 3.9%; Score 17; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.24e-12;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 GNLHYKWKQIPDCENVK 17  
 |||||||  
 QY 271 GNLHYKWKQIPDCENVK 287  
 |||||||

RESULT 10  
 ID PCT-US93-07545-243 STANDARD; PRT; 17 AA.  
 XX xxxxxx  
 AC  
 XX  
 DT  
 XX  
 DE Sequence 243, Application PC/TUS9307545  
 CC  
 CC Sequence 243, Application PC/TUS9307545  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Robert G. Urban  
 CC APPLICANT: Roman M. Chicz  
 CC APPLICANT: Dario A. A. Vignali  
 CC APPLICANT: Mary L. Hedley  
 CC APPLICANT: Lawrence J. Stern  
 CC APPLICANT: Jack L. Strominger  
 CC TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
 CC NUMBER OF SEQUENCES: 273  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: Fish & Richardson  
 CC STREET: 225 Franklin Street  
 CC CITY: Boston  
 CC STATE: Massachusetts  
 CC COUNTRY: U.S.A.  
 CC ZIP: 02110-2804  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 CC COMPUTER: IBM PS/2 Model 502 or 55SX  
 CC OPERATING SYSTEM: MS-DOS (Version 5.0)  
 CC SOFTWARE: WordPerfect (Version 5.1)  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US93/07545  
 CC FILING DATE: 19930811  
 CC CLASSIFICATION:  
 CC PRIOR APPLICATION DATA:  
 CC APPLICATION NUMBER: 07/925,460  
 CC FILING DATE: August 11, 1992  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Clark, Paul T.  
 CC REGISTRATION NUMBER: 30,162

US-09-240-675-2.rai

CC LENGTH: 17  
CC TYPE: amino acid  
CC STRANDEDNESS:  
CC TOPOLOGY: linear  
CC  
SQ SEQUENCE 17 AA: 2072 MW: 1573 CN;  
  
Query Match 3.9%; Score 17; DB 2; Length 17;  
Best Local Similarity 100.0%;  
Pred. No. 1,24e-12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

RESULT 12

XX  
AC  
XX  
XXXXXX

Sequence 9, Application US/08328256  
DE  
XX  
Sequence 9, Application US/00300056  
XX

CC APPLICANT: RATOVIJSKI, Edward

CC TITLE OF INVENTION: PREPARATION AND USE  
CC NUMBER OF SEQUENCES: 12  
CC CORRESPONDENCE ADDRESS:  
CC

CC ADDRESS: BROWDY AND NEIMARK  
CC STREET: 419 Seventh Street, N.W., Suite 300  
CC City: Washington  
CC STATE: D.C.  
CC COUNTRY: USA  
CC ZIP: 20004  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/328,256  
CC FILING DATE: 24-OCT-1994  
CC

CC PRIOR APPLICATION DATA: IL 107378  
CC APPLICATION NUMBER: 24-OCT-1993  
CC FILING DATE: 24-OCT-1993  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: BROWDY, Roger L.  
CC REGISTRATION NUMBER: REVEL-13  
CC REFERENCE/DOCKET NUMBER: 25,618  
CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 202-628-5197  
CC TELEFAX: 202-737-3528  
CC TELEX: 248633  
CC INFORMATION FOR SEQ ID NO: 9:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 56 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide  
SQ SEQUENCE 56 AA: 6323 MW: 16937 CN:  
Query Match: 3.7% Score 16; DB 1; Length 56;  
Best Local Similarity 100.0%; Pred. No. 3.39e-11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db 1 PLVYVCYKARAHYME 16  
|||||

CC Patent No. 5643749

388



CC COUNTRY: US  
CC ZIP: 92037  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/241,387  
CC FILING DATE: 10-MAY-1994  
CC CLASSIFICATION: 530  
CC PRIORITY APPLICATION DATA:  
CC APPLICATION NUMBER: USSN 07/695,564  
CC FILING DATE: 03-MAY-1004  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Fitting, Thomas  
CC REGISTRATION NUMBER: 34,163  
CC REFERENCE/DOCKET NUMBER: TSR241.001  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619-554-2937  
CC TELEFAX: 619-554-6312  
CC INFORMATION FOR SEQ ID NO: 9:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 153 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: unknown  
CC MOLECULE TYPE: protein  
CC HYPOTHEICAL: YES  
CC ANTI-SENSE: NO  
CC FRAGMENT TYPE: Internal  
CC FEATURE:  
CC NAME/KEY: Region  
CC LOCATION: 1..153  
CC OTHER INFORMATION: /note- "SEQ ID NO:9 is the 153  
CC OTHER INFORMATION: amino acid sequence predicted from the product  
CC OTHER INFORMATION: which results from amplification of the mouse  
CC FEATURE:  
CC NAME/KEY: Domain  
CC LOCATION: 108..112  
CC OTHER INFORMATION: /note- "The cytoplasmic sequence  
CC OTHER INFORMATION: CDFK begins at amino acid position 108."  
CC SEQUENCE 153 AA; 17843 MW; 134354 CN;  
SQ  
Query Match 1.6%; Score 7; DB 1; Length 153;  
Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 86 LVLVAVG 92  
11 LVLVAVG 17  
OY  
RESULT 16  
ID US-07-695-564-9 STANDARD; PRT; 153 AA.  
AC xxxxxx  
XX  
XX  
XX  
XX  
DE Sequence 9, Application US/07695564  
XX  
XX Sequence 9, Application US/07695564  
CC Patent No. 5310874  
CC GENERAL INFORMATION:  
CC APPLICANT: Tamura, Richard N.  
CC APPLICANT: Quaranta, Vito  
CC TITLE OF INVENTION: INTEGRIN ALPHA SUBUNIT CYTOPLASMIC  
CC TITLE OF INVENTION: DOMAIN POLYPEPTIDES, ANTIBODIES AND METHODS  
CC NUMBER OF SEQUENCES: 16  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Thomas Fitting  
CC STREET: 11300 Sorrento Valley Road, Suite 200  
CC CITY: San Diego

CC STATE: California  
CC COUNTRY: United States  
CC ZIP: 92121  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/07/695,564  
CC FILING DATE: 19910503  
CC CLASSIFICATION: 435  
CC PRIORITY APPLICATION DATA:  
CC APPLICATION NUMBER:  
CC FILING DATE:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Fitting, Thomas  
CC REGISTRATION NUMBER: 34,163  
CC REFERENCE/DOCKET NUMBER: SCRO377P  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619-546-1555  
CC INFORMATION FOR SEQ ID NO: 9:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 153 amino acids  
CC TYPE: AMINO ACID  
CC TOPOLOGY: unknown  
CC MOLECULE TYPE: protein  
CC HYPOTHEICAL: YES  
CC ANTI-SENSE: NO  
CC FRAGMENT TYPE: Internal  
CC FEATURE:  
CC NAME/KEY: Region  
CC LOCATION: 1..153  
CC OTHER INFORMATION: /note- "SPD ID NO:9 is the 153  
CC OTHER INFORMATION: amino acid sequence predicted from the product  
CC OTHER INFORMATION: which results from amplification of the mouse  
CC OTHER INFORMATION: ALPHA 3B CDNA with primers 2032/2033."  
CC FEATURE:  
CC NAME/KEY: Domain  
CC LOCATION: 108..112  
CC OTHER INFORMATION: /note- "The cytoplasmic sequence  
CC OTHER INFORMATION: CDFK begins at amino acid position 108."  
CC SEQUENCE 153 AA; 17843 MW; 134354 CN;  
SQ  
Query Match 1.6%; Score 7; DB 1; Length 153;  
Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 86 LVLVAVG 92  
11 LVLVAVG 17  
OY  
RESULT 17  
ID PCT-US94-14277-3 STANDARD; PRT; 202 AA.  
AC xxxxxx  
XX  
XX  
XX  
XX  
XX  
DE Sequence 3, Application PC/TUS9414277  
XX  
XX Sequence 3, Application PC/TUS9414277  
CC GENERAL INFORMATION:  
CC APPLICANT: Aguet, Michel  
CC APPLICANT: Bonni, Ruth  
CC APPLICANT: Hemmi, Silvio  
CC TITLE OF INVENTION: Receptor Subunit Polypeptides  
CC NUMBER OF SEQUENCES: 8  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Genentech, Inc.  
CC STREET: 460 Point San Bruno Blvd  
CC CITY: South San Francisco

CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94080  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: patin (Genentech)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PC7/US94/14277  
CC FILING DATE: 07-DEC-1994  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/164596  
CC FILING DATE: 09-DEC-1993  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Love, Richard B.  
CC REGISTRATION NUMBER: 34,659  
CC REFERENCE/DOCKET NUMBER: 866PCT  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415/225-5530  
CC TELEFAX: 415/952-9881  
CC TELEX: 910/371-7168  
CC INFORMATION FOR SEQ ID NO: 3:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 202 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC SEQ SEQUENCE 202 AA; 23375 MW; 241129 CN;  
  
Query Match 1.68; Score 7; DB 4; Length 202;  
Best Local Similarity 100.08; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 168 PETTYCL 174  
1111111  
QY 194 PETTYCL 200  
  
RESULT 18  
ID US-08-943-087-50 STANDARD; PRT; 221 AA.  
XX xxxxxx  
DE Sequence 50, Application US/08943087  
CC Sequence 50, Application US/08943087  
CC Patent No. 5945511  
CC GENERAL INFORMATION:  
CC APPLICANT: Lok, SI  
CC APPLICANT: rho, Choon J.  
CC APPLICANT: jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.  
CC APPLICANT: Whitmore, Theodore E.  
CC APPLICANT: Fairish, Theresa M.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East  
CC CITY: Seattle  
CC STATE: WA  
CC COUNTRY: USA  
CC ZIP: 98102  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FastSeq for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/943.087

CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/803.305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lunn, Paul G  
CC REGISTRATION NUMBER: 32,743  
CC REFERENCE/DOCKET NUMBER: 96-24C1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEX:  
CC INFORMATION FOR SEQ ID NO: 50:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 221 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
CC SEQ SEQUENCE 221 AA; 25263 MW; 276613 CN;  
  
Query Match 1.68; Score 7; DB 2; Length 221;  
Best Local Similarity 100.08; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 107 QIGPPEV 113  
1111111  
QY 127 QIGPPEV 133  
  
RESULT 19  
ID US-08-943-087-54 STANDARD; PRT; 221 AA.  
XX xxxxxx  
DE Sequence 54, Application US/08943087  
CC Sequence 54, Application US/08943087  
CC Patent No. 5945511  
CC GENERAL INFORMATION:  
CC APPLICANT: Lok, SI  
CC APPLICANT: rho, Choon J.  
CC APPLICANT: jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.  
CC APPLICANT: Whitmore, Theodore E.  
CC APPLICANT: Fairish, Theresa M.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East  
CC CITY: Seattle  
CC STATE: WA  
CC COUNTRY: USA  
CC ZIP: 98102  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FastSeq for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/943.087  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/803.305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lunn, Paul G

CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEEX:  
CC INFORMATION FOR SEQ ID NO.: 58:

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CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: internal
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SO SEQUENCE 221 AA; 25235 MW; 277495 CN;

Query Match 1.6%; Score 7; DB 2; Length 221;  
Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 107 QIGPPEV 113

OY 127 QIGPPEV 133

RESULT 22  
ID US-08-943-087-56 STANDARD; PRT: 221 AA.

AC xxxxxx

1

Sequence 56, Application US/08943087

Sequence 56, Application US/08943087  
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: LOK, SI

APPLICANT: Kuo, Choon J.

APPLICANT: Jelmeberg, Anna C.

APPLICANT: Adams, Robyn L.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Farrah, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: ZymoGenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943.087

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24CI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 221 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE 221 AA; 25207 MW; 276174 CN;

Query Match 1.6%; Score 7; DB 2; Length 221;

Best Local Similarity 100.0%; Pred. No. 2.03e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 107 QIGPPEV 113

OY 127 QIGPPEV 133

RESULT 23  
ID US-08-961-264-3 STANDARD; PRT: 258 AA.

AC xxxxxx

Sequence 3, Application US/08961264

Sequence 3, Application US/08961264  
Patent No. 6025331

GENERAL INFORMATION:

APPLICANT: Moses, Marsha A.

APPLICANT: Langer, Robert S.

APPLICANT: Wiederschain, Dimitri G.

APPLICANT: Wu, Immin

APPLICANT: Sytkowski, Arthur

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: COMPRISING TROPONIN SUBUNITS, FRAGMENTS AND ANALOGS

TITLE OF INVENTION: THEREOF AND METHODS OF THEIR USE TO INHIBIT ANGIOGENESIS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,264

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/602,941

FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,452

REFERENCE/DOCKET NUMBER: 8657-021-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864/9741

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 258 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6025331e

FEATURE:

NAME/KEY: peptide

LOCATION: 1..258

OTHER INFORMATION: //label= Human Fast Skeletal Beta

OTHER INFORMATION: Troponin T

SEQUENCE 258 AA; 30596 MW; 286474 CN;

Query Match 1.6%; Score 7; DB 3; Length 258;

Best Local Similarity 100.0%; Pred. No. 2.03e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 108 RIRAEKE 114

OY 103 RIRAEKE 109

```

DE      Sequence 8, Application PC/TUS9414277
XX
CC      Sequence 8, Application PC/TUS9414277
CC      .GENERAL INFORMATION:
CC      APPLICANT: Aguet, Michel
CC      APPLICANT: Bohnl, Ruth
CC      APPLICANT: Hemml, Silvio
CC      TITLE OF INVENTION: Receptor Subunit Polypeptides
CC      NUMBER OF SEQUENCES: 8
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Genentech, Inc.
CC      STREET: 460 Point San Bruno Blvd
CC      CITY: South San Francisco
CC      STATE: California
CC      COUNTRY: USA
CC      ZIP: 94080
CC
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: patin (Genentech)
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: PCT/US94/14277
CC      FILING DATE: 07-DEC-1994
CC      CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 08/164596
CC      FILING DATE: 09-DEC-1993
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Love, Richard B.
CC      REGISTRATION NUMBER: 34,659
CC      REFERENCE/DOCKET NUMBER: 866PCT
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 415/225-5530
CC      TELEFAX: 415/952-9881
CC      TELEX: 910/371-7168
CC      INFORMATION FOR SEQ ID NO: 8:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 337 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
SO      SEQUENCE 337 AA; 37820 MW; 633736 CN;

Query Match          1.6%; Score 7; DB 4; Length 337;
Best Local Similarity 100.0%; Fred.No. 2.03e+01;
Matches       7; Conservative    0; Mismatches     0; Indels   0; Gaps   0;

DB      142 PPENIEV 148
QY      231 PPENIEV 237
        |||||
ID      US-08-943-087-20          STANDARD:      PRT.:      553 AA.
XX      xxxxxx
DT
DE      Sequence 20, Application US/08943087
XX      Sequence 20, Application US/08943087
CC      Patent No. 5945511
CC      GENERAL INFORMATION:
CC      APPLICANT: Lok, Si
CC      APPLICANT: Kho, Choon J.
CC      APPLICANT: Jelmeberg, Anna C.
CC      APPLICANT: Adams, Robyn L.
CC      APPLICANT: Whitmore, Theodore E.
CC      APPLICANT: Farran, Theresa M.
CC      TITLE OF INVENTION: CYTOKINE RECEPTOR

```

```

CC      ZIP: 98102
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Diskette
CC      COMPUTER: IBM Compatible
CC      OPERATING SYSTEM: DOS
CC      SOFTWARE: FASTSEQ for Windows Version 2.0
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/943,087
CC      FILING DATE:
CC      CLASSIFICATION: 536
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 08/803,305
CC      FILING DATE: 20-FEB-1997
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Luna, Paul G
CC      REGISTRATION NUMBER: 32,743
CC      REFERENCE/DOCKET NUMBER: 96-24C1
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: 206-442-6627
CC      TELEFAX: 206-442-6678
CC      TELEX:
CC      INFORMATION FOR SEQ ID NO: 40:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 553 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      FRAGMENT TYPE: internal
CC      SEQUENCE: 553 AA; 62533 MW; 1648042 CN;
SQ
Query Match 1.6%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 136 QIGPEV 142
YY 127 QIGPEV 133
RESULT 28
ID US-08-943-087-16 STANDARD: PRT; 553 AA.
XX
XX AC xxxxxx
XX DT
XX
XX Sequence 16, Application US/08943087
DE
XX Sequence 16, Application US/08943087
CC
CC Sequence 16, Application US/08943087
CC Patent No. 5945511
CC GENERAL INFORMATION:
CC APPLICANT: Lok, SI
CC APPLICANT: Kho, Choon J.
CC APPLICANT: Delmberg, Anna C.
CC APPLICANT: Adams, Robyn L.
CC APPLICANT: Whitmore, Theodore E.
CC APPLICANT: Farrah, Theresa M.
CC TITLE OF INVENTION: CYTOKINE RECEPTOR
CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC City: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:

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CC APPLICATION NUMBER: US/08/943,087  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/803,305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lunn, Paul G.  
CC REGISTRATION NUMBER: 32,743  
CC REFERENCE/DOCKET NUMBER: 96-24C1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEX:  
CC INFORMATION FOR SEQ ID NO: 16:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 553 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
CC SEQUENCE 553 AA; 62533 MW; 1648042 CN;  
SO  
  
Query Match 1.6%; Score 7; DB 2; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 136 QIGPPEV 142  
1111111  
QY 127 QIGPPEV 133  
  
RESULT 29  
ID US-08-943-087-22 STANDARD; PRT; 553 AA.  
XX  
AC xxxxxx  
XX  
DT  
DE Sequence 22, Application US/08943087  
XX  
CC Sequence 22, Application US/08943087  
CC Patent No. 5945511  
CC GENERAL INFORMATION:  
CC APPLICANT: Lok, Si  
CC APPLICANT: Kho, Choon J.  
CC APPLICANT: Jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.  
CC APPLICANT: Whitmore, Theodore E.  
CC APPLICANT: Fairah, Theresa M.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East  
CC CITY: Seattle  
CC STATE: WA  
CC COUNTRY: USA  
CC ZIP: 98102  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FastSeq for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/943,087  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/803,305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:

CC NAME: Lunn, Paul G.  
CC REGISTRATION NUMBER: 32,743  
CC REFERENCE/DOCKET NUMBER: 96-24C1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEX:  
CC INFORMATION FOR SEQ ID NO: 22:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 553 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
CC SEQUENCE 553 AA; 62533 MW; 1648042 CN;  
SO  
  
Query Match 1.6%; Score 7; DB 2; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 136 QIGPPEV 142  
1111111  
QY 127 QIGPPEV 133  
  
RESULT 30  
ID US-08-943-087-42 STANDARD; PRT; 553 AA.  
XX  
AC xxxxxx  
XX  
DT  
DE Sequence 42, Application US/08943087  
XX  
CC Sequence 42, Application US/08943087  
CC Patent No. 5945511  
CC GENERAL INFORMATION:  
CC APPLICANT: Lok, Si  
CC APPLICANT: Kho, Choon J.  
CC APPLICANT: Jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.  
CC APPLICANT: Whitmore, Theodore E.  
CC APPLICANT: Fairah, Theresa M.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East  
CC CITY: Seattle  
CC STATE: WA  
CC COUNTRY: USA  
CC ZIP: 98102  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FastSeq for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/943,087  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/803,305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lunn, Paul G.  
CC REGISTRATION NUMBER: 32,743  
CC REFERENCE/DOCKET NUMBER: 96-24C1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEX:

CC INFORMATION FOR SEQ ID NO: 42:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 553 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
CC SEQUENCE 553 AA; 6253 MW; 1648042 CN;

Query Match 1.68; Score 7; DB 2; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 136 QIGPPEV 142  
1111111  
QY 127 QIGPPEV 133

RESULT 31  
ID US-08-943-087-28 STANDARD; PRT; 553 AA.  
AC xxxxxx  
XX  
XX  
XX  
DE Sequence 28, Application US/08943087  
XX  
CC Sequence 28, Application US/08943087  
CC Patent No. 5945511  
CC GENERAL INFORMATION:  
CC APPLICANT: Lok, Si  
CC APPLICANT: Kho, Choon J.  
CC APPLICANT: Jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.  
CC APPLICANT: Whitmore, Theodore E.  
CC APPLICANT: Farrah, Theresa M.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East  
CC CITY: Seattle  
CC STATE: WA  
CC COUNTRY: USA  
CC ZIP: 98102  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FASTSEQ for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/943,087  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/803,305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lunn, Paul G  
CC REGISTRATION NUMBER: 32,743  
CC REFERENCE/DOCKET NUMBER: 96-24C1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEX:  
CC INFORMATION FOR SEQ ID NO: 28:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 553 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein

CC FRAGMENT TYPE: internal  
CC SEQUENCE 553 AA; 6253 MW; 1648042 CN;

Query Match 1.68; Score 7; DB 2; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 136 QIGPPEV 142  
1111111  
QY 127 QIGPPEV 133

RESULT 32  
ID US-08-943-087-30 STANDARD; PRT; 553 AA.  
AC xxxxxx  
XX  
XX  
XX  
DE Sequence 30, Application US/08943087  
XX  
CC Sequence 30, Application US/08943087  
CC Patent No. 5945511  
CC GENERAL INFORMATION:  
CC APPLICANT: Lok, Si  
CC APPLICANT: Kho, Choon J.  
CC APPLICANT: Jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.  
CC APPLICANT: Whitmore, Theodore E.  
CC APPLICANT: Farrah, Theresa M.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East  
CC CITY: Seattle  
CC STATE: WA  
CC COUNTRY: USA  
CC ZIP: 98102  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FASTSEQ for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/943,087  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/803,305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lunn, Paul G  
CC REGISTRATION NUMBER: 32,743  
CC REFERENCE/DOCKET NUMBER: 96-24C1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEX:  
CC INFORMATION FOR SEQ ID NO: 30:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 553 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
CC SEQUENCE 553 AA; 6253 MW; 1648042 CN;

Query Match 1.68; Score 7; DB 2; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



DB 136 QIGPEV 142  
111111  
QY 127 QIGPEV 133

RESULT 33  
US-08-943-087-48 STANDARD; PRT; 553 AA.

Sequence 48, Application US/08943087

Sequence 48, Application US/08943087  
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, S1

APPLICANT: Kho, Choon J.

APPLICANT: Jelmeberg, Anna C.

APPLICANT: Adams, Robyn L.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Farrah, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,087

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE 553 AA: 62533 MW; 1648042 CN;

DB 136 QIGPEV 142  
111111

QY 127 QIGPEV 133

Query Match 1.6%; Score 7; DB 2; Length 553;

Best Local Similarity 100.0%; Pred. No. 2.03e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 34  
US-08-943-087-32 STANDARD; PRT; 553 AA.

XX  
AC xxxxxx  
XX  
DT  
XX  
DE  
XX

Sequence 32, Application US/08943087

Sequence 32, Application US/08943087  
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, S1

APPLICANT: Kho, Choon J.

APPLICANT: Jelmeberg, Anna C.

APPLICANT: Adams, Robyn L.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Farrah, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,087

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE 553 AA: 62533 MW; 1648042 CN;

DB 136 QIGPEV 142  
111111

QY 127 QIGPEV 133

Query Match 1.6%; Score 7; DB 2; Length 553;

Best Local Similarity 100.0%; Pred. No. 2.03e+01;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 35  
US-08-943-087-44 STANDARD; PRT; 553 AA.

xxxxxx

Sequence 44, Application US/08943087

CC Sequence: 44, Application US/08943087  
CC Patent No. 5945511  
CC GENERAL INFORMATION:  
CC APPLICANT: Lok, Si  
CC APPLICANT: Kho, Choon J.  
CC APPLICANT: Jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.  
CC APPLICANT: Whitmore, Theodore E.  
CC APPLICANT: Fairah, Theresa M.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East  
CC CITY: Seattle  
CC STATE: WA  
CC COUNTRY: USA  
CC ZIP: 98102  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FASTSEQ for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/943,087  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/803,305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lunn, Paul G.  
CC REGISTRATION NUMBER: 32,743  
CC REFERENCE/DOCKET NUMBER: 96-24C1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEX:  
CC INFORMATION FOR SEQ ID NO: 44:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 553 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
CC SEQUENCE 553 AA: 62533 MM: 1648042 CN;  
SQ  
Query Match 1.68; Score 7; DB 2; Length 553;  
Best Local Similarity 100.08; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 136 QIGPPEV 142  
QY 127 QIGPPEV 133  
RESULT 36  
ID US-08-943-087-2 STANDARD; PRT; 553 AA.  
XX xxxxxx  
AC  
DT  
XX  
DE Sequence 2, Application US/08943087  
XX Sequence 2, Application US/08943087  
CC Patent No. 5945511  
CC GENERAL INFORMATION:  
CC APPLICANT: Lok, Si  
CC APPLICANT: Kho, Choon J.  
CC APPLICANT: Jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.

CC APPLICANT: Whitmore, Theodore E.  
CC APPLICANT: Fairah, Theresa M.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East  
CC CITY: Seattle  
CC STATE: WA  
CC COUNTRY: USA  
CC ZIP: 98102  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FASTSEQ for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/943,087  
CC FILING DATE:  
CC CLASSIFICATION: 536  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/803,305  
CC FILING DATE: 20-FEB-1997  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lunn, Paul G.  
CC REGISTRATION NUMBER: 32,743  
CC REFERENCE/DOCKET NUMBER: 96-24C1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 206-442-6627  
CC TELEFAX: 206-442-6678  
CC TELEX:  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 553 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
CC SEQUENCE 553 AA: 62533 MM: 1648042 CN;  
SQ  
Query Match 1.68; Score 7; DB 2; Length 553;  
Best Local Similarity 100.08; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 136 QIGPPEV 142  
QY 127 QIGPPEV 133  
RESULT 37  
ID US-08-943-087-18 STANDARD; PRT; 553 AA.  
XX xxxxxx  
AC  
DT  
XX  
DE Sequence 18, Application US/08943087  
XX Sequence 18, Application US/08943087  
CC Patent No. 5945511  
CC GENERAL INFORMATION:  
CC APPLICANT: Lok, Si  
CC APPLICANT: Kho, Choon J.  
CC APPLICANT: Jelmeberg, Anna C.  
CC APPLICANT: Adams, Robyn L.  
CC APPLICANT: Whitmore, Theodore E.  
CC APPLICANT: Fairah, Theresa M.  
CC TITLE OF INVENTION: CYTOKINE RECEPTOR  
CC NUMBER OF SEQUENCES: 60  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Zymogenetics, Inc.  
CC STREET: 1201 Eastlake Avenue East

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CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943,087
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: 08/803,305
CC FILING DATE: 20-FEB-1997
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Lunn, Paul G
CC REGISTRATION NUMBER: 32,743
CC REFERENCE/DOCKET NUMBER: 96-24C1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 206-442-6627
CC TELEFAX: 206-442-6678
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 46:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 553 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC FRAGMENT TYPE: Internal
CC SEQUENCE 553 AA; 62533 MW; 1648042 CN;
SQ
Query Match 1.6%; Score 7; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 136 QIGPEPV 142
|||
|||
OY 127 QIGPEPV 133
RESULT 39
ID US-08-943-087-34 STANDARD; PRT; 553 AA.
XX xxxxxx
DT
DE Sequence 34, Application US/08943087
XX
XX Patent No. 5945511
CC
CC GENERAL INFORMATION:
CC APPLICANT: Lok, SI
CC APPLICANT: Kho, Choon J.
CC APPLICANT: Jelmeberg, Anna C.
CC APPLICANT: Adams, Robyn L.
CC APPLICANT: Whitmore, Theodore E.
CC APPLICANT: Farhan, Theresa M.
CC TITLE OF INVENTION: CYTOKINE RECEPTOR
CC NUMBER OF SEQUENCES: 60
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Zymogenetics, Inc.
CC STREET: 1201 Eastlake Avenue East
CC CITY: Seattle
CC STATE: WA
CC COUNTRY: USA
CC ZIP: 98102
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/943,087
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIORITY APPLICATION DATA:

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CC APPLICATION NUMBER: 08/803,305  
 CC FILING DATE: 20-FEB-1997  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Lunn, Paul G  
 CC REGISTRATION NUMBER: 32,743  
 CC REFERENCE/DOCKET NUMBER: 96-24C1  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 206-442-6627  
 CC TELEFAX: 206-442-6678  
 CC TELEX:  
 CC INFORMATION FOR SEQ ID NO: 34:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 553 amino acids  
 CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC FRAGMENT TYPE: internal  
 CC SEQUENCE 553 AA; 6253 MW; 1648042 CN;

Query Match 1.6%; Score 7; DB 2; Length 553;  
 Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 136 QIGPPEV 142  
 11111111  
 0Y 127 QIGPPEV 133

RESULT 40  
 ID US-08-943-087-38 STANDARD; PRT; 553 AA.

xxxxxx

Sequence 38, Application US/08943087

CC Sequence 38, Application US/08943087

CC Patent No. 5945511

CC GENERAL INFORMATION:

CC APPLICANT: Lok, Si

CC APPLICANT: Kho, Choon J.

CC APPLICANT: Jelmeberg, Anna C.

CC APPLICANT: Adams, Robyn L.

CC APPLICANT: Whitmore, Theodore E.

CC APPLICANT: Parrish, Theresa M.

CC TITLE OF INVENTION: CYTOKINE RECEPTOR

CC NUMBER OF SEQUENCES: 60

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Zymogenetics, Inc.

CC STREET: 1201 Eastlake Avenue East

CC CITY: Seattle

CC STATE: WA

CC COUNTRY: USA

CC ZIP: 98102

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette

CC COMPUTER: IBM Compatible

CC OPERATING SYSTEM: DOS

CC SOFTWARE: FASTSEQ for Windows Version 2.0

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/943,087

CC FILING DATE:

CC CLASSIFICATION: 536

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/803,305

CC FILING DATE: 20-FEB-1997

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Lunn, Paul G

CC REGISTRATION NUMBER: 32,743

CC REFERENCE/DOCKET NUMBER: 96-24C1

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 206-442-6627  
 CC TELEFAX: 206-442-6678  
 CC TELEX:  
 CC INFORMATION FOR SEQ ID NO: 38:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 553 amino acids  
 CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC FRAGMENT TYPE: internal  
 CC SEQUENCE 553 AA; 6253 MW; 1648042 CN;

Query Match 1.6%; Score 7; DB 2; Length 553;  
 Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 136 QIGPPEV 142  
 11111111  
 0Y 127 QIGPPEV 133

RESULT 41  
 ID US-08-943-087-26 STANDARD; PRT; 553 AA.

xxxxxx

Sequence 26, Application US/08943087

CC Sequence 26, Application US/08943087

CC Patent No. 5945511

CC GENERAL INFORMATION:

CC APPLICANT: Lok, Si

CC APPLICANT: Kho, Choon J.

CC APPLICANT: Jelmeberg, Anna C.

CC APPLICANT: Adams, Robyn L.

CC APPLICANT: Whitmore, Theodore E.

CC APPLICANT: Parrish, Theresa M.

CC TITLE OF INVENTION: CYTOKINE RECEPTOR

CC NUMBER OF SEQUENCES: 60

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Zymogenetics, Inc.

CC STREET: 1201 Eastlake Avenue East

CC CITY: Seattle

CC STATE: WA

CC COUNTRY: USA

CC ZIP: 98102

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Diskette

CC COMPUTER: IBM Compatible

CC OPERATING SYSTEM: DOS

CC SOFTWARE: FASTSEQ for Windows Version 2.0

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/943,087

CC FILING DATE:

CC CLASSIFICATION: 536

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/803,305

CC FILING DATE: 20-FEB-1997

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Lunn, Paul G

CC REGISTRATION NUMBER: 32,743

CC REFERENCE/DOCKET NUMBER: 96-24C1

CC TELECOMMUNICATION INFORMATION:

CC TELEFAX: 206-442-6678

CC TELEX:

CC INFORMATION FOR SEQ ID NO: 26:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 553 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC FRAGMENT TYPE: internal  
SQ SEQUENCE 553 AA; 62533 MW; 1648042 CN;

Query Match 1.68; Score 7; DB 2; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 136 QIGPPEV 142  
111111  
OY 127 QIGPPEV 133

RESULT 42  
ID US-08-943-087-14 STANDARD; PRT; 553 AA.  
XX xxxxxx

Sequence 14, Application US/08943087

Sequence 14, Application US/08943087  
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Kho, Choon J.

APPLICANT: Jelmeberg, Anna C.

APPLICANT: Adams, Rodyn L.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Farrah, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,087

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE 553 AA; 62533 MW; 1648042 CN;

Query Match 1.68; Score 7; DB 2; Length 553;

Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 136 QIGPPEV 142  
111111  
OY 127 QIGPPEV 133

RESULT 43  
ID US-08-943-087-36 STANDARD; PRT; 553 AA.  
XX xxxxxx

Sequence 36, Application US/08943087

Sequence 36, Application US/08943087  
Patent No. 5945511

GENERAL INFORMATION:

APPLICANT: Lok, Si

APPLICANT: Kho, Choon J.

APPLICANT: Jelmeberg, Anna C.

APPLICANT: Adams, Rodyn L.

APPLICANT: Whitmore, Theodore E.

APPLICANT: Farrah, Theresa M.

TITLE OF INVENTION: CYTOKINE RECEPTOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics, Inc.

STREET: 1201 Eastlake Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,087

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/803,305

FILING DATE: 20-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-24C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX:

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE 553 AA; 62533 MW; 1648042 CN;

Query Match 1.68; Score 7; DB 2; Length 553;

Best Local Similarity 100.0%; Pred. No. 2.03e+01;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 136 QIGPPEV 142  
111111  
OY 127 QIGPPEV 133

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XX Sequence 2, Application US/09016000
XX
CC Sequence 2, Application US/09016000
CC Patent No. 5962232
CC GENERAL INFORMATION:
CC APPLICANT: Hillman, Jennifer L.
CC APPLICANT: Lal, Preeti
CC APPLICANT: Bandman, Olga
CC APPLICANT: Akerbloom, Ingrid E.
CC APPLICANT: Shah, Puri V
CC APPLICANT: Corley, Neil C.
CC APPLICANT: Guegler, Karl G.
CC TITLE OF INVENTION: PROTEIN KINASE MOLECULES
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Incyte Pharmaceuticals, Inc.
CC STREET: 3174 Porter Drive
CC City: Palo Alto
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FASTSEQ for Windows Version 2.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/09/016, 000
CC FILING DATE: HEREWITH
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Billings, Lucy J
CC REGISTRATION NUMBER: 36,749
CC REFERENCE/DOCKET NUMBER: PF-0465 US
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 650-855-0555
CC TELEFAX: 650-845-4166
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 688 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC IMMEDIATE SOURCE:
CC LIBRARY: HEARNOT01
CC CLONE: 307624
CC SEQUENCE 688 AA; 77471 MW; 2333783 CN;
SO
Query Match 1.6%; Score 7; DB 2; Length 688;
Best Local Similarity 100.0%; Pred.No. 2.03e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 297 AERTIE 303
OY 380 AERTIE 386

```



\*\*\*\*\*  
 W P O S E R I E  
 (TM)  
 \*\*\*\*\*

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MSearch: protein - protein database search, using Smith-Waterman algorithm  
 Run on: Mon Aug 21 10:31:57 2000; MSPar time 14.09 Seconds  
 Tabular output not generated. 958.880 Million cell updates/sec

Title: >US-09-240-675-2  
 Description: (1-436) from US09240675.pep  
 Perfect Score: 436  
 Sequence: 1 MMYVLLGATTLVAVGPMV.....KSSVSDAVCEKTRKPGNTSK 436

Scoring table: TABLE uniprottable  
 Gap 60

Searched: 85661 segs, 30989116 residues

Post-processing: Minimum Match 0%  
 Listing first 1000 summaries

Database: swiss-prot  
 1:swissprot

Statistics: Mean 3.766; Variance 0.410; scale 9.184

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	436	100.0	557	1	INRL_HUMAN INTERFERON-ALPHA/BETA	0.00e+00
2	15	3.4	560	1	INRL_SHEEP INTERFERON-ALPHA/BETA	1.71e-21
3	13	3.0	560	1	INRL_BOVIN INTERFERON-ALPHA/BETA	1.40e-15
4	11	2.5	590	1	INRL_MOUSE INTERFERON-ALPHA/BETA	5.20e-10
5	7	1.6	11	1	BRK_MSEFL MEGASCOTILANTININ (6-TNR	1.63e+00
6	7	1.6	53	1	ATP8_COTUA ATP SYNTHASE PROTEIN 8	1.63e+00
7	7	1.6	195	1	AAAT_HDVM1 DELTA ANTIGEN	1.63e+00
8	7	1.6	252	1	TRT3_COTUA TROPONIN T, FAST SKELE	1.63e+00
9	7	1.6	252	1	TRT3_HUMAN TROPONIN T, FAST SKELE	1.63e+00
10	7	1.6	258	1	TRT3_RAT TROPONIN T, FAST SKELE	1.63e+00
11	7	1.6	262	1	TRT3_CHICK TROPONIN T, FAST SKELE	1.63e+00
12	7	1.6	278	1	TRT3_RABIT TROPONIN T, FAST SKELE	1.63e+00
13	7	1.6	337	1	INGS_HUMAN INTERFERON-GAMMA RECEPTOR	1.63e+00
14	7	1.6	353	1	FIXB_RHIME INTERFERON-GAMMA RECEPTOR	1.63e+00
15	7	1.6	369	1	FIXB_RHISM INTERFERON-GAMMA RECEPTOR	1.63e+00
16	7	1.6	369	1	FIXB_AZCCA INTERFERON-GAMMA RECEPTOR	1.63e+00
17	7	1.6	369	1	FIXB_BRAJA INTERFERON-GAMMA RECEPTOR	1.63e+00
18	7	1.6	423	1	PUR6_CAEEL PROBABLE MULTIFUNCTIONAL PROTEIN	1.63e+00
19	7	1.6	423	1	PUR6_RAT PROBABLE MULTIFUNCTIONAL PROTEIN	1.63e+00
20	7	1.6	425	1	PUR6_HUMAN MULTIFUNCTIONAL PROTEIN	1.63e+00
21	7	1.6	426	1	PUR6_CHICK MULTIFUNCTIONAL PROTEIN	1.63e+00
22	7	1.6	442	1	YAL7_SYNY3 PUTATIVE AMONIDUM TRAN	1.63e+00
23	7	1.6	450	1	VGIM_HSVB GLYCOPROTEIN M.	1.63e+00

24	7	1.6	681	1	MAOC_ECOLI MAOC PROTEIN (PHENYLAC	1.63e+00
25	7	1.6	687	1	CATE_RHIME CATECHINASE	1.63e+00
26	7	1.6	698	1	UVRB_MYCTU UVRB	1.63e+00
27	7	1.6	1051	1	IT3A_HUMAN INTEGRIN ALPHA-3 PRECU	1.63e+00
28	7	1.6	1053	1	IT3A_MOUSE INTEGRIN ALPHA-3 PRECU	1.63e+00
29	7	1.6	1091	1	MSH3_MOUSE MSH3	1.63e+00
30	7	1.6	2205	1	POLG_POL2M POLG	1.63e+00
31	7	1.6	2206	1	POLG_POL3 POLG	1.63e+00
32	7	1.6	2206	1	POLG_POL3L POLG	1.63e+00
33	7	1.6	2214	1	POLG_POL2L POLG	1.63e+00
34	7	1.6	2214	1	POLG_POL2L POLG	1.63e+00
35	7	1.6	3744	1	YHP9_YEAST YHP9	1.63e+00
36	7	1.4	53	1	RUBR_PIRFU RUBR	1.07e+02
37	7	1.4	75	1	YCB1_PORPU YCB1	1.07e+02
38	6	1.4	80	1	LEFA_NPPOP LATE EXPRESSION FACTOR	1.07e+02
39	6	1.4	80	1	TYRO_FELCA TYROSINASE (EC 1.14.18	1.07e+02
40	6	1.4	84	1	DMP_BPT5 DMP PROTEIN (FRAGMENT	1.07e+02
41	6	1.4	85	1	CYCB_PLEBO CYCB	1.07e+02
42	6	1.4	86	1	CYCB_ANAVA CYCB	1.07e+02
43	6	1.4	98	1	CERA_CERCE CERASTOXYL (EC 3.4.21.	1.07e+02
44	6	1.4	105	1	NIPM_BOVIN NADH-UBIQUINONE OXIDOR	1.07e+02
45	6	1.4	110	1	YCX1_CHLPP CYTOCHROME C6 PRECURSO	1.07e+02
46	6	1.4	111	1	CYCB_ANASP CYTOCHROME C6 PRECURSO	1.07e+02
47	6	1.4	111	1	CYCB_ANASP CYTOCHROME C6 PRECURSO	1.07e+02
48	6	1.4	112	1	YPMC_ECOLI SMALL INDUCIBLE MOBILIZAT	1.07e+02
49	6	1.4	112	1	SYZT_HUMAN ONCOPROTEIN INDUCED PR	1.07e+02
50	6	1.4	115	1	OR11_MOUSE 50S RIBOSOMAL PROTEIN	1.07e+02
51	6	1.4	115	1	RL19_THEMA UREASE ACCESSORY PROTE	1.07e+02
52	6	1.4	117	1	DRER_BACPA EYES ABSENT HOMOLOG 4	1.07e+02
53	6	1.4	119	1	EY4A_CHICK EYES ABSENT HOMOLOG 4	1.07e+02
54	6	1.4	119	1	EY4A_FUGRU EYES ABSENT HOMOLOG 4	1.07e+02
55	6	1.4	119	1	EY4A_CHICK EYES ABSENT HOMOLOG 3	1.07e+02
56	6	1.4	119	1	EY4A_CHICK EYES ABSENT HOMOLOG 3	1.07e+02
57	6	1.4	125	1	CHH5_PENJP CRUSTACEAN HYPERGLYCEN	1.07e+02
58	6	1.4	127	1	TRBC_RHISM PROBABLE CONUTICAL TRAN	1.07e+02
59	6	1.4	129	1	C356_RHOA GLUTAMYL AMINOPEPTIDAS	1.07e+02
60	6	1.4	133	1	AMPE_RAT CONUTICAL TRANSFER PROT	1.07e+02
61	6	1.4	134	1	TRBC_AGT6 L-LACTATE DEHYDROGENAS	1.07e+02
62	6	1.4	134	1	LDH_LISMO L-LACTATE DEHYDROGENAS	1.07e+02
63	6	1.4	136	1	LYGE_MOUSE HYPOHETICAL 18.3 KDA	1.07e+02
64	6	1.4	137	1	Y074_MYCGE HYPOHETICAL 19.2 KDA	1.07e+02
65	6	1.4	142	1	YNER_BACSU HYPOHETICAL 17.0 KDA	1.07e+02
66	6	1.4	144	1	WAP3_PIG WAP-3 PROTEIN PRECURSO	1.07e+02
67	6	1.4	145	1	IL2_CANFA INTERLEUKIN-2 PRECURSO	1.07e+02
68	6	1.4	155	1	GRP_BOMOR GASTRIN-RELEASING PEPT	1.07e+02
69	6	1.4	156	1	Y015_BPT4 HYPOHETICAL 18.3 KDA	1.07e+02
70	6	1.4	157	1	Y015_METTH HYPOHETICAL 18.3 KDA	1.07e+02
71	6	1.4	157	1	EMPI_HUMAN EPIHETICAL MEMBRANE PR	1.07e+02
72	6	1.4	159	1	HS12_DAUCA 18.0 KDA CLASS. I HEAT	1.07e+02
73	6	1.4	161	1	HOXO_ALCEU HYDROGENASE EXPRESSION	1.07e+02
74	6	1.4	162	1	PHCA_CVACA C-PHYCOCYANIN ALPHA CH	1.07e+02
75	6	1.4	164	1	GREX_MYCLE TRANSCRIPTION ELONGATI	1.07e+02
76	6	1.4	164	1	GREX_MYCLE TRANSCRIPTION ELONGATI	1.07e+02
77	6	1.4	166	1	Y021_BPHPI HYPOHETICAL 19.2 KDA	1.07e+02
78	6	1.4	167	1	CD3D_SHEEP T-CELL SURFACE GLYCOPR	1.07e+02
79	6	1.4	177	1	YDAB_MYCBO HYPOHETICAL 19.3 KDA	1.07e+02
80	6	1.4	179	1	Y053_SYNY3 HYPOHETICAL 20.1 KDA	1.07e+02
81	6	1.4	181	1	YMD6_YEAST HYPOHETICAL 20.7 KDA	1.07e+02
82	6	1.4	186	1	GREP_BACSU GREP PROTEIN (HSP-70 C	1.07e+02
83	6	1.4	186	1	DNA_WOLSP CHROMOSOMAL REPLICATIO	1.07e+02
84	6	1.4	187	1	SPAI_PIG SODIUM/POTASSIUM ATPAS	1.07e+02
85	6	1.4	187	1	US51_YEAST U6 SNRNA-ASSOCIATED PR	1.07e+02
86	6	1.4	189	1	EXBI_HELPY PUTATIVE BIOPOLYMER TR	1.07e+02
87	6	1.4	192	1	PEP_AQUAE PEPTIDYL-TRNA HYDROLAS	1.07e+02
88	6	1.4	194	1	Y210_AQUAE HYPOHETICAL PROTEIN A	1.07e+02
89	6	1.4	194	1	RS7_ARCFU 30S RIBOSOMAL PROTEIN	1.07e+02
90	6	1.4	195	1	AAAT_HDVM2 DELTA ANTIGEN	1.07e+02
91	6	1.4	195	1	AAAT_HDVM3 DELTA ANTIGEN	1.07e+02
92	6	1.4	195	1	IBBR_OYRSA BOWMAN-BIRK TYPE BRAN	1.07e+02
93	6	1.4	195	1	RS7_SULAC 30S RIBOSOMAL PROTEIN	1.07e+02
94	6	1.4	199	1	Y186_MYCTU HYPOHETICAL 20.8 KDA	1.07e+02
95	6	1.4	199	1	R13B_YEAST 60S RIBOSOMAL PROTEIN	1.07e+02
96	6	1.4	199	1	R13A_YEAST 60S RIBOSOMAL PROTEIN	1.07e+02



97	6	1.4	201	1	OSMY_ECOLI	OSMOTICALLY INDUCIBLE	1.07e+02	170	6	1.4	317	1	FMF_BACSU	METHIONYL-TRNA FORMYL	1.07e+02
98	6	1.4	205	1	AANT_HIVMO	URACIL ANTIGEN	1.07e+02	171	6	1.4	322	1	YK02_YEAST	HYPOTHETICAL 36.6 KDA	1.07e+02
99	6	1.4	206	1	UPP_MYCPN	URACIL PHOSPHORIBOSYL	1.07e+02	172	6	1.4	322	1	YK02_YEAST	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
100	6	1.4	208	1	NO4M_MICEP	NADH-UBIQUINONE OXIDOR	1.07e+02	173	6	1.4	323	1	YK02_YEAST	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
101	6	1.4	213	1	HIX_HUMAN	HISTONE H1X	1.07e+02	174	6	1.4	323	1	YK02_YEAST	HYPOTHETICAL 35.9 KDA	1.07e+02
102	6	1.4	214	1	AANT_HDVNA	DELTA ANTIGEN	1.07e+02	175	6	1.4	324	1	HME2_MOUSE	HEPC PROTEIN (EC 3.4.-	1.07e+02
103	6	1.4	214	1	AANT_HDVNA	DELTA ANTIGEN	1.07e+02	176	6	1.4	326	1	Y168_HUMAN	HOMEOBOX PROTEIN ENGRA	1.07e+02
104	6	1.4	218	1	IM23_SCHNA	23 KDA INTEGRAL MEMBRA	1.07e+02	177	6	1.4	331	1	PELB_COLU	HYPOTHETICAL PROTEIN K	1.07e+02
105	6	1.4	218	1	IM23_SCHNA	23 KDA INTEGRAL MEMBRA	1.07e+02	178	6	1.4	331	1	PELB_COLU	PECTATE LYASE B PRECUR	1.07e+02
106	6	1.4	218	1	IM23_SCHNA	23 KDA INTEGRAL MEMBRA	1.07e+02	179	6	1.4	336	1	GLP2_EBV	GLP2 PROTEIN HOMOLOG.	1.07e+02
107	6	1.4	218	1	IM23_SCHNA	23 KDA INTEGRAL MEMBRA	1.07e+02	180	6	1.4	336	1	GLP2_EBV	GLP2 PROTEIN HOMOLOG.	1.07e+02
108	6	1.4	219	1	ATP6_ONCMA	ATP SYNTHASE T CHAIN (	1.07e+02	181	6	1.4	339	1	R1R2_DICCI	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
109	6	1.4	221	1	EPD1_ONCMA	EPENDYMIN I PRECURSOR	1.07e+02	182	6	1.4	339	1	R1R2_DICCI	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
110	6	1.4	221	1	GCHI_ECOLI	GTP CYCLOHYDROLASE I (	1.07e+02	183	6	1.4	343	1	PSB8_HUMAN	HOMEOBOX PROTEIN HOX-D	1.07e+02
111	6	1.4	221	1	EPD1_ECOLI	EPENDYMIN PRECURSOR (E	1.07e+02	184	6	1.4	346	1	TAS_ECOLI	PROSTAGN PRECURSOR (E	1.07e+02
112	6	1.4	221	1	RAN2_ARATH	GTP-BINDING NUCLEAR PR	1.07e+02	185	6	1.4	346	1	DHAS_SYNCS	ASPARTATE-SEMIALDEHYD	1.07e+02
113	6	1.4	222	1	CASB_SHEEP	BETA CASEIN PRECURSOR.	1.07e+02	186	6	1.4	348	1	TRPD_SYNCS	TRANSPANTATE PHOSPHORI	1.07e+02
114	6	1.4	222	1	CASB_SHEEP	BETA CASEIN PRECURSOR.	1.07e+02	187	6	1.4	349	1	R1R2_PLA4	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
115	6	1.4	223	1	CGL4_RABIT	HYPOTHETICAL PROTEIN M	1.07e+02	188	6	1.4	349	1	TRPD_PSELE	ANTHRANILATE PHOSPHORI	1.07e+02
116	6	1.4	223	1	CGL4_RABIT	HYPOTHETICAL PROTEIN M	1.07e+02	189	6	1.4	353	1	VP11_RDV	NONSTRUCTURAL PROTEIN	1.07e+02
117	6	1.4	223	1	ATP6_ONCMA	ATP SYNTHASE T-1MPHOCTE	1.07e+02	190	6	1.4	358	1	AROB_AERPE	3-DEHYDRODINATE SYNTH	1.07e+02
118	6	1.4	224	1	CASB_BOVIN	BETA CASEIN PRECURSOR.	1.07e+02	191	6	1.4	360	1	FIXB_AZOVI	FIXB PROTEIN.	1.07e+02
119	6	1.4	229	1	TRJ1_ECOLI	TRAJ PROTEIN.	1.07e+02	192	6	1.4	363	1	U116_VZVD	VACUOLAR ATP SYNTHASE	1.07e+02
120	6	1.4	231	1	CUT2_CAEEL	CUTICLIN 2 PRECURSOR.	1.07e+02	193	6	1.4	368	1	VATC_DICCI	VACUOLAR ATP SYNTHASE	1.07e+02
121	6	1.4	231	1	YGOQ_ECOLI	HYPOTHETICAL 24.5 KDA	1.07e+02	194	6	1.4	369	1	CYCH_BRAJA	CYCLOCHROME C-TYPE BIOL	1.07e+02
122	6	1.4	232	1	OVAX_CHICK	GENE X PROTEIN (OVALBU	1.07e+02	195	6	1.4	374	1	TR15_FUSSP	TRICHOBIENE SYNTHASE (	1.07e+02
123	6	1.4	238	1	ATP6_MYTED	ATP SYNTHASE A CHAIN (	1.07e+02	196	6	1.4	375	1	TR15_GIBSE	TRICHOBIENE SYNTHASE (	1.07e+02
124	6	1.4	239	1	R56_SCHPO	40S RIBOSOMAL PROTEIN	1.07e+02	197	6	1.4	377	1	TR15_FUSPO	TRICHOBIENE SYNTHASE (	1.07e+02
125	6	1.4	246	1	PRCA_ARCFU	PROTEASOME ALPHA SUBUN	1.07e+02	198	6	1.4	378	1	LEUK_RAT	LEUKOSTALIN PRECURSOR	1.07e+02
126	6	1.4	246	1	TRPA_RAT	TRYPSINOGEN V-A PRECUR	1.07e+02	199	6	1.4	383	1	DEMA_HUMAN	DEMATIN (ERYTHROCYTE M	1.07e+02
127	6	1.4	246	1	TRPA_RAT	TRYPSINOGEN V-A PRECUR	1.07e+02	200	6	1.4	383	1	TR15_GIBBU	TRICHOBIENE SYNTHASE (	1.07e+02
128	6	1.4	247	1	MCBF_ECOLI	MCBF PROTEIN.	1.07e+02	201	6	1.4	384	1	NK2R_MOUSE	SUBSTANCE-K RECEPTOR	1.07e+02
129	6	1.4	247	1	TRY4_RAT	TRYPSINOGEN IV PRECURS	1.07e+02	202	6	1.4	384	1	NK2R_MOUSE	SUBSTANCE-K RECEPTOR	1.07e+02
130	6	1.4	248	1	TRY1_CHICK	TRYPSINOGEN I-P3 PRECU	1.07e+02	203	6	1.4	384	1	NK2R_MOUSE	SUBSTANCE-K RECEPTOR	1.07e+02
131	6	1.4	248	1	TRY2_CHICK	TRYPSINOGEN I-P3 PRECU	1.07e+02	204	6	1.4	384	1	NK2R_MOUSE	SUBSTANCE-K RECEPTOR	1.07e+02
132	6	1.4	248	1	TRY3_CHICK	TRYPSINOGEN II-P29 PRE	1.07e+02	205	6	1.4	385	1	TR15_MYRO	TRICHOBIENE SYNTHASE (	1.07e+02
133	6	1.4	249	1	Y505_METJA	HYPOTHETICAL PROTEIN M	1.07e+02	206	6	1.4	388	1	TR15_MYRO	TRICHOBIENE SYNTHASE (	1.07e+02
134	6	1.4	250	1	Y505_METJA	HYPOTHETICAL PROTEIN M	1.07e+02	207	6	1.4	390	1	SCC1_HUMAN	SQUAMOUS CELL CARCINOM	1.07e+02
135	6	1.4	253	1	TRUA_RICPR	TRNA PSEUDOURIDINE SYN	1.07e+02	208	6	1.4	392	1	SCC2_HUMAN	SQUAMOUS CELL CARCINOM	1.07e+02
136	6	1.4	253	1	CPAD_HUMAN	CAMP-REGULATED FACTOR D	1.07e+02	209	6	1.4	392	1	NK2R_MOUSE	SUBSTANCE-K RECEPTOR	1.07e+02
137	6	1.4	256	1	M31_DICDI	CAMP-REGULATED M31 PRO	1.07e+02	210	6	1.4	394	1	RURE_ACICA	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
138	6	1.4	256	1	ATPE_HUMAN	ATP SYNTHASE B CHAIN,	1.07e+02	211	6	1.4	394	1	CC91_YEAST	CELL DIVISION CONTROL.	1.07e+02
139	6	1.4	256	1	ATPE_HUMAN	ATP SYNTHASE B CHAIN,	1.07e+02	212	6	1.4	399	1	NK2R_HUMAN	SUBSTANCE-K RECEPTOR	1.07e+02
140	6	1.4	259	1	CPAD_MOUSE	COMPLEMENT FACTOR D PR	1.07e+02	213	6	1.4	401	1	R1R2_YEAST	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
141	6	1.4	259	1	CPAD_MOUSE	COMPLEMENT FACTOR D PR	1.07e+02	214	6	1.4	401	1	R1R2_YEAST	RIBONUCLEOSIDE-DIPHOSP	1.07e+02
142	6	1.4	259	1	PPH_MYCPN	PUTATIVE PROTEIN PHOSP	1.07e+02	215	6	1.4	402	1	CHRA_ALCEU	CHROMATINE TRANSPORT PRO	1.07e+02
143	6	1.4	262	1	BCCP_SOYBN	BIOTIN CARBOXYL CARRIE	1.07e+02	216	6	1.4	403	1	NK2R_CAVPO	HOMEOBOX PROTEIN ENGRA	1.07e+02
144	6	1.4	263	1	CPAD_RAT	COMPLEMENT FACTOR D PR	1.07e+02	217	6	1.4	405	1	ASSY_BACSU	SUBSTANCE-K RECEPTOR	1.07e+02
145	6	1.4	264	1	LIPB_AERPE	PROBABLE LIPONATE-PROTE	1.07e+02	218	6	1.4	408	1	YUHB_ECOLI	HYPOTHETICAL METABOLIT	1.07e+02
146	6	1.4	266	1	APAI_CANPA	APOLIPOPROTEIN A-I PRE	1.07e+02	219	6	1.4	409	1	YMXG_BACSU	INDIAN HEDGEHOG PROTEI	1.07e+02
147	6	1.4	266	1	IF2A_METJA	PROBABLE TRANSLATION I	1.07e+02	220	6	1.4	411	1	YMXG_BACSU	INDIAN HEDGEHOG PROTEI	1.07e+02
148	6	1.4	269	1	DA80_YEAST	NITROGEN REGULATORY PR	1.07e+02	221	6	1.4	412	1	YEBD_SCHPO	HYPOTHETICAL 47.1 KDA	1.07e+02
149	6	1.4	270	1	CH14_PHAVU	ENDOCYTININASE PRA PREC	1.07e+02	222	6	1.4	413	1	CATD_HUMAN	CATHEPSIN D PRECURSOR	1.07e+02
150	6	1.4	280	1	PH32_HUMAN	PUTATIVE 32 KDA HEART	1.07e+02	223	6	1.4	413	1	PBP2_YEAST	PAR1-BINDING PROTEIN 2	1.07e+02
151	6	1.4	283	1	YB89_METJA	HYPOTHETICAL PROTEIN M	1.07e+02	224	6	1.4	419	1	PEXA_PICPA	PEROXISOME ASSEMBLY PR	1.07e+02
152	6	1.4	283	1	YB89_METJA	HYPOTHETICAL PROTEIN M	1.07e+02	225	6	1.4	421	1	YB10_ECOLI	HYPOTHETICAL 47.3 KDA	1.07e+02
153	6	1.4	285	1	TPM1_DROME	TROPOMOSIN 1, MUSCLE	1.07e+02	226	6	1.4	426	1	YB08_BACSU	HOMOSERINE DEHYDROGENA	1.07e+02
154	6	1.4	288	1	YD09_SCHPO	HYPOTHETICAL 31.5 KDA	1.07e+02	227	6	1.4	433	1	YB08_BACSU	HOMOSERINE DEHYDROGENA	1.07e+02
155	6	1.4	288	1	Y143_HAEIN	HYPOTHETICAL PROTEIN H	1.07e+02	228	6	1.4	435	1	MRP_MYCE	MRP PROTEIN HOMOLOG.	1.07e+02
156	6	1.4	292	1	YGET_ECOLI	HYPOTHETICAL 31.6 KDA	1.07e+02	229	6	1.4	437	1	KDPA_CHIPN	3-DEOXY-D-MANNO-OCTULO	1.07e+02
157	6	1.4	300	1	TRT2_RABIT	TRIPONIN T, CARDIAC MO	1.07e+02	230	6	1.4	437	1	SAHH_LEIDO	ADENOSYL-HOMOCYSTEINASE	1.07e+02
158	6	1.4	302	1	VG15_BPPH8	REPLICATION PROTEIN 15	1.07e+02	231	6	1.4	437	1	HFE2_HAEIN	MINOR FIBRILAL SUBUNIT	1.07e+02
159	6	1.4	302	1	CITG_KLEPN	CITG PROTEIN.	1.07e+02	232	6	1.4	438	1	ER24_YEAST	C-14 STEROL REDUCTASE	1.07e+02
160	6	1.4	303	1	CD38_RAT	ADP-RIBOSYL CYCLASE 1	1.07e+02	233	6	1.4	443	1	COX3_HUMAN	PROTEINOME IX FARNESYL	1.07e+02
161	6	1.4	304	1	CD38_MOUSE	VOLTAGE-GATED POTASSIUM	1.07e+02	234	6	1.4	443	1	ERAH_HUMAN	GTP-BINDING PROTEIN ER	1.07e+02
162	6	1.4	304	1	CD38_MOUSE	VOLTAGE-GATED POTASSIUM	1.07e+02	235	6	1.4	449	1	PSN2_XETJA	PRESENTIN BETA.	1.07e+02
163	6	1.4	308	1	Y325_METJA	HYPOTHETICAL PROTEIN M	1.07e+02	236	6	1.4	450	1	DNA1_MYCA	CHROMOSOMAL REPLICATIO	1.07e+02
164	6	1.4	308	1	AMID_STRNA	OLIGOPEPTIDE-TRANSPORT	1.07e+02	237	6	1.4	454	1	YU06_CAEEL	PUTATIVE SERINE CARBOX	1.07e+02
165	6	1.4	312	1	CC2D_ANTMA	CELL DIVISION CONTROL.	1.07e+02	238	6	1.4	458	1	MSRE_MOUSE	MACROPHAGE SCAVENGER R	1.07e+02
166	6	1.4	313	1	Y058_YEAST	HYPOTHETICAL 35.0 KDA	1.07e+02	239	6	1.4	459	1	ND4M_STICA	NADH-UBIQUINONE OXIDOR	1.07e+02
167	6	1.4	316	1	CORA_SALTY	MAGNESIUM AND COBAL T	1.07e+02	240	6	1.4	459	1	ND4M_EFICA	NADH-UBIQUINONE OXIDOR	1.07e+02
168	6	1.4	316	1	VP23_VZVD	PROBABLE CAPSID PROTEI	1.07e+02	241	6	1.4	459	1	ND4M_MOUSE	NADH-UBIQUINONE OXIDOR	1.07e+02
169	6	1.4	316	1	CORA_ECOLI	MAGNESIUM AND COBAL T	1.07e+02	242	6	1.4	459	1	D1D1_PSEPU	D1HYDROLIPONAMIDE DEHYD	1.07e+02

243	6	1.4	462	1	MUTL_CLOTT	MUTL PROTEIN	1.07e+02	316	6	1.4	574	1	CO9_ONCAY	COMPLEMENT COMPONENT C	1.07e+02
244	6	1.4	463	1	ZABA_SCHRO	PROTEIN PHOSPHATASE PP	1.07e+02	317	6	1.4	580	1	STCD_RHME	STACHYDRINE UTILIZATIO	1.07e+02
245	6	1.4	473	1	GONB_NEOPA	ENDOGLUCANASE B PRECUR	1.07e+02	318	6	1.4	584	1	LEU1_SCHPO	PROBABLE 2-ISOPROPYLMA	1.07e+02
246	6	1.4	473	1	ENG4_YEAST	C-24(28) STEROL REDUCT	1.07e+02	319	6	1.4	589	1	STEV_CANAL	SERINE/THREONINE PROTE	1.07e+02
247	6	1.4	474	1	NU04M_DIDMA	NADH-UBIQUINONE OXIDOR	1.07e+02	320	6	1.4	591	1	VG01_VACCV	PROTEIN G1	1.07e+02
248	6	1.4	474	1	DLDD_HALVO	DIHYDROLIPOAMIDE DEHYD	1.07e+02	321	6	1.4	591	1	VG01_VACCV	PROTEIN G1	1.07e+02
249	6	1.4	476	1	YCAM_ECOLI	HYPOHETICAL 52.5 KDA	1.07e+02	322	6	1.4	591	1	VG01_VACCV	PROTEIN G1	1.07e+02
250	6	1.4	476	1	NIFD_SYNP8	NITROGENASE MOLIBDENUM	1.07e+02	323	6	1.4	591	1	VG01_VACCV	PROTEIN G1	1.07e+02
251	6	1.4	478	1	ATPB_AOUPY	ATP SYNTHASE BETA CHAI	1.07e+02	324	6	1.4	594	1	VG01_VACCV	PROTEIN G1	1.07e+02
252	6	1.4	478	1	ATPB_AOUPY	ATP SYNTHASE BETA CHAI	1.07e+02	325	6	1.4	594	1	VG01_VACCV	PROTEIN G1	1.07e+02
253	6	1.4	481	1	LMRA_STRLN	LINCAMYCIN RESISTANCE	1.07e+02	326	6	1.4	599	1	MTGS_YEAST	METHYLENTERAHDROFOL	1.07e+02
254	6	1.4	482	1	CATA_BACSU	VEGETATIVE CATALASE (E	1.07e+02	327	6	1.4	602	1	MTGS_YEAST	METHYLENTERAHDROFOL	1.07e+02
255	6	1.4	482	1	TISD_HUMAN	TISID PROTEIN (BUTYRA	1.07e+02	328	6	1.4	602	1	MTGS_YEAST	METHYLENTERAHDROFOL	1.07e+02
256	6	1.4	483	1	TRKH_ECOLI	TRK STYED POTASSIU U	1.07e+02	329	6	1.4	606	1	MTGS_YEAST	METHYLENTERAHDROFOL	1.07e+02
257	6	1.4	484	1	QAR2_LOCM1	POTASSIUM TYRAMINE RECE	1.07e+02	330	6	1.4	615	1	SPB4_YEAST	SODIUM- AND CHLORIDE-D	1.07e+02
258	6	1.4	484	1	QAR2_LOCM1	POTASSIUM TYRAMINE RECE	1.07e+02	331	6	1.4	615	1	SPB4_YEAST	SODIUM- AND CHLORIDE-D	1.07e+02
259	6	1.4	486	1	RBL1_RHOSH	RIBULOSE BIPHOSPHATE	1.07e+02	332	6	1.4	616	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
260	6	1.4	486	1	RBL1_RHOSH	RIBULOSE BIPHOSPHATE	1.07e+02	333	6	1.4	616	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
261	6	1.4	486	1	RBL1_RHOSH	RIBULOSE BIPHOSPHATE	1.07e+02	334	6	1.4	621	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
262	6	1.4	486	1	RBL1_RHOSH	RIBULOSE BIPHOSPHATE	1.07e+02	335	6	1.4	626	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
263	6	1.4	487	1	RK75_MYCTU	HYPOHETICAL 51.6 KDA	1.07e+02	336	6	1.4	627	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
264	6	1.4	488	1	RBL1_XANPL	NITROGENASE MOLIBDENUM	1.07e+02	337	6	1.4	627	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
265	6	1.4	489	1	NIFD_THIFE	NITROGENASE MOLIBDENUM	1.07e+02	338	6	1.4	627	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
266	6	1.4	490	1	YF86_METUA	HYPOHETICAL 70.9 KDA	1.07e+02	339	6	1.4	629	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
267	6	1.4	491	1	YF86_METUA	HYPOHETICAL 70.9 KDA	1.07e+02	340	6	1.4	632	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
268	6	1.4	492	1	CPA1_RAT	CYCLOCHROME P450 2A1 (E	1.07e+02	341	6	1.4	638	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
269	6	1.4	493	1	CPA9_MESAU	CYCLOCHROME P450 2A9 (E	1.07e+02	342	6	1.4	638	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
270	6	1.4	494	1	LIPH_RAT	TRIACYLGLYCEROL LIPASE	1.07e+02	343	6	1.4	639	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
271	6	1.4	495	1	CIK1_MOUSE	VOLTAGE-GATED POTASSIU	1.07e+02	344	6	1.4	639	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
272	6	1.4	495	1	CIK1_MOUSE	VOLTAGE-GATED POTASSIU	1.07e+02	345	6	1.4	639	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
273	6	1.4	495	1	CIK1_MOUSE	VOLTAGE-GATED POTASSIU	1.07e+02	346	6	1.4	642	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
274	6	1.4	504	1	SKY2_ECOLI	LYSIL-TRNA SYNTHETASE,	1.07e+02	347	6	1.4	644	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
275	6	1.4	504	1	SKY2_ECOLI	LYSIL-TRNA SYNTHETASE,	1.07e+02	348	6	1.4	644	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
276	6	1.4	507	1	KROS_CHICK	TROPOMYOSIN 1, FUSION	1.07e+02	349	6	1.4	644	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
277	6	1.4	508	1	Y020_HUMAN	HYPOHETICAL 58.1 KDA	1.07e+02	350	6	1.4	651	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
278	6	1.4	508	1	MURE_BORBU	UDP-N-ACETYLURACMOTIL	1.07e+02	351	6	1.4	652	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
279	6	1.4	510	1	YF86_METUA	HYPOHETICAL 70.9 KDA	1.07e+02	352	6	1.4	653	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
280	6	1.4	514	1	YF86_METUA	HYPOHETICAL 70.9 KDA	1.07e+02	353	6	1.4	656	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
281	6	1.4	515	1	SIR2_CANAL	REGULATORY PROTEIN SIR	1.07e+02	354	6	1.4	656	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
282	6	1.4	518	1	TPM4_DROME	TROPOMYOSIN 1, FUSION	1.07e+02	355	6	1.4	656	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
283	6	1.4	520	1	ITSN_HUMAN	INTERSECTIN (SH3 DOMAI	1.07e+02	356	6	1.4	657	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
284	6	1.4	522	1	YGF6_YEAST	HYPOHETICAL 58.1 KDA	1.07e+02	357	6	1.4	657	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
285	6	1.4	529	1	TYRO_HUMAN	TYROSINASE PRECURSOR	1.07e+02	358	6	1.4	660	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
286	6	1.4	530	1	TRPG_SALTY	ANTHRANILATE SYNTHASE	1.07e+02	359	6	1.4	661	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
287	6	1.4	530	1	TRPG_SALTY	ANTHRANILATE SYNTHASE	1.07e+02	360	6	1.4	664	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
288	6	1.4	532	1	TYRO_MOUSE	TYROSINASE PRECURSOR	1.07e+02	361	6	1.4	667	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
289	6	1.4	533	1	TYRO_MOUSE	TYROSINASE PRECURSOR	1.07e+02	362	6	1.4	667	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
290	6	1.4	534	1	TYR1_AMBME	5-6-DIHYDROXYINDOLE-2-	1.07e+02	363	6	1.4	667	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
291	6	1.4	535	1	SSDH_HUMAN	SUCCINATE SEMIALDEHYDE	1.07e+02	364	6	1.4	670	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
292	6	1.4	536	1	DTT1_YEAST	SPORE WALL MATURATION	1.07e+02	365	6	1.4	681	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
293	6	1.4	537	1	MYPH_CHICK	MYOSIN-BINDING PROTEIN	1.07e+02	366	6	1.4	683	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
294	6	1.4	538	1	EYAZ2_HUMAN	EYES ABSENT HOMOLOG 2	1.07e+02	367	6	1.4	684	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
295	6	1.4	540	1	TYRO_ORFLA	TYROSINASE PRECURSOR	1.07e+02	368	6	1.4	686	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
296	6	1.4	542	1	DAGA_ALPHA	NA(+)-LINKED D-ALANINE	1.07e+02	369	6	1.4	686	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
297	6	1.4	545	1	ICAI_RAT	INTERCELLULAR ADHESION	1.07e+02	370	6	1.4	687	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
298	6	1.4	547	1	IF37_MOUSE	EUKARYOTIC TRANSLATION	1.07e+02	371	6	1.4	690	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
299	6	1.4	548	1	IF37_MOUSE	EUKARYOTIC TRANSLATION	1.07e+02	372	6	1.4	693	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
300	6	1.4	548	1	IF37_MOUSE	EUKARYOTIC TRANSLATION	1.07e+02	373	6	1.4	695	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
301	6	1.4	551	1	REFR_SPKKA	RIPAMPICIN RESISTANCE	1.07e+02	374	6	1.4	695	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
302	6	1.4	551	1	REFR_SPKKA	RIPAMPICIN RESISTANCE	1.07e+02	375	6	1.4	696	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
303	6	1.4	551	1	REFR_SPKKA	RIPAMPICIN RESISTANCE	1.07e+02	376	6	1.4	697	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
304	6	1.4	551	1	REFR_SPKKA	RIPAMPICIN RESISTANCE	1.07e+02	377	6	1.4	699	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
305	6	1.4	553	1	MGPS2_YEAST	METHYL-ACCEPTING CHEMO	1.07e+02	378	6	1.4	702	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
306	6	1.4	554	1	MGPS2_YEAST	METHYL-ACCEPTING CHEMO	1.07e+02	379	6	1.4	710	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
307	6	1.4	555	1	DCS3_GOSAR	(+)-DETR-CADINENE SYN	1.07e+02	380	6	1.4	716	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
308	6	1.4	557	1	HLVB_SERMA	HEMOXYSTIN ACTIVATOR PR	1.07e+02	381	6	1.4	724	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
309	6	1.4	559	1	UROT_MOUSE	TISSUE PLASMINOGEN ACT	1.07e+02	382	6	1.4	727	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
310	6	1.4	559	1	UROT_MOUSE	TISSUE PLASMINOGEN ACT	1.07e+02	383	6	1.4	740	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
311	6	1.4	564	1	HCM1_YEAST	HCM1 PROTEIN	1.07e+02	384	6	1.4	742	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
312	6	1.4	566	1	UROT_BOVIN	TISSUE PLASMINOGEN ACT	1.07e+02	385	6	1.4	743	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
313	6	1.4	568	1	G6P1_CLAMI	GLUCOSE-6-PHOSPHATE 1	1.07e+02	386	6	1.4	746	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
314	6	1.4	572	1	U125_ILVT	64.1 KDA VITON PROTEI	1.07e+02	387	6	1.4	746	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02
315	6	1.4	573	1	EYAZ3_HUMAN	EYES ABSENT HOMOLOG 3	1.07e+02	388	6	1.4	746	1	YED8_SCHPO	HYPOHETICAL 70.4 KDA	1.07e+02

389	6	1.4	747	1	CIC4_RAT	CHLORIDE CHANNEL, PROTE	1.07e+02	462	6	1.4	1205	1	NCCL_MOUSE	BUNMETANIDE-SENSITIVE S	1.07e+02
390	6	1.4	747	1	VTBR_VZVD	PROBABLE DNA PACKAGING	1.07e+02	463	6	1.4	1209	1	DNBI_HSVB	MAJOR DNA-BINDING PROT	1.07e+02
391	6	1.4	747	1	CIC4_MOUSE	CHLORIDE CHANNEL, PROTE	1.07e+02	464	6	1.4	1212	1	NCCL_HUMAN	BUNMETANIDE-SENSITIVE S	1.07e+02
392	6	1.4	760	1	CIC4_HUMAN	CHLORIDE CHANNEL, PROTE	1.07e+02	465	6	1.4	1275	1	TRF_DROME	TRANSIENT-RECEPTOR-POT	1.07e+02
393	6	1.4	762	1	TRPG_NEUCR	ANTHRANILATE SYNTHASE	1.07e+02	466	6	1.4	1315	1	CAIH_MOUSE	COLLAGEN ALPHA 1(XVII)	1.07e+02
394	6	1.4	763	1	IF39_YEAST	EUKARYOTIC TRANSLATION	1.07e+02	467	6	1.4	1325	1	YAB6_SCHRO	HYPOTHETICAL 145.8 KDA	1.07e+02
395	6	1.4	766	1	EVA_DROME	DEVELOPMENTAL PROTEIN	1.07e+02	468	6	1.4	1332	1	XKDO_SCHRO	PHASE-LIKE ELEMENT PBS	1.07e+02
396	6	1.4	768	1	TRPG_COCHIE	ANTHRANILATE SYNTHASE	1.07e+02	469	6	1.4	1358	1	SIR4_YEAST	MITOGEN-ACTIVATED PROT	1.07e+02
397	6	1.4	795	1	P5CS_MOUSE	DELTA 1-PYRROLINE-5-C	1.07e+02	470	6	1.4	1374	1	M3K5_HUMAN	REGULATORY PROTEIN SIR	1.07e+02
398	6	1.4	795	1	AFSK_STRGR	SERINE/THREONINE PROTE	1.07e+02	471	6	1.4	1379	1	M3K5_MOUSE	MITOGEN-ACTIVATED PROT	1.07e+02
399	6	1.4	807	1	AFSK_STRGR	SERINE/THREONINE PROTE	1.07e+02	472	6	1.4	1391	1	M157_YEAST	MITOGEN-ACTIVATED PROT	1.07e+02
400	6	1.4	814	1	POL_IPMAT	PROBABLE POLYPROPONE	1.07e+02	473	6	1.4	1429	1	L112_CAEEL	LIN-12 PROTEIN PRECURS	1.07e+02
401	6	1.4	817	1	YGBL_YEAST	HYPOTHETICAL 95.4 KDA	1.07e+02	474	6	1.4	1444	1	ADP1_MYCG	ADHESIN P1 PRECURSOR (	1.07e+02
402	6	1.4	830	1	YGBL_HSV62	GLYCOPROTEIN B PRECURS	1.07e+02	475	6	1.4	1473	1	TOP2_ARATH	DNA TOPOISOMERASE II (	1.07e+02
403	6	1.4	830	1	YGBL_HSV60	GLYCOPROTEIN B PRECURS	1.07e+02	476	6	1.4	1495	1	A2MG_MOUSE	ALPHA-2-MACROGLOBULIN	1.07e+02
404	6	1.4	830	1	YGBL_HSV66	GLYCOPROTEIN B PRECURS	1.07e+02	477	6	1.4	1497	1	TRR2_CAEEL	SEX-DETERMINING TRANSF	1.07e+02
405	6	1.4	830	1	PRN2_MYXXA	SERINE/THREONINE-PROTE	1.07e+02	478	6	1.4	1548	1	MOR_LEITR	MULTIDRUG RESISTANCE P	1.07e+02
406	6	1.4	831	1	IF2_RICPR	TRANSLATION INITIATION	1.07e+02	479	6	1.4	1589	1	CC25_YEAST	CELL DIVISION CONTROL	1.07e+02
407	6	1.4	831	1	SAS3_YEAST	SAS3 PROTEIN.	1.07e+02	480	6	1.4	1596	1	G113_HUMAN	ZINC FINGER PROTEIN GL	1.07e+02
408	6	1.4	839	1	YDDB_HAEIN	HYPOTHETICAL PROTEIN H	1.07e+02	481	6	1.4	1678	1	CLH_DROME	CLATHRIN HEAVY CHAIN.	1.07e+02
409	6	1.4	845	1	Y4FA_RHISN	PROBABLE CHEMORECEPT	1.07e+02	482	6	1.4	1738	1	CO4_MOUSE	COMPLEMENT C4 PRECURSO	1.07e+02
410	6	1.4	859	1	PM52_MOUSE	PM51 PROTEIN HOMOLOG 2	1.07e+02	483	6	1.4	1745	1	ZOI_MOUSE	TIGHT JUNCTION PROTEIN	1.07e+02
411	6	1.4	868	1	MCN2_YEAST	MINICHROMOSOME MAINTEN	1.07e+02	484	6	1.4	1763	1	POLN_PCE9	NON-STRUCTURAL POLYPRO	1.07e+02
412	6	1.4	869	1	YD95_YEAST	HYPOTHETICAL 98.7 KDA	1.07e+02	485	6	1.4	2139	1	CRB_DROME	CROMBS PROTEIN PRECURS	1.07e+02
413	6	1.4	872	1	ADHE_GLOAB	ALDEHYDE-ALCOHOL DEHID	1.07e+02	486	6	1.4	2292	1	POLG_EMCVB	GENOME POLYPROTEIN (CO	1.07e+02
414	6	1.4	877	1	DPOL_LACLC	DNA POLYMERASE 1 (EC 2	1.07e+02	487	6	1.4	2292	1	POLG_EMCVB	GENOME POLYPROTEIN (CO	1.07e+02
415	6	1.4	885	1	AR36_SCHPO	ARG31 PROTEIN PRECURSO	1.07e+02	488	6	1.4	2366	1	TOXB_CLODI	TOXIN B.	1.07e+02
416	6	1.4	887	1	YAV5_SCHPO	PROBABLE ATP-DEPENDENT	1.07e+02	489	6	1.4	2524	1	NOTC_XENIA	NEUROGENIC LOCUS NOTCH	1.07e+02
417	6	1.4	892	1	IF2_CHLTR	TRANSLATION INITIATION	1.07e+02	490	6	1.4	2663	1	CENE_HUMAN	CENTROMERIC PROTEIN E	1.07e+02
418	6	1.4	909	1	CT1A_FUSSO	CUTINASE TRANSCRIPTION	1.07e+02	491	6	1.4	3411	1	POLG_YEY1	GENOME POLYPROTEIN (CO	1.07e+02
419	6	1.4	909	1	MC2_YEAST	MC2 PROTEIN.	1.07e+02	492	6	1.4	3411	1	POLG_YEY2	GENOME POLYPROTEIN (CO	1.07e+02
420	6	1.4	919	1	GLK3_RAT	GLUTAMATE RECEPTOR, IO	1.07e+02	493	6	1.4	3491	1	ERY1_SACER	ERYTHRONOLIDE SYNTHASE	1.07e+02
421	6	1.4	919	1	GLK3_HUMAN	GLUTAMATE RECEPTOR, IO	1.07e+02	494	6	1.4	3672	1	LM2_CAEEL	LAMININ-LIKE PROTEIN K	1.07e+02
422	6	1.4	919	1	EXL3_HUMAN	EXOSTOSIN-LIKE 3 (PUTA	1.07e+02	495	6	1.4	3898	1	POLG_HCVB	GENOME POLYPROTEIN.	1.07e+02
423	6	1.4	922	1	LCN2_LACLA	LACTICIN 481/LACTOCOCC	1.07e+02	496	6	1.4	4036	1	RRPL_DUGCV	RNA-DIRECTED RNA POLYM	1.07e+02
424	6	1.4	927	1	B3AT_CHICK	BAND 3 ANION TRANSPORT	1.07e+02	497	6	1.4	4092	1	DYHC_YEAST	DYSCIN HEAVY CHAIN, CY	1.07e+02
425	6	1.4	927	1	B3AT_RAT	BAND 3 ANION EXCHANGE	1.07e+02	498	6	1.4	4568	1	DYHC_CAEEL	DYSCIN HEAVY CHAIN, CY	1.07e+02
426	6	1.4	929	1	B3AT_MOUSE	BAND 3 ANION EXCHANGE	1.07e+02	499	6	1.4	4969	1	RYNC_RABIT	RYANODINE RECEPTOR, CA	1.07e+02
427	6	1.4	932	1	SECA_SYNY3	PREPROTEIN TRANSLOCASE	1.07e+02	500	6	1.4	5179	1	MC2_HUMAN	MUCIN 2 PRECURSOR (INT	1.07e+02
428	6	1.4	932	1	HIRL_SCHPO	HISTONE TRANSCRIPTION	1.07e+02	501	6	1.4	55	1	YP18_CLOHE	MUCIN 2 PRECURSOR (INT	1.07e+02
429	6	1.4	941	1	MSH1_SCHPO	MUTS. PROTEIN HOMOLOG 1	1.07e+02	502	6	1.4	56	1	YOR7_LEYVI	HYPOTHETICAL 6.5 KDA P	1.07e+02
430	6	1.4	942	1	AMPN_MANSE	AMINOPEPTIDASE N (EC 3	1.07e+02	503	6	1.4	62	1	YVLP_MYCRA	HYPOTHETICAL 6.5 KDA P	1.07e+02
431	6	1.4	944	1	V335_YEAST	VACUOLAR PROTEIN SORTI	1.07e+02	504	6	1.4	67	1	TRPF_METO	HYPOTHETICAL PROTEIN A	1.07e+02
432	6	1.4	953	1	YC07_YEAST	HYPOTHETICAL 107.9 KDA	1.07e+02	505	6	1.4	72	1	YHEU_ECOLI	HYPOTHETICAL 8.5 KDA P	1.07e+02
433	6	1.4	956	1	GLK4_HUMAN	GLUTAMATE RECEPTOR, IO	1.07e+02	506	6	1.4	72	1	YF77_HAEIN	HYPOTHETICAL 8.9 KDA P	1.07e+02
434	6	1.4	956	1	GLK4_RAT	GLUTAMATE RECEPTOR, IO	1.07e+02	507	6	1.4	73	1	YOR6_LEYVI	HYPOTHETICAL 8.9 KDA P	1.07e+02
435	6	1.4	984	1	KBP1_CHICK	NUCLEAR FACTOR NF-KAPB	1.07e+02	508	6	1.4	73	1	YOR6_LEYVI	HYPOTHETICAL 8.9 KDA P	1.07e+02
436	6	1.4	985	1	ENV_ROMAY	ENV POLYPROTEIN (COAT	1.07e+02	509	6	1.4	74	1	YMOG_SALTY	HYPOTHETICAL PROTEIN A	1.07e+02
437	6	1.4	992	1	EBN6_EBV	EBNA-6 NUCLEAR PROTEIN	1.07e+02	510	6	1.4	78	1	YPOK_ECOLI	HYPOTHETICAL 7.7 KDA P	1.07e+02
438	6	1.4	1002	1	MMUA_MYCTU	PUTATIVE MEMBRANE PROT	1.07e+02	511	6	1.4	84	1	YV77_YEAST	HYPOTHETICAL 9.7 KDA P	1.07e+02
439	6	1.4	1005	1	MMUA_DICDI	LYSOSOMAL ALPHAN-MANNOS	1.07e+02	512	6	1.4	87	1	YVNC_ECOLI	HYPOTHETICAL 11.2 KDA	1.07e+02
440	6	1.4	1008	1	MMUA_MYCLE	PUTATIVE MEMBRANE PROT	1.07e+02	513	6	1.4	87	1	YVNC_ECOLI	HYPOTHETICAL 11.2 KDA	1.07e+02
441	6	1.4	1015	1	DNM3_MOUSE	DNA LIGASE-III (EC 6.5	1.07e+02	514	6	1.4	93	1	YVAL_RHISP	INSERTION ELEMENT ISR1	1.07e+02
442	6	1.4	1025	1	SLAP_CAUCR	S-LAYER PROTEIN (PARAC	1.07e+02	515	6	1.4	95	1	YV12_CLOHE	HYPOTHETICAL 10.7 KDA	1.07e+02
443	6	1.4	1043	1	EF3A_YEAST	ELONGATION FACTOR 3A (	1.07e+02	516	6	1.4	97	1	YHBY_ECOLI	HYPOTHETICAL 10.8 KDA	1.07e+02
444	6	1.4	1043	1	EF3B_YEAST	ELONGATION FACTOR 3B (	1.07e+02	517	6	1.4	102	1	YH82_ECOLI	INSERTION ELEMENTS-IS1	1.07e+02
445	6	1.4	1049	1	EF3_CANAL	ELONGATION FACTOR 3 (E	1.07e+02	518	6	1.4	104	1	YV04_YEAST	HYPOTHETICAL 11.7 KDA	1.07e+02
446	6	1.4	1051	1	ITV3_CRISP	INTEGRIN ALPHA-3 PRECU	1.07e+02	519	6	1.4	107	1	YV65_MYCTU	HYPOTHETICAL 13.0 KDA	1.07e+02
447	6	1.4	1053	1	RROC_BROTH	DNA-DIRECTED RNA POLYM	1.07e+02	520	6	1.4	113	1	YKRS_CAEEL	HYPOTHETICAL 11.3 KDA	1.07e+02
448	6	1.4	1056	1	MUC5_HUMAN	TRACHEOBRONCHIAL MUCIN	1.07e+02	521	6	1.4	114	1	YVCA_YEREN	HYPOTHETICAL 13.1 KDA	1.07e+02
449	6	1.4	1070	1	RPOB_TOBAC	DNA-DIRECTED RNA POLYM	1.07e+02	522	6	1.4	114	1	YV11_METUA	HYPOTHETICAL PROTEIN M	1.07e+02
450	6	1.4	1072	1	CARB_ECOLI	CARBAMOYL-PHOSPHATE SY	1.07e+02	523	6	1.4	115	1	YVXA_BACSU	HYPOTHETICAL 13.0 KDA	1.07e+02
451	6	1.4	1073	1	ITAB_MOUSE	INTEGRIN ALPHA-6 PRECU	1.07e+02	524	6	1.4	116	1	YV92_YEAST	HYPOTHETICAL 13.4 KDA	1.07e+02
452	6	1.4	1074	1	CARB_SALTY	CARBAMOYL-PHOSPHATE SY	1.07e+02	525	6	1.4	119	1	YV05_YEAST	HYPOTHETICAL 13.9 KDA	1.07e+02
453	6	1.4	1076	1	HSEB_CAVPO	HEAT-STABLE ENTEROTOXIN	1.07e+02	526	6	1.4	120	1	YVBI_ECOLI	HYPOTHETICAL 13.9 KDA	1.07e+02
454	6	1.4	1081	1	PDR6_YEAST	PILOTROPIC DRUG RESIST	1.07e+02	527	6	1.4	120	1	YH88_YEAST	HYPOTHETICAL 14.0 KDA	1.07e+02
455	6	1.4	1087	1	XYNX_CLODM	EXOGLUCANASE XYNA PREC	1.07e+02	528	6	1.4	122	1	YH88_YEAST	VERY HYPOTHETICAL 14.2	1.07e+02
456	6	1.4	1118	1	YPT4_CAEEL	HYPOTHETICAL 127.3 KDA	1.07e+02	529	6	1.4	123	1	YOD9_CAEEL	HYPOTHETICAL 14.8 KDA	1.07e+02
457	6	1.4	1132	1	JAK2_RAT	TYROSINE-PROTEIN KINAS	1.07e+02	530	6	1.4	123	1	YOFB_HAEIN	HYPOTHETICAL 15.0 KDA	1.07e+02
458	6	1.4	1132	1	JAK2_RAT	TYROSINE-PROTEIN KINAS	1.07e+02	531	6	1.4	125	1	YMB3_YEAST	HYPOTHETICAL 15.0 KDA	1.07e+02
459	6	1.4	1141	1	MEM2_CAEEL	MEMBRANE-ASSOCIATED PR	1.07e+02	532	6	1.4	125	1	YNL6_CAEEL	HYPOTHETICAL 13.9 KDA	1.07e+02
460	6	1.4	1175	1	PTNF_RAT	PROTEIN-TYROSINE PHOSP	1.07e+02	533	6	1.4	126	1	YNL6_CAEEL	HYPOTHETICAL 14.4 KDA	1.07e+02
461	6	1.4	1176	1	PTNF_MOUSE	PROTEIN-TYROSINE PHOSP	1.07e+02	534	6	1.4	127	1	YVAA_ECOLI	HYPOTHETICAL 14.4 KDA	1.07e+02

535	5	1.1	129	1	YE02_YEAST	HYPOTHETICAL 14.4 KDA	3.04e+03	608	5	1.1	242	1	YURK_BACSU	HYPOTHETICAL TRANSRIP	3.04e+03
536	5	1.1	129	1	YOFX_BACSU	HYPOTHETICAL 13.9 KDA	3.04e+03	609	5	1.1	245	1	YOD1_CAEEL	HYPOTHETICAL 28.3 KDA	3.04e+03
537	5	1.1	132	1	YXEC_BACSU	HYPOTHETICAL 15.7 KDA	3.04e+03	610	5	1.1	246	1	YP73_MCTU	HYPOTHETICAL 26.2 KDA	3.04e+03
538	5	1.1	134	1	YORD_TV1	HYPOTHETICAL 15.4 KDA	3.04e+03	611	5	1.1	248	1	YINL_LISMO	HYPOTHETICAL OXIDOREDU	3.04e+03
539	5	1.1	135	1	YN82_YEAST	HYPOTHETICAL 14.7 KDA	3.04e+03	612	5	1.1	248	1	YNHD_ECOLI	PROBABLE ATP-DEPENDENT	3.04e+03
540	5	1.1	135	1	YI04_METJA	HYPOTHETICAL PROTEIN M	3.04e+03	613	5	1.1	250	1	YMI9_MCTU	HYPOTHETICAL 26.9 KDA	3.04e+03
541	5	1.1	138	1	YNCG_CAEEL	HYPOTHETICAL 15.3 KDA	3.04e+03	614	5	1.1	259	1	YG31_YEAST	HYPOTHETICAL 27.2 KDA	3.04e+03
542	5	1.1	143	1	YORH_TV1	HYPOTHETICAL 16.6 KDA	3.04e+03	615	5	1.1	260	1	YOGK_BACSU	HYPOTHETICAL ABC TRANS	3.04e+03
543	5	1.1	143	1	YP99_MCTU	HYPOTHETICAL 15.0 KDA	3.04e+03	616	5	1.1	262	1	YXBG_BACSU	HYPOTHETICAL OXIDOREDU	3.04e+03
544	5	1.1	145	1	YME6_YEAST	HYPOTHETICAL 16.9 KDA	3.04e+03	617	5	1.1	262	1	YKVA_CAEEL	HYPOTHETICAL 30.0 KDA	3.04e+03
545	5	1.1	145	1	YJEC_SCHPO	HYPOTHETICAL 16.8 KDA	3.04e+03	618	5	1.1	265	1	YRR4_MYCA	HYPOTHETICAL 31.5 KDA	3.04e+03
546	5	1.1	148	1	YJEE_STRCO	HYPOTHETICAL 15.8 KDA	3.04e+03	619	5	1.1	270	1	YOPF_BACSU	HYPOTHETICAL 30.3 KDA	3.04e+03
547	5	1.1	148	1	YPT3_STRCO	HYPOTHETICAL 15.9 KDA	3.04e+03	620	5	1.1	270	1	YKRB_YEAST	HYPOTHETICAL 30.7 KDA	3.04e+03
548	5	1.1	149	1	YOBH_BACSU	HYPOTHETICAL 17.1 KDA	3.04e+03	621	5	1.1	273	1	YGF0_YEAST	HYPOTHETICAL 30.8 KDA	3.04e+03
549	5	1.1	150	1	YVY3_AGRF9	HYPOTHETICAL 16.6 KDA	3.04e+03	622	5	1.1	273	1	ZN80_PONPY	ZINC FINGER PROTEIN 80	3.04e+03
550	5	1.1	150	1	YV024_BPHP1	POTATIVE TAIL TDBE PRO	3.04e+03	623	5	1.1	273	1	ZN80_PANTR	ZINC FINGER PROTEIN 80	3.04e+03
551	5	1.1	151	1	YV28_AOGAE	HYPOTHETICAL 17.5 KDA	3.04e+03	624	5	1.1	273	1	ZN80_GORGO	ZINC FINGER PROTEIN 80	3.04e+03
552	5	1.1	151	1	YF23_YEAST	HYPOTHETICAL 17.5 KDA	3.04e+03	625	5	1.1	273	1	ZN80_HUMAN	ZINC FINGER PROTEIN 80	3.04e+03
553	5	1.1	155	1	YFJT_ECOLI	HYPOTHETICAL 17.1 KDA	3.04e+03	626	5	1.1	274	1	YG15_YEAST	HYPOTHETICAL 32.1 KDA	3.04e+03
554	5	1.1	155	1	YHCH_HAEN	HYPOTHETICAL 16.9 KDA	3.04e+03	627	5	1.1	275	1	YD84_YEAST	HYPOTHETICAL 30.0 KDA	3.04e+03
555	5	1.1	156	1	YMS6_CAEEL	HYPOTHETICAL 16.9 KDA	3.04e+03	628	5	1.1	276	1	YGEF_ECOLI	HYPOTHETICAL 28.4 KDA	3.04e+03
556	5	1.1	158	1	YN19_YEAST	HYPOTHETICAL 17.1 KDA	3.04e+03	629	5	1.1	280	1	YGX4_YEAST	HYPOTHETICAL 32.0 KDA	3.04e+03
557	5	1.1	159	1	YZ81_MCTU	HYPOTHETICAL 16.4 KDA	3.04e+03	630	5	1.1	281	1	YH71_AEP3E	HYPOTHETICAL PROTEIN A	3.04e+03
558	5	1.1	159	1	YEB7_YEAST	HYPOTHETICAL 16.7 KDA	3.04e+03	631	5	1.1	281	1	YK45_SYNY3	HYPOTHETICAL 30.4 KDA	3.04e+03
559	5	1.1	160	1	YGAD_PSEPU	HYPOTHETICAL 19.0 KDA	3.04e+03	632	5	1.1	281	1	YKX5_BACSU	HYPOTHETICAL 33.3 KDA	3.04e+03
560	5	1.1	167	1	YP74_MCTU	HYPOTHETICAL 19.0 KDA	3.04e+03	633	5	1.1	282	1	YK05_YEAST	HYPOTHETICAL 32.1 KDA	3.04e+03
561	5	1.1	167	1	YV20_HAEN	HYPOTHETICAL PROTEIN H	3.04e+03	634	5	1.1	284	1	YV26_YEAST	HYPOTHETICAL 32.3 KDA	3.04e+03
562	5	1.1	167	1	YPA2_ASCIM	HYPOTHETICAL 19.7 KDA	3.04e+03	635	5	1.1	285	1	YK26_YEAST	HYPOTHETICAL 32.3 KDA	3.04e+03
563	5	1.1	168	1	YH11_AZOB	HYPOTHETICAL 18.6 KDA	3.04e+03	636	5	1.1	286	1	YMD3_CAEEL	HYPOTHETICAL 32.1 KDA	3.04e+03
564	5	1.1	169	1	YS41_PNECA	POTATIVE 40S RIBOSOMAL	3.04e+03	637	5	1.1	286	1	YGBB_EDRIC	HYPOTHETICAL 30.6 KDA	3.04e+03
565	5	1.1	170	1	YH83_YEAST	HYPOTHETICAL 19.8 KDA	3.04e+03	638	5	1.1	288	1	YOD5_CAEEL	HYPOTHETICAL 33.2 KDA	3.04e+03
566	5	1.1	175	1	YH1E_ECOLI	HYPOTHETICAL 20.6 KDA	3.04e+03	639	5	1.1	289	1	YRAN_BACSU	HYPOTHETICAL TRANSRIP	3.04e+03
567	5	1.1	175	1	YPEV_LACDL	HYPOTHETICAL TRANSPORT	3.04e+03	640	5	1.1	289	1	YFK2_YEAST	HYPOTHETICAL 31.9 KDA	3.04e+03
568	5	1.1	179	1	YPOL_THFEL	HYPOTHETICAL PROTEIN I	3.04e+03	641	5	1.1	292	1	YKFA_YEAST	HYPOTHETICAL 32.1 KDA	3.04e+03
569	5	1.1	180	1	YRBI_HAEN	HYPOTHETICAL PROTEIN H	3.04e+03	642	5	1.1	292	1	YKVA_YEAST	HYPOTHETICAL 34.5 KDA	3.04e+03
570	5	1.1	183	1	ZE82_MAIZE	ZEIN-BETA-PRCUCSOR (Z	3.04e+03	643	5	1.1	293	1	ZN80_MACMO	ZINC FINGER PROTEIN 80	3.04e+03
571	5	1.1	188	1	YI41_LACAC	HYPOTHETICAL 22.0 KDA	3.04e+03	644	5	1.1	295	1	YF1E_ECOLI	HYPOTHETICAL TRANSRIP	3.04e+03
572	5	1.1	189	1	YVYD_BACSU	HYPOTHETICAL 22.0 KDA	3.04e+03	645	5	1.1	295	1	YUST_BACSU	HYPOTHETICAL TRANSRIP	3.04e+03
573	5	1.1	189	1	YNOO_YEAST	VERY HYPOTHETICAL 21.7	3.04e+03	646	5	1.1	295	1	YF1F_YEAST	HYPOTHETICAL PROTEIN I	3.04e+03
574	5	1.1	189	1	YPT2_CAEEL	HYPOTHETICAL 21.6 KDA	3.04e+03	647	5	1.1	297	1	YMY9_YEAST	HYPOTHETICAL 34.0 KDA	3.04e+03
575	5	1.1	191	1	YGL2_STRCO	HYPOTHETICAL 20.1 KDA	3.04e+03	648	5	1.1	299	1	YHND_BACSU	HYPOTHETICAL OXIDOREDU	3.04e+03
576	5	1.1	193	1	YRAP_HAEN	HYPOTHETICAL PROTEIN H	3.04e+03	649	5	1.1	301	1	YHND_BACSU	HYPOTHETICAL 33.7 KDA	3.04e+03
577	5	1.1	194	1	YMP9_CAEEL	HYPOTHETICAL 22.0 KDA	3.04e+03	650	5	1.1	301	1	YGLD_BACST	HYPOTHETICAL 35.5 KDA	3.04e+03
578	5	1.1	196	1	YKGG_ECOLI	HYPOTHETICAL 23.3 KDA	3.04e+03	651	5	1.1	301	1	YMI6_MCTU	HYPOTHETICAL 31.7 KDA	3.04e+03
579	5	1.1	198	1	YMO3_YEAST	HYPOTHETICAL 22.7 KDA	3.04e+03	652	5	1.1	301	1	YNT4_YEAST	HYPOTHETICAL 34.1 KDA	3.04e+03
580	5	1.1	200	1	YPT2_SCHPO	YPT1-RELATED PROTEIN 2	3.04e+03	653	5	1.1	302	1	YHCF_BACSU	HYPOTHETICAL 33.7 KDA	3.04e+03
581	5	1.1	201	1	YR63_SCHPO	HYPOTHETICAL 23.2 KDA	3.04e+03	654	5	1.1	302	1	YV95_CAEEL	HYPOTHETICAL 34.8 KDA	3.04e+03
582	5	1.1	203	1	YH14_YEAST	HYPOTHETICAL 20.6 KDA	3.04e+03	655	5	1.1	303	1	YFBU_HAEN	HYPOTHETICAL PROTEIN H	3.04e+03
583	5	1.1	204	1	YIR8_YEAST	HYPOTHETICAL 22.8 KDA	3.04e+03	656	5	1.1	305	1	YHDM_HAEN	POTATIVE AMINO-ACID AB	3.04e+03
584	5	1.1	207	1	YI0R_CVMI	HYPOTHETICAL PROTEIN I	3.04e+03	657	5	1.1	307	1	YK35_YEAST	HYPOTHETICAL 36.1 KDA	3.04e+03
585	5	1.1	208	1	YPD3_CAEEL	HYPOTHETICAL 24.4 KDA	3.04e+03	658	5	1.1	308	1	YMI6_MYCLE	HYPOTHETICAL 32.9 KDA	3.04e+03
586	5	1.1	210	1	YIHA_ECOLI	HYPOTHETICAL GTP-BINDI	3.04e+03	659	5	1.1	308	1	YF05_HAEN	HYPOTHETICAL PROTEIN H	3.04e+03
587	5	1.1	212	1	YGBL_ECOLI	HYPOTHETICAL 23.2 KDA	3.04e+03	660	5	1.1	309	1	YVBS_BACSU	HYPOTHETICAL 34.5 KDA	3.04e+03
588	5	1.1	213	1	YI11_ARCFU	HYPOTHETICAL PROTEIN A	3.04e+03	661	5	1.1	310	1	YFDC_ECOLI	HYPOTHETICAL 34.5 KDA	3.04e+03
589	5	1.1	214	1	YGO10_XENIA	OOCYTE ZINC FINGER PRO	3.04e+03	662	5	1.1	310	1	YK01_YEAST	HYPOTHETICAL 36.1 KDA	3.04e+03
590	5	1.1	215	1	YG39_YEAST	HYPOTHETICAL 24.8 KDA	3.04e+03	663	5	1.1	315	1	YP76_CAEEL	HYPOTHETICAL 36.7 KDA	3.04e+03
591	5	1.1	216	1	YGD7_YEAST	HYPOTHETICAL 25.0 KDA	3.04e+03	664	5	1.1	319	1	YKRB_BACSU	HYPOTHETICAL 33.6 KDA	3.04e+03
592	5	1.1	217	1	YGB9_METH	HYPOTHETICAL PROTEIN M	3.04e+03	665	5	1.1	319	1	YHAI_CRP	HYPOTHETICAL PROTEIN 1	3.04e+03
593	5	1.1	217	1	YVFA_BACSU	HYPOTHETICAL 25.1 KDA	3.04e+03	666	5	1.1	320	1	YIHT_YEAST	HYPOTHETICAL 36.9 KDA	3.04e+03
594	5	1.1	218	1	YV22_CAEEL	HYPOTHETICAL 24.2 KDA	3.04e+03	667	5	1.1	325	1	YKOD_BACSU	HYPOTHETICAL 36.4 KDA	3.04e+03
595	5	1.1	220	1	YV53_YEAST	GTP-BINDING PROTEIN TP	3.04e+03	668	5	1.1	326	1	YF02_MCPN	HYPOTHETICAL ABC TRANS	3.04e+03
596	5	1.1	222	1	YKGH_ECOLI	HYPOTHETICAL 25.6 KDA	3.04e+03	669	5	1.1	330	1	YETR_BACSU	HYPOTHETICAL 35.8 KDA	3.04e+03
597	5	1.1	225	1	YRNI_CAEEL	HYPOTHETICAL 25.2 KDA	3.04e+03	670	5	1.1	331	1	YZ44_METJA	HYPOTHETICAL PROTEIN M	3.04e+03
598	5	1.1	227	1	YVPA_METFE	HYPOTHETICAL 24.7 KDA	3.04e+03	671	5	1.1	332	1	YVIA_HAEN	HYPOTHETICAL PROTEIN M	3.04e+03
599	5	1.1	228	1	YR16_MCTU	HYPOTHETICAL 24.6 KDA	3.04e+03	672	5	1.1	338	1	YFVY_ECOLI	POTATIVE ARSENICAL PDM	3.04e+03
600	5	1.1	229	1	YRHM_ECOLI	TRNA (GUANOSINE-2'-O-)	3.04e+03	673	5	1.1	338	1	YJHR_ECOLI	HYPOTHETICAL 38.0 KDA	3.04e+03
601	5	1.1	231	1	YEA4_YEAST	HYPOTHETICAL 25.1 KDA	3.04e+03	674	5	1.1	340	1	YV65_CAEEL	HYPOTHETICAL 38.8 KDA	3.04e+03
602	5	1.1	232	1	YV23_YEAST	HYPOTHETICAL 26.3 KDA	3.04e+03	675	5	1.1	340	1	YV51_YEAST	HYPOTHETICAL 39.8 KDA	3.04e+03
603	5	1.1	238	1	YV23_AGRV1	HYPOTHETICAL 26.7 KDA	3.04e+03	676	5	1.1	341	1	YVX8_BACSU	HYPOTHETICAL 40.6 KDA	3.04e+03
604	5	1.1	238	1	YFBN_ECOLI	HYPOTHETICAL 28.0 KDA	3.04e+03	677	5	1.1	342	1	YV22_YEAST	HYPOTHETICAL 38.6 KDA	3.04e+03
605	5	1.1	239	1	YV22_CAEEL	HYPOTHETICAL 26.6 KDA	3.04e+03	678	5	1.1	346	1	YV20_MCTU	HYPOTHETICAL 38.6 KDA	3.04e+03
606	5	1.1	239	1	YVGE_EDMIC	HYPOTHETICAL 26.0 KDA	3.04e+03	679	5	1.1	346	1	YV53_CAEEL	HYPOTHETICAL 38.8 KDA	3.04e+03
607	5	1.1	241	1	YV12_METJA	HYPOTHETICAL PROTEIN M	3.04e+03	680	5	1.1	347	1	YV7_YEAST	HYPOTHETICAL 38.1 KDA	3.04e+03

681	5	1.1	347	1	YPFG_ECOLI	HYPOTHETICAL 38.7 KDA	3.0e+03	754	5	1.1	449	1	YJCD_ECOLI	HYPOTHETICAL 45.7 KDA	3.0e+03
682	5	1.1	349	1	YHNT_ECOLI	HYPOTHETICAL 38.5 KDA	3.0e+03	755	5	1.1	452	1	YH24_ECOLI	HYPOTHETICAL 51.2 KDA	3.0e+03
683	5	1.1	352	1	ZINC_MOUSE	ZINC FINGER PROTEIN 18	3.0e+03	756	5	1.1	452	1	Z185_HUMAN	ZINC FINGER PROTEIN 18	3.0e+03
684	5	1.1	360	1	YOFI_CAEEL	HYPOTHETICAL 39.7 KDA	3.0e+03	757	5	1.1	453	1	YW5_CAEEL	HYPOTHETICAL 49.8 KDA	3.0e+03
685	5	1.1	361	1	YMOI_CAEEL	PROBABLE G PROTEIN-COU	3.0e+03	758	5	1.1	455	1	Y142_MYCTO	HYPOTHETICAL 48.1 KDA	3.0e+03
686	5	1.1	366	1	YOCF_BACSU	HYPOTHETICAL 41.5 KDA	3.0e+03	759	5	1.1	456	1	YW5_CAEEL	HYPOTHETICAL 51.6 KDA	3.0e+03
687	5	1.1	366	1	YHRO_YEAST	HYPOTHETICAL 42.3 KDA	3.0e+03	760	5	1.1	456	1	YMOI_YEAST	HYPOTHETICAL 51.6 KDA	3.0e+03
688	5	1.1	367	1	YMI1_PASTE	HYPOTHETICAL 43.7 KDA	3.0e+03	761	5	1.1	457	1	YMS9_YEAST	HYPOTHETICAL 52.2 KDA	3.0e+03
689	5	1.1	371	1	YMP4_STRCO	HYPOTHETICAL PROTEIN I	3.0e+03	762	5	1.1	457	1	YK90_HAEIN	HYPOTHETICAL SODIUM-DE	3.0e+03
690	5	1.1	371	1	YHDI_BACSU	HYPOTHETICAL 42.5 KDA	3.0e+03	763	5	1.1	457	1	YK90_HAEIN	HYPOTHETICAL 51.8 KDA	3.0e+03
691	5	1.1	374	1	YNGC_YEAST	HYPOTHETICAL 43.9 KDA	3.0e+03	764	5	1.1	463	1	YNAJ_BACSU	HYPOTHETICAL SYMPTOMER	3.0e+03
692	5	1.1	376	1	YOT3_CAEEL	HYPOTHETICAL 42.0 KDA	3.0e+03	765	5	1.1	464	1	YV5_CAEEL	HYPOTHETICAL 51.9 KDA	3.0e+03
693	5	1.1	377	1	YPRG_BACSU	HYPOTHETICAL 42.6 KDA	3.0e+03	766	5	1.1	465	1	YX43_RHIME	HYPOTHETICAL 53.8 KDA	3.0e+03
694	5	1.1	378	1	ZP47_BRAHE	POU DOMAIN PROTEIN ZP-	3.0e+03	767	5	1.1	466	1	YX18_CAEEL	HYPOTHETICAL 53.8 KDA	3.0e+03
695	5	1.1	384	1	YSG7_YEAST	HYPOTHETICAL 43.5 KDA	3.0e+03	768	5	1.1	468	1	YPS7_CAEEL	POTATIVE SERINE/THREON	3.0e+03
696	5	1.1	385	1	YCT2_BACFI	HYPOTHETICAL 43.4 KDA	3.0e+03	769	5	1.1	469	1	YMS_CAEEL	POTATIVE SERINE/THREON	3.0e+03
697	5	1.1	387	1	YF20_METJA	HYPOTHETICAL 40.5 KDA	3.0e+03	770	5	1.1	471	1	YH24_CRYPA	HYPOTHETICAL 54.3 KDA	3.0e+03
698	5	1.1	389	1	YMB2_YEAST	HYPOTHETICAL 42.9 KDA	3.0e+03	771	5	1.1	472	1	YH24_CRYPA	HYPOTHETICAL 54.3 KDA	3.0e+03
699	5	1.1	390	1	YFBE_ECOLI	HYPOTHETICAL 42.9 KDA	3.0e+03	772	5	1.1	474	1	YMS5_TRYAB	VARIANT SURFACE GLYCOP	3.0e+03
700	5	1.1	392	1	Y178_ARCFU	HYPOTHETICAL 43.2 KDA	3.0e+03	773	5	1.1	476	1	YG32_YEAST	HYPOTHETICAL 53.4 KDA	3.0e+03
701	5	1.1	393	1	YHFC_ECOLI	HYPOTHETICAL 43.2 KDA	3.0e+03	774	5	1.1	477	1	YH24_CRYPA	HYPOTHETICAL 54.9 KDA	3.0e+03
702	5	1.1	394	1	YHFC_ECOLI	HYPOTHETICAL 43.4 KDA	3.0e+03	775	5	1.1	479	1	YH24_CRYPA	HYPOTHETICAL 54.9 KDA	3.0e+03
703	5	1.1	396	1	YH24_CAEEL	HYPOTHETICAL 45.2 KDA	3.0e+03	776	5	1.1	482	1	YH24_CAEEL	HYPOTHETICAL 54.9 KDA	3.0e+03
704	5	1.1	397	1	YH24_CAEEL	HYPOTHETICAL 44.5 KDA	3.0e+03	777	5	1.1	482	1	YH24_CAEEL	HYPOTHETICAL 54.9 KDA	3.0e+03
705	5	1.1	398	1	YH24_CAEEL	HYPOTHETICAL 43.3 KDA	3.0e+03	778	5	1.1	484	1	YH24_CAEEL	HYPOTHETICAL 54.9 KDA	3.0e+03
706	5	1.1	398	1	YH24_CAEEL	POTATIVE CYTOCHROME P4	3.0e+03	779	5	1.1	486	1	YH24_CAEEL	HYPOTHETICAL 54.9 KDA	3.0e+03
707	5	1.1	399	1	YF07_METJA	HYPOTHETICAL 43.8 KDA	3.0e+03	780	5	1.1	488	1	YH24_CAEEL	HYPOTHETICAL 54.7 KDA	3.0e+03
708	5	1.1	400	1	YHIN_ECOLI	HYPOTHETICAL 43.8 KDA	3.0e+03	781	5	1.1	491	1	YH24_CAEEL	HYPOTHETICAL 54.7 KDA	3.0e+03
709	5	1.1	402	1	YH24_CAEEL	HYPOTHETICAL 43.2 KDA	3.0e+03	782	5	1.1	491	1	YH24_CAEEL	HYPOTHETICAL 54.7 KDA	3.0e+03
710	5	1.1	402	1	YH24_CAEEL	HYPOTHETICAL 43.2 KDA	3.0e+03	783	5	1.1	491	1	YH24_CAEEL	HYPOTHETICAL 54.7 KDA	3.0e+03
711	5	1.1	403	1	YH24_CAEEL	HYPOTHETICAL 43.7 KDA	3.0e+03	784	5	1.1	497	1	YH24_CAEEL	HYPOTHETICAL 54.2 KDA	3.0e+03
712	5	1.1	403	1	YH24_CAEEL	HYPOTHETICAL 43.7 KDA	3.0e+03	785	5	1.1	497	1	YH24_CAEEL	HYPOTHETICAL 54.2 KDA	3.0e+03
713	5	1.1	404	1	YH24_CAEEL	HYPOTHETICAL 45.1 KDA	3.0e+03	786	5	1.1	498	1	YH24_CAEEL	HYPOTHETICAL 55.6 KDA	3.0e+03
714	5	1.1	404	1	YH24_CAEEL	PROBABLE AMINOTRANSFER	3.0e+03	787	5	1.1	498	1	YH24_CAEEL	HYPOTHETICAL 55.6 KDA	3.0e+03
715	5	1.1	405	1	YH24_CAEEL	POTATIVE GTP-BINDING P	3.0e+03	788	5	1.1	499	1	YH24_CAEEL	HYPOTHETICAL 56.5 KDA	3.0e+03
716	5	1.1	405	1	YH24_CAEEL	HYPOTHETICAL 47.8 KDA	3.0e+03	789	5	1.1	500	1	YH24_CAEEL	HYPOTHETICAL 56.5 KDA	3.0e+03
717	5	1.1	407	1	YH24_CAEEL	HYPOTHETICAL 44.3 KDA	3.0e+03	790	5	1.1	501	1	YH24_CAEEL	HYPOTHETICAL 54.5 KDA	3.0e+03
718	5	1.1	408	1	YH24_CAEEL	HYPOTHETICAL 45.1 KDA	3.0e+03	791	5	1.1	503	1	YH24_CAEEL	HYPOTHETICAL 55.6 KDA	3.0e+03
719	5	1.1	408	1	YH24_CAEEL	HYPOTHETICAL 45.1 KDA	3.0e+03	792	5	1.1	503	1	YH24_CAEEL	HYPOTHETICAL 55.6 KDA	3.0e+03
720	5	1.1	411	1	YH24_CAEEL	HYPOTHETICAL 45.0 KDA	3.0e+03	793	5	1.1	504	1	YH24_CAEEL	HYPOTHETICAL 55.8 KDA	3.0e+03
721	5	1.1	411	1	YH24_CAEEL	HYPOTHETICAL 45.2 KDA	3.0e+03	794	5	1.1	505	1	YH24_CAEEL	HYPOTHETICAL 58.3 KDA	3.0e+03
722	5	1.1	413	1	YH24_CAEEL	HYPOTHETICAL 47.4 KDA	3.0e+03	795	5	1.1	514	1	YH24_CAEEL	HYPOTHETICAL 58.3 KDA	3.0e+03
723	5	1.1	413	1	YH24_CAEEL	HYPOTHETICAL 47.0 KDA	3.0e+03	796	5	1.1	516	1	YH24_CAEEL	HYPOTHETICAL 59.8 KDA	3.0e+03
724	5	1.1	413	1	YH24_CAEEL	HYPOTHETICAL 47.7 KDA	3.0e+03	797	5	1.1	518	1	YH24_CAEEL	HYPOTHETICAL 59.8 KDA	3.0e+03
725	5	1.1	414	1	YH24_CAEEL	HYPOTHETICAL 47.4 KDA	3.0e+03	798	5	1.1	519	1	YH24_CAEEL	HYPOTHETICAL 59.8 KDA	3.0e+03
726	5	1.1	414	1	YH24_CAEEL	HYPOTHETICAL 47.0 KDA	3.0e+03	799	5	1.1	520	1	YH24_CAEEL	HYPOTHETICAL 58.0 KDA	3.0e+03
727	5	1.1	415	1	YH24_CAEEL	HYPOTHETICAL 47.6 KDA	3.0e+03	800	5	1.1	523	1	YH24_CAEEL	HYPOTHETICAL 61.7 KDA	3.0e+03
728	5	1.1	415	1	YH24_CAEEL	HYPOTHETICAL 47.6 KDA	3.0e+03	801	5	1.1	527	1	YH24_CAEEL	HYPOTHETICAL 61.7 KDA	3.0e+03
729	5	1.1	419	1	YH24_CAEEL	HYPOTHETICAL 45.0 KDA	3.0e+03	802	5	1.1	529	1	YH24_CAEEL	HYPOTHETICAL 58.3 KDA	3.0e+03
730	5	1.1	421	1	YH24_CAEEL	HYPOTHETICAL 45.4 KDA	3.0e+03	803	5	1.1	529	1	YH24_CAEEL	HYPOTHETICAL 59.0 KDA	3.0e+03
731	5	1.1	421	1	YH24_CAEEL	HYPOTHETICAL 46.6 KDA	3.0e+03	804	5	1.1	533	1	YH24_CAEEL	HYPOTHETICAL 59.0 KDA	3.0e+03
732	5	1.1	422	1	YH24_CAEEL	PUTATIVE NA(+)/H(+) EX	3.0e+03	805	5	1.1	534	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
733	5	1.1	423	1	YH24_CAEEL	HYPOTHETICAL 46.9 KDA	3.0e+03	806	5	1.1	535	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
734	5	1.1	423	1	YH24_CAEEL	HYPOTHETICAL 46.3 KDA	3.0e+03	807	5	1.1	536	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
735	5	1.1	423	1	YH24_CAEEL	HYPOTHETICAL 49.0 KDA	3.0e+03	808	5	1.1	539	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
736	5	1.1	424	1	YH24_CAEEL	HYPOTHETICAL 49.0 KDA	3.0e+03	809	5	1.1	540	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
737	5	1.1	425	1	YH24_CAEEL	HYPOTHETICAL 45.8 KDA	3.0e+03	810	5	1.1	541	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
738	5	1.1	425	1	YH24_CAEEL	HYPOTHETICAL 49.1 KDA	3.0e+03	811	5	1.1	541	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
739	5	1.1	428	1	YH24_CAEEL	HYPOTHETICAL 48.3 KDA	3.0e+03	812	5	1.1	543	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
740	5	1.1	428	1	YH24_CAEEL	HYPOTHETICAL 48.3 KDA	3.0e+03	813	5	1.1	543	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
741	5	1.1	430	1	YH24_CAEEL	HYPOTHETICAL 44.9 KDA	3.0e+03	814	5	1.1	544	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
742	5	1.1	430	1	YH24_CAEEL	HYPOTHETICAL 49.8 KDA	3.0e+03	815	5	1.1	547	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
743	5	1.1	431	1	YH24_CAEEL	HYPOTHETICAL 50.3 KDA	3.0e+03	816	5	1.1	551	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
744	5	1.1	432	1	YH24_CAEEL	HYPOTHETICAL 49.7 KDA	3.0e+03	817	5	1.1	552	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
745	5	1.1	432	1	YH24_CAEEL	HYPOTHETICAL 48.6 KDA	3.0e+03	818	5	1.1	552	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
746	5	1.1	437	1	YH24_CAEEL	HYPOTHETICAL 48.6 KDA	3.0e+03	819	5	1.1	558	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
747	5	1.1	438	1	YH24_CAEEL	HYPOTHETICAL 48.6 KDA	3.0e+03	820	5	1.1	562	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
748	5	1.1	438	1	YH24_CAEEL	HYPOTHETICAL 48.6 KDA	3.0e+03	821	5	1.1	564	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
749	5	1.1	439	1	YH24_CAEEL	HYPOTHETICAL 48.6 KDA	3.0e+03	822	5	1.1	568	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
750	5	1.1	443	1	YH24_CAEEL	HYPOTHETICAL 48.6 KDA	3.0e+03	823	5	1.1	568	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
751	5	1.1	446	1	YH24_CAEEL	HYPOTHETICAL 48.6 KDA	3.0e+03	824	5	1.1	571	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
752	5	1.1	446	1	YH24_CAEEL	HYPOTHETICAL 48.6 KDA	3.0e+03	825	5	1.1	571	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03
753	5	1.1	447	1	YH24_CAEEL	HYPOTHETICAL 48.6 KDA	3.0e+03	826	5	1.1	577	1	YH24_CAEEL	THROMBOXANE-A SYNTHASE	3.0e+03

827	5	1.1	581	1	YMM7_YEAST	HYPOTHETICAL 65.2 KDA	3.04e+03	900	5	1.1	776	1	YLA4_CAEEL	HYPOTHETICAL 86.9 KDA	3.04e+03
828	5	1.1	585	1	YK56_CAEEL	HYPOTHETICAL 68.3 KDA	3.04e+03	901	5	1.1	780	1	YOM1_CAEEL	HYPOTHETICAL 88.3 KDA	3.04e+03
829	5	1.1	585	1	YK58_YEAST	HYPOTHETICAL 65.3 KDA	3.04e+03	902	5	1.1	782	1	YNN2_YEAST	HYPOTHETICAL 88.8 KDA	3.04e+03
830	5	1.1	587	1	YID6_YEAST	HYPOTHETICAL 65.3 KDA	3.04e+03	903	5	1.1	786	1	YSA8_CAEEL	HYPOTHETICAL 84.3 KDA	3.04e+03
831	5	1.1	587	1	YKRO_YEAST	HYPOTHETICAL 67.5 KDA	3.04e+03	904	5	1.1	796	1	YEZ2_YEAST	POTATIVE 90.2 KDA ZINC	3.04e+03
832	5	1.1	593	1	YK28_YEAST	POTATIVE TRANSPORTER Y	3.04e+03	905	5	1.1	799	1	ZEK1_MOUSE	ZINC FINGER X-CHROMOSOM	3.04e+03
833	5	1.1	597	1	YKPA_KLUFA	HYPOTHETICAL KILLER PL	3.04e+03	906	5	1.1	800	1	ZEK1_MOUSE	ZINC FINGER X-CHROMOSOM	3.04e+03
834	5	1.1	599	1	YV06_CAEEL	HYPOTHETICAL 66.2 KDA	3.04e+03	907	5	1.1	801	1	ZEK1_MOUSE	ZINC FINGER X-CHROMOSOM	3.04e+03
835	5	1.1	607	1	YK28_CAEEL	HYPOTHETICAL 66.2 KDA	3.04e+03	908	5	1.1	804	1	YNA4_CAEEL	HYPOTHETICAL 91.0 KDA	3.04e+03
836	5	1.1	607	1	YKRO_YEAST	HYPOTHETICAL 70.2 KDA	3.04e+03	909	5	1.1	805	1	ZEK1_MOUSE	ZINC FINGER X-CHROMOSOM	3.04e+03
837	5	1.1	610	1	YKRO_YEAST	PROBABLE ATP-DEPENDENT	3.04e+03	910	5	1.1	807	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
838	5	1.1	610	1	YKRO_YEAST	POTATIVE ABC TRANSPORT	3.04e+03	911	5	1.1	811	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
839	5	1.1	614	1	YK28_CAEEL	HYPOTHETICAL 69.0 KDA	3.04e+03	912	5	1.1	821	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
840	5	1.1	615	1	YK28_CAEEL	HYPOTHETICAL 69.0 KDA	3.04e+03	913	5	1.1	823	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
841	5	1.1	618	1	YK28_CAEEL	POTATIVE 70.4 KDA TRAN	3.04e+03	914	5	1.1	829	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
842	5	1.1	624	1	YK28_CAEEL	HYPOTHETICAL 71.4 KDA	3.04e+03	915	5	1.1	832	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
843	5	1.1	627	1	YK28_CAEEL	HYPOTHETICAL 70.9 KDA	3.04e+03	916	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
844	5	1.1	630	1	YK28_CAEEL	HYPOTHETICAL 70.9 KDA	3.04e+03	917	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
845	5	1.1	632	1	YK28_CAEEL	HYPOTHETICAL 69.8 KDA	3.04e+03	918	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
846	5	1.1	633	1	YK28_CAEEL	HYPOTHETICAL 73.0 KDA	3.04e+03	919	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
847	5	1.1	633	1	YK28_CAEEL	HYPOTHETICAL 73.0 KDA	3.04e+03	920	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
848	5	1.1	636	1	YK28_CAEEL	HYPOTHETICAL 67.4 KDA	3.04e+03	921	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
849	5	1.1	638	1	YK28_CAEEL	HYPOTHETICAL 71.7 KDA	3.04e+03	922	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
850	5	1.1	642	1	YK28_CAEEL	HYPOTHETICAL 71.2 KDA	3.04e+03	923	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
851	5	1.1	644	1	YK28_CAEEL	TRANSPOSABLE ELEMENT H	3.04e+03	924	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
852	5	1.1	644	1	YK28_CAEEL	HYPOTHETICAL 74.0 KDA	3.04e+03	925	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
853	5	1.1	646	1	YK28_CAEEL	HYPOTHETICAL 70.5 KDA	3.04e+03	926	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
854	5	1.1	648	1	YK28_CAEEL	ZINC FINGER PROTEIN 20	3.04e+03	927	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
855	5	1.1	653	1	YK28_CAEEL	HYPOTHETICAL 75.9 KDA	3.04e+03	928	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
856	5	1.1	653	1	YK28_CAEEL	HYPOTHETICAL 75.9 KDA	3.04e+03	929	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
857	5	1.1	655	1	YK28_CAEEL	HYPOTHETICAL 75.9 KDA	3.04e+03	930	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
858	5	1.1	660	1	YK28_CAEEL	HYPOTHETICAL 73.9 KDA	3.04e+03	931	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
859	5	1.1	667	1	YK28_CAEEL	HYPOTHETICAL 73.9 KDA	3.04e+03	932	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
860	5	1.1	676	1	YK28_CAEEL	HYPOTHETICAL 76.2 KDA	3.04e+03	933	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
861	5	1.1	678	1	YK28_CAEEL	HYPOTHETICAL 72.8 KDA	3.04e+03	934	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
862	5	1.1	679	1	YK28_CAEEL	HYPOTHETICAL 75.4 KDA	3.04e+03	935	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
863	5	1.1	683	1	YK28_CAEEL	ZINC FINGER PROTEIN 26	3.04e+03	937	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
864	5	1.1	683	1	YK28_CAEEL	HYPOTHETICAL 80.2 KDA	3.04e+03	938	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
865	5	1.1	688	1	YK28_CAEEL	HYPOTHETICAL 80.2 KDA	3.04e+03	939	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
867	5	1.1	689	1	YK28_CAEEL	HYPOTHETICAL 81.0 KDA	3.04e+03	940	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
868	5	1.1	689	1	YK28_CAEEL	HYPOTHETICAL 81.0 KDA	3.04e+03	941	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
869	5	1.1	691	1	YK28_CAEEL	HYPOTHETICAL 81.0 KDA	3.04e+03	942	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
870	5	1.1	692	1	YK28_CAEEL	PROBABLE G PROTEIN-COU	3.04e+03	943	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
871	5	1.1	697	1	YK28_CAEEL	HYPOTHETICAL 81.2 KDA	3.04e+03	944	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
872	5	1.1	701	1	YK28_CAEEL	HYPOTHETICAL 81.2 KDA	3.04e+03	945	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
873	5	1.1	713	1	YK28_CAEEL	ZONA PELLUCIDA SPEM-B	3.04e+03	946	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
874	5	1.1	720	1	YK28_CAEEL	HYPOTHETICAL 82.1 KDA	3.04e+03	947	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
875	5	1.1	721	1	YK28_CAEEL	HYPOTHETICAL 84.0 KDA	3.04e+03	948	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
876	5	1.1	725	1	YK28_CAEEL	HYPOTHETICAL 84.0 KDA	3.04e+03	949	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
877	5	1.1	732	1	YK28_CAEEL	HYPOTHETICAL 81.8 KDA	3.04e+03	950	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
878	5	1.1	733	1	YK28_CAEEL	HYPOTHETICAL 81.0 KDA	3.04e+03	951	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
879	5	1.1	735	1	YK28_CAEEL	HYPOTHETICAL 80.5 KDA	3.04e+03	952	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
880	5	1.1	737	1	YK28_CAEEL	HYPOTHETICAL 84.6 KDA	3.04e+03	953	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
881	5	1.1	742	1	YK28_CAEEL	ZINC FINGER AUTOSOMAL	3.04e+03	954	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
882	5	1.1	742	1	YK28_CAEEL	HYPOTHETICAL 84.2 KDA	3.04e+03	955	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
883	5	1.1	743	1	YK28_CAEEL	HYPOTHETICAL 84.0 KDA	3.04e+03	956	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
884	5	1.1	744	1	YK28_CAEEL	HYPOTHETICAL 80.2 KDA	3.04e+03	957	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
885	5	1.1	745	1	YK28_CAEEL	ZONA PELLUCIDA SPEM-B	3.04e+03	958	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
886	5	1.1	745	1	YK28_CAEEL	ZONA PELLUCIDA SPEM-B	3.04e+03	959	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
887	5	1.1	747	1	YK28_CAEEL	HYPOTHETICAL 83.2 KDA	3.04e+03	960	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
888	5	1.1	750	1	YK28_CAEEL	HYPOTHETICAL 81.0 KDA	3.04e+03	961	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
889	5	1.1	751	1	YK28_CAEEL	HYPOTHETICAL 81.0 KDA	3.04e+03	962	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
890	5	1.1	754	1	YK28_CAEEL	HYPOTHETICAL 83.4 KDA	3.04e+03	963	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
891	5	1.1	757	1	YK28_CAEEL	HYPOTHETICAL 88.3 KDA	3.04e+03	964	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
892	5	1.1	758	1	YK28_CAEEL	HYPOTHETICAL 88.3 KDA	3.04e+03	965	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
893	5	1.1	759	1	YK28_CAEEL	HYPOTHETICAL 87.4 KDA	3.04e+03	966	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
894	5	1.1	764	1	YK28_CAEEL	HYPOTHETICAL 87.2 KDA	3.04e+03	967	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
895	5	1.1	765	1	YK28_CAEEL	HYPOTHETICAL 82.7 KDA	3.04e+03	968	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
896	5	1.1	766	1	YK28_CAEEL	HYPOTHETICAL 86.9 KDA	3.04e+03	969	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
897	5	1.1	767	1	YK28_CAEEL	POTATIVE CYSTEINYL-TRN	3.04e+03	970	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
898	5	1.1	767	1	YK28_CAEEL	HYPOTHETICAL 86.6 KDA	3.04e+03	971	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03
899	5	1.1	770	1	YK28_CAEEL	HYPOTHETICAL 84.2 KDA	3.04e+03	972	5	1.1	833	1	YNA1_MOUSE	HYPOTHETICAL 91.0 KDA	3.04e+03



973 5 1.1 1286 1 YKVS\_YEAST HYPOTHETICAL 140.4 KDA 3.04e+03  
 974 5 1.1 1308 1 YKVS\_YEAST TRANSPOSOM T11 HYPOHE 3.04e+03  
 975 5 1.1 1328 1 YKVS\_YEAST TRANSPOSOM T11 PROTEIN 3.04e+03  
 976 5 1.1 1358 1 Z261\_HUMAN ZINC FINGER PROTEIN 26 3.04e+03  
 977 5 1.1 1361 1 YME9\_YEAST HYPOTHETICAL 153.8 KDA 3.04e+03  
 978 5 1.1 1391 1 YLDS\_CAEEL HYPOTHETICAL 157.0 KDA 3.04e+03  
 979 5 1.1 1403 1 YGN1\_YEAST HYPOTHETICAL 163.2 KDA 3.04e+03  
 980 5 1.1 1411 1 YM42\_YEAST HYPOTHETICAL 162.7 KDA 3.04e+03  
 981 5 1.1 1420 1 YM8\_YEAST HYPOTHETICAL 163.6 KDA 3.04e+03  
 982 5 1.1 1541 1 YH6\_YEAST HYPOTHETICAL 175.8 KDA 3.04e+03  
 983 5 1.1 1585 1 YH6\_BACSU HYPOTHETICAL 171.0 KDA 3.04e+03  
 984 5 1.1 1592 1 YHDS\_YEAST PROBABLE APP-DEPENDENT 3.04e+03  
 985 5 1.1 1612 1 YP2B\_CRILO DNA TOPOISOMERASE II, 3.04e+03  
 986 5 1.1 1626 1 YP2B\_HUMAN DNA TOPOISOMERASE II, 3.04e+03  
 987 5 1.1 1636 1 YN7\_YEAST HYPOTHETICAL 186.8 KDA 3.04e+03  
 988 5 1.1 1679 1 YME9\_YEAST HYPOTHETICAL 187.1 KDA 3.04e+03  
 989 5 1.1 1736 1 ZOI\_HUMAN TIGHT JUNCTION PROTEIN 3.04e+03  
 990 5 1.1 1748 1 YNR2\_YEAST HYPOTHETICAL 196.1 KDA 3.04e+03  
 991 5 1.1 1753 1 YNR2\_YEAST HYPOTHETICAL 195.4 KDA 3.04e+03  
 992 5 1.1 1769 1 YNR9\_YEAST HYPOTHETICAL 200.0 KDA 3.04e+03  
 993 5 1.1 1941 1 YRM8\_CAEEL HYPOTHETICAL 216.3 KDA 3.04e+03  
 994 5 1.1 1967 1 YG50\_YEAST PUTATIVE HELICASE YGR2 3.04e+03  
 995 5 1.1 2111 1 YP84\_CAEEL HYPOTHETICAL 216.3 KDA 3.04e+03  
 996 5 1.1 2298 1 YP84\_CAEEL HYPOTHETICAL 216.3 KDA 3.04e+03  
 997 5 1.1 2717 1 YP84\_CAEEL HYPOTHETICAL 216.3 KDA 3.04e+03  
 998 5 1.1 3443 1 YP84\_CAEEL HYPOTHETICAL 216.3 KDA 3.04e+03  
 999 5 1.1 3443 1 YP84\_CAEEL HYPOTHETICAL 216.3 KDA 3.04e+03  
 1000 5 1.1 4385 1 YP73\_CAEEL HYPOTHETICAL 486.0 KDA 3.04e+03

## ALIGNMENTS

RESULT 1 STANDARD: PRT: 557 AA.  
 ID INRL HUMAN  
 AC P17181  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA-CHAIN PRECURSOR (IFN-ALPHA-REC).  
 GN IFNARI OR IFNAR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 90124632.  
 RA Uze G., Lutfalla G., Gresser I.,  
 RT "Genetic transfer of a functional human interferon" alpha receptor  
 RT into mouse cells: cloning and expression of its cDNA."  
 RL Cell 60:225-234(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92129376.  
 RA Lutfalla G., Gardiner K., Proudhon D., Vieh E., Uze G.,  
 RT "The structure of the human interferon alpha/beta receptor gene."  
 RL J. Biol. Chem. 267:2802-2809(1992).  
 RN [3]  
 RP PHOSPHORYLATION BY TYR2.  
 RX MEDLINE: 95059042.  
 RA Coleman J. O., Yan H., Domanski P., Hande R., Smalley D.,  
 RA Mullerstein J., Witte M., Krishnan K., Krolewski J.,  
 RT "Direct binding to and tyrosine phosphorylation of the alpha subunit  
 RT of the type I interferon receptor by p135tyk2 tyrosine kinase."  
 RL Mol. Cell. Biol. 14:8133-8142(1994).  
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE  
 CC I TRMS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS  
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-ALPHA AND BETA-  
 CC SUBUNITS THEMSELVES.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND  
 CC EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.  
 CC -1- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYR2 TYROSINE KINASE.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: J03171; AAA52730.1; -  
 DR EMBL: X60459; CAA42992.1; -  
 DR PIR: A32694; A32694.  
 DR PIR: S17112; S17112.  
 DR MIM: 107450; -  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;  
 KW Phosphorylation.  
 FT SIGNAL 1 27  
 FT CHAIN 28 557  
 FT POTENTIAL.  
 FT INTERFERON-ALPHA/BETA RECEPTOR ALPHA  
 FT CHAIN.  
 FT DOMAIN 28 436  
 FT TRANSMEM 437 457  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 79 87  
 FT BY SIMILARITY.  
 FT DISULFID 199 220  
 FT BY SIMILARITY.  
 FT MOD\_RES 466 466  
 FT PHOSPHORYLATION (BY TYR2) (PROBABLE).  
 FT MOD\_RES 481 481  
 FT PHOSPHORYLATION (BY TYR2) (PROBABLE).  
 FT CARBOHYD 50 50  
 FT POTENTIAL.  
 FT CARBOHYD 58 58  
 FT POTENTIAL.  
 FT CARBOHYD 81 81  
 FT POTENTIAL.  
 FT CARBOHYD 88 88  
 FT POTENTIAL.  
 FT CARBOHYD 110 110  
 FT POTENTIAL.  
 FT CARBOHYD 172 172  
 FT POTENTIAL.  
 FT CARBOHYD 254 254  
 FT POTENTIAL.  
 FT CARBOHYD 313 313  
 FT POTENTIAL.  
 FT CARBOHYD 314 314  
 FT POTENTIAL.  
 FT CARBOHYD 376 376  
 FT POTENTIAL.  
 FT CARBOHYD 416 416  
 FT POTENTIAL.  
 FT CARBOHYD 433 433  
 FT POTENTIAL.  
 FT VARIANT 168 168  
 FT L -> V  
 FT /FTID=VAR.002717.  
 FT G -> A (IN REF. 2).  
 FT CONFLICT 17 17  
 FT SEQUENCE 557 AA; 63525 MW; 0F6744C8A1ADB273 CRC64;  
 SQ  
 Query Match 100.0%; Score 436; DB 1; Length 557;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;  
 Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 MAAVLLGATTLVLA VAGPWWLSAAGGRNLSPOKVEVDIIDDFILRMNSDSYGVNT 60  
 Oy 1 MAAVLLGATTLVLA VAGPWWLSAAGGRNLSPOKVEVDIIDDFILRMNSDSYGVNT 60  
 Db 61 FSPDYQKGMNWKLSGCCNITSTKCFSSLAKLVNVEIKLRIRAEKNTSSYEDSF 120  
 Oy 61 FSPDYQKGMNWKLSGCCNITSTKCFSSLAKLVNVEIKLRIRAEKNTSSYEDSF 120  
 Db 61 FSPDYQKGMNWKLSGCCNITSTKCFSSLAKLVNVEIKLRIRAEKNTSSYEDSF 120  
 Oy 61 FSPDYQKGMNWKLSGCCNITSTKCFSSLAKLVNVEIKLRIRAEKNTSSYEDSF 120  
 Db 121 TPFRAOIGPEVLEAEADRAIVHISPGTDSVMALDGLSTFYSLIIRNSSGVEERI 180  
 Oy 121 TPFRAOIGPEVLEAEADRAIVHISPGTDSVMALDGLSTFYSLIIRNSSGVEERI 180  
 Db 181 ENIYSRRKIKLSPETTYCLVKAKALLSMKIGVSPVHCITKTVNELPPENIEVSQ 240  
 Oy 181 ENIYSRRKIKLSPETTYCLVKAKALLSMKIGVSPVHCITKTVNELPPENIEVSQ 240  
 Db 241 NQNVLLKMDTYYAMTQVOMLAFLKRNQGNHLYKKOJPDCCNVYTTQCVFQNFQK 300  
 Oy 241 NQNVLLKMDTYYAMTQVOMLAFLKRNQGNHLYKKOJPDCCNVYTTQCVFQNFQK 300  
 Db 241 NQNVLLKMDTYYAMTQVOMLAFLKRNQGNHLYKKOJPDCCNVYTTQCVFQNFQK 300  
 Oy 241 NQNVLLKMDTYYAMTQVOMLAFLKRNQGNHLYKKOJPDCCNVYTTQCVFQNFQK 300  
 Db 301 GIYLLRQASDGNNTSMSEIKPDTEIOAFLPPVNNISLSDFHIYIGAPQSGNTP 360  
 Oy 301 GIYLLRQASDGNNTSMSEIKPDTEIOAFLPPVNNISLSDFHIYIGAPQSGNTP 360  
 Db 361 VIQDYPLIYEITFEMNTSNAERKIIERTDVYVNLPLTYVYCVKAAHTMDERLNSV 420

OY 361 VIADYPLIEILMENTSNMERKIKEDVYTPNKLPLTYCVKARAHMDKLNKSSV 420  
 DB 421 FSDAVCEKTRPGNTSK 436  
 OY 421 FSDAVCEKTRPGNTSK 436

RESULT 2  
 ID INRI-SHEEP STANDARD: PRT; 560 AA.  
 AC Q28589; Q95206;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)  
 DE (INTERFERON-ALPHA/BETA RECEPTOR-1).  
 GN IFNAR1 OR IFNAR.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-ENDOMETRIUM;  
 RX MEDLINE: 97135690.  
 RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;  
 RT "Structure of an ovine interferon receptor and its expression in  
 RT endometrium."  
 RL J. Mol. Endocrinol. 17:207-215(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-ENDOMETRIUM;  
 RX MEDLINE: 98006426.  
 RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;  
 RT "Molecular cloning of ovine and bovine type I interferon receptor  
 RT subunits from uteri, and endometrial expression of messenger  
 RT ribonucleic acid for ovine receptors during the estrous cycle and  
 RT pregnancy."  
 RL Endocrinology 138:4757-4767(1997).  
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE  
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS  
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA- AND BETA-  
 CC SUBUNITS THEMSELVES.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT  
 CC CONCEPTUS AT DAY 15 OF PREGNANCY.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC -----  
 CC EMBL: X95939; CAA65183.1;  
 CC DR EMBL: U65978; AAB84231.1;  
 CC PFAM: PF00041; fn3; 1.  
 CC Receptor; Transmembrane; Glycoprotein; Signal.  
 CC BY SIMILARITY.  
 CC SIGNAL 1 24  
 CC CHAIN 25 560  
 CC INTERFERON-ALPHA/BETA RECEPTOR ALPHA  
 CC CHAIN.  
 CC EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 25 437  
 CC DOMAIN 438 458  
 CC POTENTIAL.  
 CC CITOPLASMIC (POTENTIAL).  
 CC DISULFID 459 560  
 CC BY SIMILARITY.  
 CC CARBOHYD 76 84  
 CC BY SIMILARITY.  
 CC CARBOHYD 199 220  
 CC POTENTIAL.  
 CC CARBOHYD 47 47  
 CC POTENTIAL.  
 CC CARBOHYD 55 55  
 CC POTENTIAL.  
 CC CARBOHYD 85 85  
 CC POTENTIAL.  
 CC CARBOHYD 108 108  
 CC POTENTIAL.

FT CARBOHYD 109 109 POTENTIAL.  
 FT CARBOHYD 172 172 POTENTIAL.  
 FT CARBOHYD 222 222 POTENTIAL.  
 FT CARBOHYD 285 285 POTENTIAL.  
 FT CARBOHYD 313 313 POTENTIAL.  
 FT CARBOHYD 359 359 POTENTIAL.  
 FT CARBOHYD 377 377 POTENTIAL.  
 FT CARBOHYD 434 434 POTENTIAL.  
 FT CARBOHYD 434 434 POTENTIAL.  
 FT CONFLICT 352 352 S -> G (IN REF. 2).  
 FT CONFLICT 522 522 A -> D (IN REF. 2).  
 SQ SEQUENCE 560 AA; 63918 MW; E7198A1905D4805C CRC64;  
 Query Match 3.48; Score 15; DB 1; Length 560;  
 Best Local Similarity 100.0%; Pred. No. 1,71e-21;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 395 PNKPLTYCVKARA 409  
 OY 394 PNKPLTYCVKARA 408  
 RESULT 3  
 ID INRI BOVIN STANDARD: PRT; 560 AA.  
 AC Q04730;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).  
 GN IFNAR1 OR IFNAR.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-LUNG;  
 RX MEDLINE: 93076908.  
 RA Mouchel-Viehl E., Luftalla G., Mogenssen K.E., Uze G.;  
 RT "Specific antiviral activities of the human alpha interferons are  
 RT determined at the level of receptor (IFNAR) structure."  
 RL FEBS Lett. 313:255-259(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE: 93305725.  
 RA Lim J.-K., Langer J.A.;  
 RT "Cloning and characterization of a bovine alpha interferon receptor."  
 RT Blooming. Biophys. Acta 1173:314-319(1993).  
 CC -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE  
 CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS  
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA- AND BETA-  
 CC SUBUNITS THEMSELVES.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT  
 CC CONCEPTUS AT DAY 15 OF PREGNANCY.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC -----  
 CC EMBL: X68443; CAA48484.1;  
 CC DR EMBL: L06320; AAO2571.1;  
 CC PIR: S33770; S33770;  
 CC PIR: S27387; S27387;  
 CC PFAM: PF00041; fn3; 1.  
 CC Receptor; Transmembrane; Glycoprotein; Signal.  
 CC BY SIMILARITY.  
 CC SIGNAL 1 24  
 CC CHAIN 25 560  
 CC INTERFERON-ALPHA/BETA RECEPTOR ALPHA  
 CC CHAIN.  
 CC EXTRACELLULAR (POTENTIAL).  
 CC DOMAIN 25 437



FT	43	POTENTIAL
FT	109	POTENTIAL

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae

CC Coturnix.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LIVER;  
 RA Ramirez V., Morals R.;  
 RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONMEMBRANIC COMPONENT  
 CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.  
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.  
 CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.  
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 CC  
 CC EMBL: U36794; AAA76731.1;  
 DR PFAA; PF00895; ATP-synt\_8; 1;  
 KM Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.  
 FT TRANSMEM 8  
 RL J. Biol. Chem. 264:12482-12491(1989).  
 SQ SEQUENCE 55 AA; 6494 MW; B284AFD91399AE1B CRC64;

Query Match 1.6%; Score 7; DB 1; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 18 FTYSLI 24  
 OY 163 FTYSLI 169

RESULT 7  
 ID AANT\_HDV\_M1 STANDARD; PRT; 195 AA.  
 AC P25881;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 01-MAY-1992 (Rel. 22, Last annotation update)  
 DE DELTA ANTIGEN.  
 CC Hepatitis delta virus (isolate Japanese M-1) (HDV).  
 CC Viruses; Deltavirus.  
 CC [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91012805.  
 RA Imazeki F., Omata M., Ono M.  
 RL "Heterogeneity and evolution rates of delta virus RNA sequences."  
 RL J. Virol. 64:5594-5599(1990).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
 CC -1- PTM: PHOSPHORYLATED.  
 CC -1- DISEASE: BINDS SPECIFICALLY TO ANTISERA FROM PATIENTS WITH CHRONIC  
 CC HEPATITIS DELTA VIRAL INFECTIONS.  
 CC -1- MISCELLANEOUS: DELTA ANTIGEN BINDS SPECIFICALLY TO HDV RNA.  
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 CC  
 CC EMBL: D90190; BAA14214.1;  
 DR PIR; A36409; SAVIUM.  
 DR PFAA; PF01517; HDV\_ag; 1;  
 KM Antigen; RNA-binding; Nuclear protein; Phosphorylation.  
 SQ SEQUENCE 195 AA; 21811 MW; FOAF63C16F746F1 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 195;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 116 AAGKRL 122  
 OY 24 AAGKRL 30

RESULT 8  
 ID TRT3\_COTJA STANDARD; PRT; 252 AA.  
 AC P06398; P06397;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE TROPONIN T, FAST SKELETAL MUSCLE ISOPFORM.  
 CC Coturnix coturnix japonica (Japanese quail).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Coturnix.  
 CC [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 89308680.  
 RA Bucher E.A., de la Brousse F.C., Emerson C.P. Jr.;  
 RT "Developmental and muscle-specific regulation of avian fast skeletal  
 RT tropoin T isoform expression by mRNA splicing."  
 RL J. Biol. Chem. 264:12482-12491(1989).  
 RL [2]  
 RP SEQUENCE OF 108-252 FROM N.A.  
 RX MEDLINE; 86033836.  
 RA Hastings K.E.M., Bucher E.A., Emerson C.P. Jr.;  
 RT "Generation of tropoin T isoforms by alternative RNA splicing in  
 RT avian skeletal muscle. Conserved and divergent features in birds and  
 RT mammals."  
 RL J. Biol. Chem. 260:13699-13703(1985).  
 CC -1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF  
 CC TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS  
 CC CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST THREE ISOPFORMS ARE PRODUCED BY  
 CC ALTERNATIVE SPLICING.  
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 CC  
 CC EMBL: M26600; AAA49506.1;  
 DR EMBL; M26599; AAA49505.1;  
 DR EMBL; M11685; AAA49504.1;  
 DR EMBL; M11684; AAA49503.1;  
 DR PIR; A03084; TPQJ72.  
 DR PIR; A03084; TPQJ71.  
 DR PFAA; PF00992; Tropoin; 1.  
 KM Muscle protein; Alternative splicing; Multigene family;  
 KW Phosphorylation.  
 FT INIT MET 0  
 FT MOD. RES 1 1  
 FT VARSPPLIC 27 30  
 FT VARSPPLIC 225 237  
 FT LTRRRRLQSLSEF -> VTLRRRIQDAKH (IN AN  
 FT ISOFORM)  
 SQ SEQUENCE 252 AA; 29967 MW; 67FED1A595C3C997 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 104 RIRAEKE 110  
 OY 103 RIRAEKE 109

RESULT 9  
 ID TRT3\_HUMAN STANDARD; PRT; 257 AA.

AC P45378; 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE TROPONIN T, FAST SKELETAL MUSCLE ISOFORM BETA (BETA TMTF).  
 GN TMTF3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP TISSUE-FETAL SKELETAL MUSCLE;  
 RX MEDLINE; 94226695.  
 RA Wu O.-I., Jha P.K., Raychowdhury M.K., Du Y., Leavis P.C.,  
 RA Sakar S.;  
 RT Isolation and characterization of human fast skeletal beta tropoin  
 RT cDNA: comparative sequence analysis of isoforms and insight into  
 RT the evolution of members of a multigene family.";  
 RL DNA Cell Biol. 13:217-233(1994).  
 CC -1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF  
 CC TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS  
 CC CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.  
 CC -1- TISSUE SPECIFICITY: IN FETAL AND ADULT FAST SKELETAL MUSCLES, WITH  
 CC A HIGHER LEVEL EXPRESSION IN FETAL THAN IN ADULT MUSCLE.  
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 CC -----  
 DR EMBL; M21984; AAA36777.1; -  
 DR MIM; 6006932; -  
 DR PFM; PF00992; Tropoin; 1.  
 DR Muscle protein; Multigene family; Phosphorylation.  
 KW INT\_MET 0 0 BY SIMILARITY.  
 FT MOD\_RES 1 1 PHOSPHORYLATION (BY CK2)  
 FT (BY SIMILARITY).  
 SQ SEQUENCE 257 AA; 30465 MW; FA33B3626BE597D9 CRC64;  
 Query Match 1 68; Score 7; DR 1; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 107 RIRAKE 113  
 113  
 103 RIRAKE 109  
 109  
 RESULT 10  
 ID TMTF3\_RAT STANDARD; PRT; 258 AA.  
 AC P09739; P09740;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS BETA/ALPHA (BETA/ALPHA  
 DE TMTF).  
 GN TMTF3.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 86281691.  
 RA Bretthart R.E., Nadal-Ginard B.;  
 RT "Complete nucleotide sequence of the fast skeletal tropoin T gene.  
 RT Alternatively spliced exons exhibit unusual interspecies  
 RT divergence.";  
 RL J. Mol. Biol. 188:313-324(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RX MEDLINE; 85201690.  
 RA Bretthart R.E., Nguyen H.T., Medford R.M., Destree A.T., Mahdavi V.,  
 RA Nadal-Ginard B.;  
 RT "Integrate combinatorial patterns of exon splicing generate multiple  
 RT regulated tropoin T isoforms from a single gene.";  
 RL Cell 41:67-82(1985).  
 CC -1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF  
 CC TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS  
 CC CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 44 ISOFORMS ARE PRODUCED BY  
 CC ALTERNATIVE SPLICING. THE ALPHA AND BETA FORMS ARE PRODUCED BY THE  
 CC USE OF MUTUALLY EXCLUSIVE EXONS.  
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 CC -----  
 DR EMBL; M15202; CAB24794.1; -  
 DR EMBL; M15202; AAA96446.1; -  
 DR EMBL; M15202; CAB24796.1; -  
 DR EMBL; M15202; CAB24802.1; -  
 DR EMBL; M15202; CAB24798.1; -  
 DR EMBL; M15202; CAB24789.1; -  
 DR EMBL; M15202; CAB24800.1; -  
 DR EMBL; M15202; CAB24809.1; -  
 DR EMBL; M15202; CAB24803.1; -  
 DR EMBL; M15202; CAB24793.1; -  
 DR EMBL; M15202; CAB24791.1; -  
 DR EMBL; M15202; AAA96447.1; -  
 DR EMBL; M15202; AAA96442.1; -  
 DR EMBL; M15202; AAA96443.1; -  
 DR EMBL; M15202; CAB24810.1; -  
 DR EMBL; M15202; CAB24806.1; -  
 DR EMBL; M15202; AAA96452.1; -  
 DR EMBL; M15202; CAB24797.1; -  
 DR EMBL; M15202; CAB24801.1; -  
 DR EMBL; M15202; AAA96455.1; -  
 DR EMBL; M15202; AAA96457.1; -  
 DR EMBL; M15202; AAA96458.1; -  
 DR EMBL; M15202; AAA96459.1; -  
 DR EMBL; M15202; CAB24790.1; -  
 DR EMBL; M15202; CAB24804.1; -  
 DR EMBL; M15202; CAB24808.1; -  
 DR EMBL; M15202; CAB24805.1; -  
 DR EMBL; M15202; AAA96460.1; -  
 DR EMBL; M15202; CAB24795.1; -  
 DR EMBL; M15202; AAA96462.1; -  
 DR EMBL; M15202; CAB24791.1; -  
 DR EMBL; M15202; CAB24807.1; -  
 DR EMBL; M15202; AAA96469.1; -  
 DR EMBL; M15202; CAB24792.1; -  
 DR EMBL; M15202; AAA96466.1; -  
 DR EMBL; M15202; AAA96470.1; -  
 DR EMBL; M15202; AAA96478.1; -  
 DR EMBL; M15202; AAA96479.1; -  
 DR EMBL; M15202; AAA96480.1; -  
 DR PIR; A24824; A24824.  
 DR PFM; PF00992; Tropoin; 1.  
 DR Muscle protein; Multigene family; Alternative splicing; Phosphorylation.  
 KW INT\_MET 0 0 BY SIMILARITY.  
 FT MOD\_RES 1 1 PHOSPHORYLATION (BY CK2)  
 FT (BY SIMILARITY).  
 VARSPIC 9 14 MISSING (IN SOME CLASS 1 ISOFORMS).

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SQ  SEQUENCE 262 AA; 31010 MM; F6B867C9ACE77ED CRC64;
Query Match 1.6%; Score 7; DB 1; Length 262;
Best Local Similarity 100.0%; Pred. No. 1.63e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 114 KIRAKE 120
OY 103 KIRAKE 109

RESULT 12
AC P02641.P19349; P19350; PRT; 278 AA.
AC 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS.
CN TNNNT3.
OS Oryctolagus cuniculus (Rabbit).
OC Mammalia; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eumaryota; Euthera; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE OF 1-10: 17-43 AND 56-278.
RX MEDLINE; 77118575.
RA Pearlstone J.R., Johnson P., Carpenter M.R., Smillie L.B.;
RT "Primary structure of rabbit skeletal muscle troponin-T. Sequence
RT determination of the NH2-terminal fragment CB3 and the complete
RT sequence of troponin-T.";
RL J. Biol. Chem. 252:983-989(1977).
RN [2]
RP SEQUENCE OF 1-66 FROM N.A., AND ALTERNATIVE SPLICING.
RC STAIN-NEW ZEALAND WHITE; TISSUE-SKELETAL MUSCLE;
RX MEDLINE; 93345743.
RA Briggs M.M., Schachat F.;
RT "Origin of fetal troponin T: developmentally regulated splicing of a
RT new exon in the fast troponin T gene.";
RL Dev. Biol. 158:503-509(1993).
RN [3]
RP SEQUENCE OF 1-66 FROM N.A., AND ALTERNATIVE SPLICING.
RC STAIN-NEW ZEALAND WHITE; TISSUE-SKELETAL MUSCLE;
RX MEDLINE; 90323375.
RA Briggs M.M., McGlinch H.D., Schachat F.;
RT "Transitions from fetal to fast troponin T isoforms are coordinated
RT with changes in tropomyosin and alpha-actinin isoforms in developing
RT rabbit skeletal muscle.";
RL Dev. Biol. 140:253-260(1990).
RN [4]
RP SEQUENCE OF 1-66 FROM N.A., AND ALTERNATIVE SPLICING.
RC STAIN-NEW ZEALAND WHITE; TISSUE-SKELETAL MUSCLE;
RA Briggs M.M., Schachat F.;
RT Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1-43 AND 56-65.
RC STAIN-NEW ZEALAND WHITE; TISSUE-SKELETAL MUSCLE;
RX MEDLINE; 89199646.
RA Briggs M.M., Schachat F.;
RT "N-terminal amino acid sequences of three functionally different
RT troponin T isoforms from rabbit fast skeletal muscle.";
RL J. Mol. Biol. 206:245-249(1999).
RN [6]
RP PHOSPHORYLATION SITES.
RX MEDLINE; 77157104.
RA Molr A.J.G., Cole H.A., Perry S.V.;
RT "The phosphorylation sites of troponin T from white skeletal muscle
RT and the effects of interaction with troponin C on their
RT phosphorylation by phosphorylase kinase.";
RL Biochem. J. 161:371-382(1977).
RN [7]
RP FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF
RP TROPONIN, THE THIN FILAMENT REGULATOR-COMPLEX WHICH CONTERS
RP CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
RP -1- ALTERNATIVE PRODUCTS: MANY DIFFERENT ISOFORMS ARE GENERATED BY A
RP DIFFERENTIAL RNA SPLICING MECHANISM. THE FORM TNNI1 IS SHOWN

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 CC -----  
 CC EMBL: 004970; AAA16023.1; -  
 CC EMBL: 004971; AAA16024.1; -  
 CC EMBL: 004972; AAA16025.1; -  
 CC EMBL: 004973; AAA16026.1; -  
 CC EMBL: 004974; AAA16027.1; -  
 CC EMBL: 004975; AAA16028.1; -  
 CC EMBL: 004976; AAA16029.1; -  
 CC EMBL: 004977; AAA16030.1; -  
 CC EMBL: 004978; AAA16031.1; -  
 CC PIR: A03083; TPPTS.  
 CC PIR: S03590; S03590.  
 CC PIR: S03591; S03591.  
 CC PIR: S03592; S03592.  
 CC PIR: PF00992; Tropoin; 1.  
 CC PIR: PF00992; Tropoin; 1.  
 CC Muscle protein; Multigene family; Phosphorylation; Acetylation;  
 CC Alternative splicing.  
 CC INIT MET 0  
 CC MOD RES 1 1 ACETYLATION.  
 CC MOD RES 1 1 PHOSPHORYLATION (BY CK2).  
 CC VASPLIC 11 16 MISSING (IN TNT2F, TNT2.5F AND TNT4F).  
 CC VASPLIC 22 38 MISSING (IN TNT3, TNT3F AND TNT4F).  
 CC VASPLIC 32 38 MISSING (IN TNT2, TNT2FA AND TNT2.5F).  
 CC VASPLIC 44 55 MISSING (IN TNT1F, TNT2F, TNT2FA,  
 CC TNT2.5F, TNT3F AND TNT4F).  
 CC O -> E (IN REF. 1).  
 CC VH -> HV (IN REF. 1 AND 5).  
 CC CONFLICT 19 19  
 CC CONFLICT 35 36  
 CC CONFLICT 61 61 MISSING (IN REF. 1).  
 CC SEQUENCE 278 AA; 32903 MM; 3D5A7E5F661E4CA9 CMC64;  
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 CC Query Match 1.6%; Score 7; DB 1; Length 278;  
 CC Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC Db 128 RIRAEKE 134  
 CC 103 RIRAEKE 109  
 CC  
 CC RESULT 13  
 CC ID INGS HUMAN STANDARD; PRT; 337 AA.  
 CC AC P38484;  
 CC DT 01-OCT-1994 (Rel. 30, Created)  
 CC DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 CC DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 CC DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA  
 CC RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).  
 CC GN IFNGR2 OR IFNGT1.  
 CC OS Homo sapiens (Human).  
 CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 CC RN (1)  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE-LONG FIBROBLAST;  
 CC RX MEDLINE; 94170380.  
 CC RA Soh J., Donnelly R.J., Kosenko S., Mariano T.M., Cook J.R.,  
 CC Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;  
 CC "Identification and sequence of an accessory factor required for  
 CC activation of the human interferon gamma receptor.";  
 CC Cell 76:793-802(1994).  
 CC RL (2)  
 CC RP SEQUENCE OF 1-24 FROM N.A.

RX MEDLINE; 97067142.  
 RA Rhee S., Ebersperger C., Dembic Z., Pestka S.;  
 RT "The structure of the gene for the second chain of the human  
 RT interferon gamma receptor.";  
 RL J. Biol. Chem. 271:28947-28952(1996).  
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR  
 CC SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF  
 CC THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO  
 CC INTERACT WITH GAF, JAK1, AND/OR JAK2.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC -----  
 CC EMBL: 005875; AAA16955.1; -  
 CC EMBL: 005877; AAA16956.1; -  
 CC EMBL: 068755; AAC52066.1; -  
 CC MIM; 147369;  
 CC PIR: PF00041; fn3; 1.  
 CC PIR: PF00041; fn3; 1.  
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 CC SIGNAL 1 27  
 CC CHAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN.  
 CC DOMAIN 28 247 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 248 268 CYTOPLASMIC (POTENTIAL).  
 CC DOMAIN 269 337 POTENTIAL.  
 CC CARBOHYD 56 56 POTENTIAL.  
 CC CARBOHYD 85 85 POTENTIAL.  
 CC CARBOHYD 110 110 POTENTIAL.  
 CC CARBOHYD 137 137 POTENTIAL.  
 CC CARBOHYD 219 219 POTENTIAL.  
 CC CARBOHYD 231 231 POTENTIAL.  
 CC VARIANT 64 64 R -> Q.  
 CC SEQUENCE 337 AA; 37834 MM; 18C61B10AD90E509 CMC64;  
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 CC Query Match 1.6%; Score 7; DB 1; Length 337;  
 CC Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC Db 142 PENIEV 148  
 CC 231 PENIEV 237  
 CC  
 CC RESULT 14  
 CC ID FIXB RHINE STANDARD; PRT; 353 AA.  
 CC AC P09819;  
 CC DT 01-MAR-1989 (Rel. 10, Created)  
 CC DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 CC DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 CC DE FIXB PROTEIN.  
 CC GN FIXB.  
 CC OS Rhizobium meliloti (Sinorhizobium meliloti).  
 CC CC Plasmid; psyma (megaplasmid 1).  
 CC CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 CC CC Rhizobiaceae; Sinorhizobium.  
 CC RN (1)  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN-1021;  
 CC RX MEDLINE; 87137267.  
 CC RA Earl C.D., Ronson C.W., Ausubel F.M.;  
 CC "Genetic and structural analysis of the Rhizobium meliloti fixA,  
 CC fixB, fixC, and fixX genes.";  
 CC J. Bacteriol. 169:1127-1136(1987).  
 CC RL (1)  
 CC RP FUNCTION: MAY PLAY A ROLE IN A REDOX PROCESS INVOLVED IN NITROGEN  
 CC FIXATION.

CC -1- SUBUNIT: FIXA AND FIXB FORM A HETERODIMER (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE ETP ALPHA-SUBUNIT / FIXB FAMILY.  
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 CC -----  
 CC EMBL: M15546; AAA21769.1; -  
 CC PIR: B26952; B26952.  
 CC PFAM: PF00766; ETP\_alpha.1.  
 CC PROSITE: PS00696; ETP\_ALPHA.1.  
 CC Electron transport; Flavoprotein; FAD; Nitrogen fixation;  
 CC Plasmid.  
 CC NP\_BIND 283 311 FAD (ADP PART) (POTENTIAL).  
 CC SEQUENCE 353 AA; 37786 MW; 8142B04B4C08546 CRC64;  
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 CC Query Match 1.6%; Score 7; DB 1; Length 353;  
 CC Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC Db 109 LGATTL 115  
 CC | | | | |  
 CC OY 5 LGATTL 11  
 CC -----  
 CC RESULT 15  
 CC ID FIXA\_RHISN STANDARD; PRT; 369 AA.  
 CC AC Q53209;  
 CC DT 01-NOV-1997 (Rel. 35; Created)  
 CC DT 01-NOV-1997 (Rel. 35; Last sequence update)  
 CC DT 15-FEB-2000 (Rel. 39; Last annotation update)  
 CC DE FIXB PROTEIN.  
 CC GN FIXB OR Y4YA.  
 CC OS Rhizobium sp. (strain NGR234).  
 CC OG Plasmid sym pNGR234a.  
 CC OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 CC CC Rhizobiaceae; Rhizobium.  
 CC [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE: 97305956.  
 CC RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,  
 CC Perret X.;  
 CC FT "Molecular basis of symbiosis between Rhizobium and legumes.";  
 CC RL Nature 387:394-401(1997).  
 CC [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RX MEDLINE: 96389014.  
 CC RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;  
 CC FT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.  
 CC NGR334 using dye terminators and a thermostable 'sequenase' a  
 CC beginning.";  
 CC RL Genome Res. 6:590-600(1996).  
 CC -1- FUNCTION: MAY PLAY A ROLE IN A REDOX PROCESS INVOLVED IN NITROGEN  
 CC FIXATION.  
 CC -1- SUBUNIT: FIXA AND FIXB FORM A HETERODIMER (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE ETP ALPHA-SUBUNIT / FIXB FAMILY.  
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 CC -----  
 CC EMBL: Z68203; CAA92416.1; -  
 CC EMBL: AF000100; AAB91889.1; -  
 CC PFAM: PF00766; ETP\_alpha.1.  
 CC PROSITE: PS00696; ETP\_ALPHA.1.  
 CC DR

KW Electron transport; Flavoprotein; FAD; Nitrogen fixation; Plasmid.  
 FT NP\_BIND 299 327 FAD (ADP PART) (POTENTIAL).  
 CC SEQUENCE 369 AA; 39851 MW; C4B5DB56FA1C08A CRC64;  
 CC -----  
 CC Query Match 1.6%; Score 7; DB 1; Length 369;  
 CC Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC Db 125 LGATTL 131  
 CC | | | | |  
 CC OY 5 LGATTL 11  
 CC -----  
 CC RESULT 16  
 CC ID FIXB\_AZOCA STANDARD; PRT; 369 AA.  
 CC AC P26483;  
 CC DT 01-AUG-1992 (Rel. 23; Created)  
 CC DT 01-AUG-1992 (Rel. 23; Last sequence update)  
 CC DT 15-FEB-2000 (Rel. 39; Last annotation update)  
 CC DE FIXB PROTEIN.  
 CC GN FIXB.  
 CC OS Azorhizobium caulinodans.  
 CC OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 CC CC Hyphomicrobium group; Azorhizobium.  
 CC [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN-OR5571;  
 CC RX MEDLINE: 91203829.  
 CC RA Argiont F., Kaminski P.A., Hennecke H., Elmerich C.;  
 CC FT "Nucleotide sequence of the fixABC region of Azorhizobium caulinodans  
 CC OR5571: similarity of the fixB product with eukaryotic flavoproteins,  
 CC RT Mol. Gen. Genet. 225:514-520(1991).  
 CC -1- FUNCTION: MAY PLAY A ROLE IN A REDOX PROCESS INVOLVED IN NITROGEN  
 CC FIXATION.  
 CC -1- SUBUNIT: FIXA AND FIXB FORM A HETERODIMER (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE ETP ALPHA-SUBUNIT / FIXB FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: X55450; CAA39092.1; -  
 CC PIR: S14071; S14071.  
 CC DR HSPD: P13804; LEFV.  
 CC DR PFAM: PF00766; ETP\_alpha.1.  
 CC DR PROSITE: PS00696; ETP\_ALPHA.1.  
 CC KW Electron transport; Flavoprotein; FAD; Nitrogen fixation.  
 CC FT NP\_BIND 289 327 FAD (ADP PART) (POTENTIAL).  
 CC SEQUENCE 369 AA; 39712 MW; F73BA68B40C751BB CRC64;  
 CC -----  
 CC Query Match 1.6%; Score 7; DB 1; Length 369;  
 CC Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC Db 125 LGATTL 131  
 CC | | | | |  
 CC OY 5 LGATTL 11  
 CC -----  
 CC RESULT 17  
 CC ID FIXB\_BRAJA STANDARD; PRT; 369 AA.  
 CC AC P10449;  
 CC DT 01-MAR-1999 (Rel. 10; Created)  
 CC DT 01-OCT-1996 (Rel. 34; Last sequence update)  
 CC DT 15-FEB-2000 (Rel. 39; Last annotation update)  
 CC DE FIXB PROTEIN.  
 CC GN GN  
 CC OS Bradyrhizobium japonicum.

CC -1- CATALYTIC ACTIVITY: 1-(5-PHOSPHORIBOSYL)-5-AMINO-4-IMIDAZOLE-  
CC CARBOXYLATE - 1-(5-PHOSPHORIBOSYL)-5-AMINOIMIDAZOLE + CO(2).  
CC PATHWAY: SIXTH AND SEVENTH STEP IN DE NOVO PURINE BIOSYNTHESIS.  
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE SAICAR  
CC SYNTHETASE FAMILY.  
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE AIR  
CC CARBOXYLASE FAMILY.  
CC -----  
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CC  
CC DR EMBL: U39848; AAA80690.1; -  
CC DR WORKPBR, B0286.3; CR03863.  
CC DR PFAM; PF00731; AIRC: 1.  
CC DR PFAM; PF01259; SAICAR\_Synth; 1.  
CC DR PROSITE; PS01057; SAICAR\_SYNTHETASE.1; 1.  
CC DR PROSITE; PS01057; SAICAR\_SYNTHETASE.2; 1.  
CC KW Hypothetical protein; Multifunctional enzyme; Purine biosynthesists;  
KW Lysase; Ligase; Decarboxylase.  
KW DOMAIN 1 263 SAICAR\_SYNTHETASE.  
KW DOMAIN 264 423 AIR CARBOXYLASE.  
SQ SEQUENCE 423 AA; 46978 MW; 101CD65318C480AA CRC64;  
  
Query Match 1.6%; Score 7; DB 1; Length 423;  
Best Local Similarity 100.0%; Pred. No. 1,636+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 112 FLKRNPG 118  
|||||||  
Qy 265 FLKRNPG 271  
  
RESULT 19 STANDARD; PRT; 425 AA.  
AC PUR6\_RAT  
AC P51583;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-FEB-2000 (Rel. 39, Last annotation update)  
DE MULTIFUNCTIONAL PROTEIN ADE2 [INCLUDES: PHOSPHORIBOSYLAMINOIMIDAZOLE-  
DE SUCCINOCARBOXYAMIDE SYNTHASE (EC 6.3.2.6) (SAICAR SYNTHETASE);  
DE PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE (EC 4.1.1.21) (AIR  
DE CARBOXYLASE) (AIRC)].  
GN PAICS OR ADE2 OR AIRC.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-FISCHER;  
RX MEDLINE; 95260861.  
RA Iwahana H., Honda S., Tsujisawa T., Takahashi Y., Adzuma K.,  
RA Katsushima R., Yamaoka T., Moritani M., Yoshimoto K., Itakura M.,  
RT "Rat genomic structure of amidophosphoribosyltransferase, cDNA  
RT sequence of aminoimidazole ribonucleotide carboxylase, and cell  
RT cycle-dependent expression of these two physically linked genes".  
RL Biochim. Biophys. Acta 1261:369-380(1995).  
CC -1- CATALYTIC ACTIVITY: ATP + 1-(5-PHOSPHORIBOSYL)-4-CARBOXY-5-  
CC AMINOIMIDAZOLE + L-ASPARATE - ADP + ORTHOPHOSPHATE + 1-(5-  
CC PHOSPHORIBOSYL)-4-(N-SUCCINOCARBOXYAMIDE)-5-AMINOIMIDAZOLE.  
CC -1- CATALYTIC ACTIVITY: 1-(5-PHOSPHORIBOSYL)-4-CARBOXY-5-  
CC CARBOXYLATE + 1-(3-PHOSPHORIBOSYL)-5-AMINOIMIDAZOLE + CO(2).  
CC -1- PATHWAY: SIXTH AND SEVENTH STEP IN DE NOVO PURINE BIOSYNTHESIS.  
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE SAICAR  
CC SYNTHETASE FAMILY.  
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE AIR  
CC CARBOXYLASE FAMILY.  
CC  
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DR EMBL; X53793; CAA37801.1; -.  
DR PIR; S14147; S14147.  
DR MIM; 172439; -.  
DR PFAM; PF00731; AIRC; 1.  
DR PFAM; PF01259; SAICAR\_synt; 1

DR EMBL; M31764; AAAA8601.1; -.  
DR EMBL; L12533; AAAA17894.1; -.  
PIR; A35641; A35641.  
DR PFAM; PF00731; AIRC\_1.  
DR PFAM; PF01259; SAICAR\_synt; 1.



DR PROSITE: PS01057; SAICAR SYNTHETASE.1; 1.  
 DR PROSITE: PS01058; SAICAR SYNTHETASE.2; 1.  
 KM Multifunctional enzyme; Purine biosynthesis; Ligase; Lyase;  
 FT Decarboxylase.  
 FT DOMAIN 1 261 SAICAR SYNTHETASE.  
 FT DOMAIN 2 426 AIR CARBOXYLASE.  
 SQ SEQUENCE 426 AA; 47240 MW; BAA90AE2AD360C CRC64;

Query Match 1.6%; Score 7; DB 1; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 109 FLKRNPG 115  
 |||||  
 QY 265 FLKRNPG 271

RESULT 22  
 ID YAL1 SYN3 STANDARD; PRT; 442 AA.  
 AC P72935;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE PUTATIVE AMMONIUM TRANSPORTER SL1017.  
 GN SL1017.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97061201.  
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Sugitani M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K.,  
 RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,  
 RA Yamada M., Yasuda M., Tabata S.;  
 RT \*Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.;  
 RL DNA Res. 3:109-136(1996).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE AMT1/MEP/NRGA FAMILY OF AMMONIUM  
 CC TRANSPORTERS (TC 2.49).  
 CC  
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CC  
 CC EMBL: D90901; BAA16952.1;  
 DR PFM: PF00909; Ammonium.transp. 1.  
 DR PROSITE: PS01219; AMMONIUM.TRANSP. 1.  
 KW Hypothetical protein; Transport; Transmembrane.  
 FT TRANSMEM 5 25 POTENTIAL.  
 FT TRANSMEM 44 64 POTENTIAL.  
 FT TRANSMEM 81 101 POTENTIAL.  
 FT TRANSMEM 104 124 POTENTIAL.  
 FT TRANSMEM 133 153 POTENTIAL.  
 FT TRANSMEM 155 175 POTENTIAL.  
 FT TRANSMEM 193 213 POTENTIAL.  
 FT TRANSMEM 240 260 POTENTIAL.  
 FT TRANSMEM 269 289 POTENTIAL.  
 FT TRANSMEM 299 319 POTENTIAL.  
 FT TRANSMEM 325 345 POTENTIAL.  
 FT TRANSMEM 354 374 POTENTIAL.  
 FT TRANSMEM 386 406 POTENTIAL.  
 SQ SEQUENCE 442 AA; 47172 MW; F3683BF3D96539E CRC64;

Query Match 1.6%; Score 7; DB 1; Length 442;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 277 LSAAAGG 283  
 |||||  
 QY 21 LSAAAGG 27

RESULT 23  
 ID VGLM\_HSVB STANDARD; PRT; 450 AA.  
 AC P28948;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE GLYCOPROTEIN M.  
 GN GM OR 52.  
 OS Equine herpesvirus type 1 (strain Abap) (EHV-1).  
 OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicelloviruses.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 92295566.  
 RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;  
 RT \*The DNA sequence of equine herpesvirus-1.\*;  
 RL Virology 189:304-316(1992).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN M.  
 CC  
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CC  
 CC EMBL: M86664; AAB02487.1;  
 DR PIR: G36800; WZBER4.  
 DR PFM: PF01528; Herpes-glycop. 1.  
 DR PRINTS: PR00333; HSV1INTEGRMP.  
 KW Transmembrane; Glycoprotein.  
 FT TRANSMEM 37 53 POTENTIAL.  
 FT TRANSMEM 111 127 POTENTIAL.  
 FT TRANSMEM 156 173 POTENTIAL.  
 FT TRANSMEM 179 195 POTENTIAL.  
 FT TRANSMEM 241 257 POTENTIAL.  
 FT TRANSMEM 271 287 POTENTIAL.  
 FT TRANSMEM 297 314 POTENTIAL.  
 FT TRANSMEM 341 358 POTENTIAL.  
 FT CARBOHYD 75 75 POTENTIAL.  
 SQ SEQUENCE 450 AA; 49221 MW; 5F1271CBDA9B0E6 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 109 TTLVIVA 115  
 |||||  
 QY 9 TTLVIVA 15  
 RESULT 24  
 ID MAOC\_ECOLI STANDARD; PRT; 681 AA.  
 AC P77455; O53009;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE MAOC PROTEIN (PHENYLACETIC ACID DEGRADATION PROTEIN PAZ).  
 GN MAOC OR PAZ.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;

RX MEDLINE: 97426617.  
 RA Blatter F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Colado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.,  
 RT "The complete genome sequence of *Escherichia coli* K-12.";  
 RL Science 277:1453-1474(1997).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-R12:  
 RX MEDLINE: 97251357.  
 RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
 RA Nakade S., Nakamura Y., Naghimoto H., Nishio Y., Oshima T., Saito N.,  
 RA Sasaki G., Seki Y., Sivasubramanian S., Tagami H., Takeda J.,  
 RA Takeuchi K., Takeuchi Y., Wada C., Yamamoto Y., Horinouchi T.,  
 RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome  
 corresponding to the 28.0-40.1 min region on the linkage map.";  
 RL DNA Res. 3:363-377(1996).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 11105;  
 RX Diaz E.,  
 RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
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 CC  
 DR EMBL: AEO00236; AAC74469.1;  
 DR EMBL: D90777; CAB20933.1;  
 DR EMBL: X87452; CAA66088.1;  
 DR EMBL: EGI3735; MAOC;  
 DR EMBL: PFO1575; MAOC\_1like; 1.  
 DR PFAM: PFO0171; aldehyd. 1.  
 DR PROSITE: PS00070; ALDEHYDE DEHYDR. CYS; FALSE NEG.  
 DR PROSITE: PS00687; ALDEHYDE DEHYDR. GLU; FALSE NEG.  
 KW Oxidoreductase.  
 FT ACT\_SITE 256 BY SIMILARITY.  
 FT ACT\_SITE 295 L -> V (IN REF. 3).  
 FT CONFLICT 143 143 A -> T (IN REF. 3).  
 FT CONFLICT 440 440 S -> N (IN REF. 3).  
 FT CONFLICT 611 611  
 SO SEQUENCE: 681 AA; 73002 MW; A631B97AA37A1C3E CRC64;  
 Query Match 1.68; Score: 7; DB 1; Length 681;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 587 VLSAAG 593  
 QY 20 VLSAAG 26  
 RESULT 25  
 ID CATE\_RHIME STANDARD; PRT; 687 AA.  
 AC 09X576;  
 DT 15-FEB-2000 (Rel. 39, Created)  
 DT 15-FEB-2000 (Rel. 39, Last sequence update)  
 DE CATALASE C (EC 1.11.1.6) (KAT2).  
 GN KATC OR KATC.  
 OS *Rhizobium meliloti* (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-RCR2011 / SM47;  
 RX MEDLINE: 99214118;  
 RA Sigaud S., Becquet V., Frendo P., Puppo A., Herouart D.,  
 RT "Differential regulation of two divergent Sinorhizobium meliloti genes  
 for HPII-like catalases during free-living growth and protective role  
 of both catalases during symbiosis.";  
 RL J. Bacteriol. 181:2634-2639(1999).  
 CC  
 CC -1- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES  
 CC TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.  
 CC COULD PROTECT CELLS IN NODULES WHICH HAVE A HIGH POTENTIAL TO  
 CC PRODUCE HYDROGEN PEROXIDE BECAUSE OF THE STRONG REDUCING  
 CC CONDITIONS REQUIRED FOR NITROGEN FIXATION AND THE ACTION OF  
 CC SEVERAL PROTEINS.  
 CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) - O(2) + 2 H(2)O.  
 CC -1- COFACTOR: HEME GROUP.  
 CC -1- INDUCTION: A THREEFOLD INCREASE OF THE ACTIVITY ARISES AFTER  
 CC EXPOSURE TO HEAT STRESS (37 DEGREES CELSIUS), TO SODIUM CHLORIDE  
 CC OR ETHANOL FOR ONE HOUR. NOT INDUCIBLE BY HYDROGEN PEROXIDE.  
 CC -1- MISCELLANEOUS: EITHER KATC OR KATC IS ABSOLUTELY REQUIRED FOR THE  
 CC PROTECTION OF THE NITROGEN FIXATION PROCESS.  
 CC -1- SIMILARITY: BELONGS TO THE CATALASE FAMILY, HPII SUBFAMILY.  
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 CC  
 DR EMBL: AF121348; AAD21077.1;  
 DR PROSITE: PS00437; CATALASE\_1; 1.  
 DR PROSITE: PS00438; CATALASE\_2; 1.  
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.  
 FT ACT\_SITE 88 BY SIMILARITY.  
 FT ACT\_SITE 161 161  
 FT BINDING 375 375 PROXIMAL HEME LIGAND (BY SIMILARITY).  
 FT SEQUENCE 687 AA; 76553 MW; E0C11305DB59BA3F CRC64;  
 Query Match 1.68; Score: 7; DB 1; Length 687;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 430 KLRIRAE 436  
 QY 101 KLRIRAE 107  
 RESULT 26  
 ID VVRB\_MYCTU STANDARD; PRT; 698 AA.  
 AC 006150;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE EXCINUCLEASE ABC SUBUNIT B.  
 GN VVRB OR RV1633 OR MYC01B2.25.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV;  
 RX MEDLINE: 98295987;  
 RA Cole S.T., Brosch R., Parthill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badoock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Raftery J., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,  
 RA Taylor K., Whitehead S., Barrell B.G.,  
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the  
 complete genome sequence."

RL Nature 393:537-544(1998).  
CC -1- FUNCTION: THIS IS ONE OF THE THREE SUBUNITS OF THE ABC EXCISION  
CC NUCLEASE. A DNA REPAIR ENZYME THAT CATALYZES THE EXCISION REACTION  
CC OF UV-DAMAGED NUCLEOTIDE SEGMENTS PRODUCING OLIGOMERS HAVING THE  
CC MODIFIED BASE(S). UV-B STIMULATES THE ATPASE ACTIVITY OF UVRA IN  
CC THE PRESENCE OF UV-RADIATED DOUBLE-STRANDED DNA. IT ALSO  
CC ENHANCES THE ABILITY OF UVRA TO BIND TO UV-RADIATED DOUBLE-STRANDED DNA  
CC (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE UVRA FAMILY.  
CC  
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DR EMBL: Z95554; CAB08886.1; -  
DR TUBERCULIST; RV1633; -  
DR PFAM: PF00270; DEAD. 1.  
DR PFAM: PF00271; helicase.C. 1.  
KM SOS response; Excision nuclease; DNA repair; ATP-binding.  
SQ SEQUENCE 698 AA; 78070 MW; 9252A0079699CFC62 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 698;  
Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 37 VILGAT 43  
3 VILGAT 9

RESULT 27  
ID ITA3 HUMAN STANDARD; PRT; 1051 AA.  
AC P26006;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE INTEGRIN ALPHA-3 PRECURSOR (GALACTOPROTEIN B3) (GAPB3) (VLA-3 ALPHA  
DE CHAIN) (CD49C).  
GN ITGAL3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 92011866.  
RA Takada Y., Murphy E., Pili P., Chen C., Ginsberg M.H., Hemler M.E.;  
RT "Molecular cloning and expression of the cDNA for alpha 3 subunit of  
RT human alpha 3 beta 1 (VLA-3), an integrin receptor for fibronectin,  
RT laminin, and collagen.";  
RT J. Cell Biol. 115:257-266(1991).  
RL [2]  
RN [3]  
RP SEQUENCE OF 33-1051 FROM N.A.  
RX MEDLINE: 91331981.  
RA Tsuji T., Hakomori S.-I., Osawa T.;  
RT "Identification of human galactoprotein b3, an oncogenic  
RT transformation-induced membrane glycoprotein, as VLA-3 alpha  
RT subunit: the primary structure of human integrin alpha 3.";  
RT J. Biochem. 109:659-665(1991).  
RL [3]  
RP SEQUENCE OF 33-46.  
RX MEDLINE: 87004112.  
RA Takada Y., Strominger J.L., Hemler M.E.;  
RT "The very late antigen family of heterodimers is part of a  
RT superfamily of molecules involved in adhesion and embryogenesis.";  
RT Proc. Natl. Acad. Sci. U.S.A. 84:3239-3243(1987).  
CC -1- FUNCTION: ACTS AS RECEPTOR FOR FIBRONECTIN, LAMININ AND COLLAGEN.  
CC -1- SUBUNIT: DIMER OF AN ALPHA AND BETA CHAINS. THE ALPHA CHAIN IS

CC COMPOSED OF AN HEAVY AND LIGHT CHAINS LINKED BY A DISULFIDE BOND.  
CC ALPHA-3 ASSOCIATES WITH BETA-1.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.  
CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD49C entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd49c.htm".  
CC  
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DR EMBL: M59911; AAA36120.1; -  
DR EMBL: D01038; BAA00845.1; -  
DR PIR: JX0161; JX0161.  
DR HSSP: P1215; 1A8X.  
DR PFAM: PF01839; FG-GAP. 5.  
DR PFAM: PF00357; Integrin\_A. 1.  
DR PRINTS: PRO1185; INTEGRIN.  
DR PROSITE: PS00242; INTEGRIN\_ALPHA. 1.  
KM Cell adhesion; Glycoprotein; Transmembrane; Signal; Integrin;  
KM Extracellular matrix; Cytoskeleton; Repeat.  
FT SIGNAL 1 32  
FT CHAIN 33 1051  
FT CHAIN 33 872  
FT CHAIN 876 1051  
FT CHAIN 33 991  
FT DOMAIN 992 1019  
FT DOMAIN 1020 1051  
FT DOMAIN 49 461  
FT REPEAT 120 165  
FT REPEAT 195 227  
FT REPEAT 246 279  
FT REPEAT 304 345  
FT REPEAT 366 402  
FT REPEAT 426 461  
FT DISULFID 94 103  
FT DISULFID 140 162  
FT DISULFID 185 197  
FT DISULFID 485 490  
FT DISULFID 496 550  
FT DISULFID 615 621  
FT DISULFID 694 702  
FT DISULFID 846 904  
FT DISULFID 911 916  
FT CARBOHYD 86  
FT CARBOHYD 107  
FT CARBOHYD 265  
FT CARBOHYD 500  
FT CARBOHYD 511  
FT CARBOHYD 573  
FT CARBOHYD 573  
FT CARBOHYD 573  
FT CARBOHYD 605  
FT CARBOHYD 605  
FT CARBOHYD 656  
FT CARBOHYD 697  
FT CARBOHYD 841  
FT CARBOHYD 857  
FT CARBOHYD 926  
FT CARBOHYD 935  
FT CARBOHYD 969  
SQ SEQUENCE 1051 AA; 116612 MW; EBAFA778BFF17B21 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 1051;  
Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 994 LVIVANG 1000  
11 LVIVANG 17

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FT FT DISULFID 486 491 BY SIMILARITY.
FT FT DISULFID 497 551 BY SIMILARITY.
FT FT DISULFID 616 622 BY SIMILARITY.
FT FT DISULFID 695 704 BY SIMILARITY.
FT FT DISULFID 848 906 INTERCHAIN (BY SIMILARITY).
FT FT DISULFID 913 918 BY SIMILARITY.
FT FT CARBOHYD 86 86 POTENTIAL.
FT FT CARBOHYD 501 501 POTENTIAL.
FT FT CARBOHYD 512 512 POTENTIAL.
FT FT CARBOHYD 574 574 POTENTIAL.
FT FT CARBOHYD 606 606 POTENTIAL.
FT FT CARBOHYD 657 657 POTENTIAL.
FT FT CARBOHYD 699 699 POTENTIAL.
FT FT CARBOHYD 843 843 POTENTIAL.
FT FT CARBOHYD 859 859 POTENTIAL.
FT FT CARBOHYD 925 925 POTENTIAL.
FT FT CARBOHYD 928 928 POTENTIAL.
FT FT CARBOHYD 937 937 POTENTIAL.
FT FT CARBOHYD 971 971 POTENTIAL.
FT FT VASPPLIC 1023 1053 RARRALRYEARQRAEKMSQSETERLDDY -> PTPIYR
FT FT ALPHAB-3B). IMPHYAVRIEEDNTPPGSTLPFKHM (IN ISOFOR
FT FT CONFLICT 975 975 W -> C (IN REF. 2).
FT FT CONFLICT 979 979 D -> N (IN REF. 2).
FT FT CONFLICT 1002 1002 G -> S (IN REF. 2).
SQ SQ SEQUENCE 1053 AA; 116745 MW; 6A5E8FE9DBA86D65 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 1053;
Best Local Similarity 100.0%; Pred. No. 1.63e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 996 LVLYAVG 1002
QY 11 LVLYAVG 17

RESULT 29
ID MSH3 MOUSE STANDARD; PRT; 1091 AA.
AC P13705;
DT 01-JAN-1990 (Rel. 13, Created).
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DNA MISMATCH REPAIR PROTEIN MSH3 (REPAIR-3 PROTEIN) (REP-1).
GN MSH3 OR REP-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN RP SEQUENCE FROM N.A.
RA Liu K., Niu L., Linton J.P., Crouse G.F.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN RP SEQUENCE FROM N.A.
RX MEDLINE; 95011610.
RA Liu K., Niu L., Linton J.P., Crouse G.F.;
RT "Characterization of the mouse Rep-3 gene: sequence similarities to
RT bacterial and yeast mismatch-repair proteins";
RL Gene 147:169-177(1994).
RN RP SEQUENCE OF 1.917 FROM N.A.
RX MEDLINE; 89384367.
RA Linton J.P., Yen J.-Y.J., Selby E., Chen Z., Chinsky J.M., Liu K.,
RA Kellens R.E., Crouse G.F.;
RT "Dual bidirectional promoters at the mouse dhfr locus: cloning and
RT characterization of two mRNA classes of the divergently transcribed
RT Rep-1 gene."
RL Mol. Cell. Biol. 9:3058-3072(1989).
CC 1- FUNCTION: NOT KNOWN. PROBABLE DNA-REPAIR PROTEIN.
CC 1- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MOTS FAMILY.
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ID	RESULT	30	STANDARD;	PRT;	2205 AA.
DT	POLG.POL2M				
AC	P23069;				
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-NOV-1991 (Rel. 20, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	GENOME POLYPROTEIN [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS				
DE	PCAC.10 PCAC, P3A; GENOME-LINKED PROTEIN VP6; PICORNAIN 3C				
DE	PCAC.3.4.22.28] (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D				
DE	(EC 2.7.7.48)].				
OS	poliovirus, type 2 (strain W-2);				
OC	viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;				
OC	enterovirus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 90155230.				
RA	Pearse D.C., Oh C.K., Cunningham L.L., Calenoff M., Jubelt B.;				
RT	"Localization of genomic regions specific for the attenuated, mouse-				
U	adapted poliovirus type 2 strain W-2.";				
U	J. Gen. Virol. 71:43-52(1990).				
CC	1-1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN				

RESULT	31			
ID	POLG.POL32	STANDARD;	PRT;	2206 AA.
AC	P06209;			
DT	01-JAN-1988	(Rel. 06, Created)		
DT	01-JAN-1988	(Rel. 06, Last sequence update)		
DT	15-DEC-1998	(Rel. 37, Last annotation update)		
DE	GENOME POLYPEPTIDE [CONTAINS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS			
DE	P24 TO P2C; P3A; GENOME-LINKED PROTEIN VP6; PICORNAIN 3C			
DE	(EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D			
DEL	(EC 2.7.7.48)].			
OC	Poliiovirus type 3 (strain 23127).			
OC	Viruses: ssRNA positive-strand viruses, no DNA stage; Picornaviridae;			
OC	Enteroviruses.			
RN	[1].			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE: 87010550.			
RA	Hughes P.J., Evans D.M.A., Minor P.D., Schild G.C., Almond J.W.,			
RA	Starway G.;			
RT	"The nucleotide sequence of a type 3 poliovirus isolated during a			
RT	recent outbreak of poliomyelitis in Finland."			
RT	J. Gen. Virol. 67:2093-2102(1986).			
RT	-1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN			

CC O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.  
 CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 Icosahedral units,  
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,  
 CC VP3, AND VP4.  
 CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
 CC  
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 CC  
 CC EMBL: X04468; CAA28155.1; J.  
 CC  
 CC DR PIR: A27245; GNNY27.  
 CC DR HSSP: P03302; LP1V.  
 CC DR PFAM: PF00548; Cys-protease-3C; 1.  
 CC DR PFAM: PF00947; Pico\_P2A; 1.  
 CC DR PFAM: PF01552; Pico\_P2B; 1.  
 CC DR PFAM: PF00680; RNA\_dep\_RNA\_pol; 1.  
 CC DR PFAM: PF00910; RNA\_helicase; 1.  
 CC DR PFAM: PF00073; rlv; 3.  
 CC  
 CC KM Polypeptide; Coat protein; Core protein; Transferrase;  
 CC RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate.  
 CC  
 CC FT CHAIN 2  
 CC FT CHAIN 70 340  
 CC FT CHAIN 341 578  
 CC FT CHAIN 579 878  
 CC FT CHAIN 879 1027  
 CC FT CHAIN 1028 1124  
 CC FT CHAIN 1125 1453  
 CC FT CHAIN 1454 1540  
 CC FT CHAIN 1541 1562  
 CC FT CHAIN 1563 1745  
 CC FT CHAIN 1746 2206  
 CC  
 CC FT LIPID 2  
 CC FT ACT\_SITE 1709 1709  
 CC FT ACT\_SITE 1723 1723  
 CC FT SEQUENCE 2206 AA; 245731 MW; F226AD85403C37BA CRC64;  
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 CC Query Match 1.68; Score 7; DB 1; Length 2206;  
 CC Best Local Similarity 100.00; Pred. No. 1.63e+00;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC Db 1271 AERENTS 1277  
 CC  
 CC Qy 106 AERENTS 112  
 CC  
 CC RESULT 32.  
 CC ID POLG.POL3L STANDARD: PRT: 2206 AA.  
 CC AC P03302; Q84783; Q84784; Q84785; Q84786; Q84787; Q84788; Q84789;  
 CC AC Q84790; Q98592; Q98593; Q98594;  
 CC DT 21-JUL-1986 (Rel. 01, Created)  
 CC DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 CC DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 CC DE GENOME POLYPROTEIN [COMPARIS: COAT PROTEINS VP1 TO VP4; CORE PROTEINS  
 CC P2A TO P2C; P3A; GENOME-LINKED PROTEIN VP6; PICORNAIN 3C  
 CC (EC 3.4.22.28) (PROTEASE 3C); RNA-DIRECTED RNA POLYMERASE P3D  
 CC (EC 3.4.22.28)].  
 CC OS Poliovirus type 3 (strains P3/Leon/37 and P3/Leon 12A11B).  
 CC OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 CC OC Enterovirus.  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC STRAIN-P3/LEON/37;  
 CC RX MEDLINE; 84170338.  
 CC RA Stanway G.C., Hughes P.J., Mountford R.C., Reeve P., Minor P.D.,  
 CC Schild G.C., Almond J.W.;  
 CC \*Comparison of the complete nucleotide sequences of the genomes of  
 CC the neuroinfectant poliovirus P3/Leon/37 and its attenuated Sabin

RT vaccine derivative P3/Leon 12a1b.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:1539-1543(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-P3/LEON 12A11B;  
 RX MEDLINE; 83299239.  
 RA Stanway G., Cann A.J., Hauptmann R., Hughes P., Clarke L.D.,  
 RA Mountford R.C., Minor P.D., Schild G.C., Almond J.W.;  
 RT "The nucleotide sequence of poliovirus type 3 Leon 12 alb: comparison  
 RL with poliovirus type 1.";  
 RN Nucleic Acids Res. 11:5629-5643(1983).  
 CC [3]  
 CC X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 1-878.  
 CC MEDLINE; 95120467.  
 CC RA Grant R.A., Hlreath C.N., Filman D.J., Syed R., Andries K.,  
 CC Hogle J.M.;  
 CC RT Structures of poliovirus complexes with anti-viral drugs:  
 CC implications for viral stability and drug design.";  
 CC Curr. Biol. 4:784-797(1994).  
 CC [4]  
 CC X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-878.  
 CC RA Syed R., Filman D.J., Hogle J.M.;  
 CC Submitted (MAR-1995) to the PDB data bank.  
 CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN  
 CC O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.  
 CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 Icosahedral units,  
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,  
 CC VP3, AND VP4.  
 CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
 CC -1- MISCELLANEOUS: THE SEQUENCE OF STRAIN SABIN VACCINE P3/LEON/37 IS  
 CC SHOWN.  
 CC -1- MISCELLANEOUS: THE STRAIN SABIN VACCINE P3/LEON/37 IS THE  
 CC PROGENITOR OF THE STRAIN SABIN VACCINE P3/LEON 12A11B.  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
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 CC  
 CC EMBL: K01392; AAA46914.1;  
 CC EMBL: X00925; CAA25444.1; -  
 CC DR PIR: A03900; GNNY4P.  
 CC DR PDB: 1P1V; 20-JUL-95.  
 CC DR PDB: 1PVC; 15-SEP-95.  
 CC DR PDB: 1VBA; 11-JUL-96.  
 CC DR PDB: 1VBB; 11-JUL-96.  
 CC DR PDB: 1VBC; 11-JUL-96.  
 CC DR PDB: 1VBE; 11-JUL-96.  
 CC DR PFAM: PF00548; Cys-protease-3C; 1.  
 CC DR PFAM: PF00947; Pico\_P2A; 1.  
 CC DR PFAM: PF01552; Pico\_P2B; 1.  
 CC DR PFAM: PF00680; RNA\_dep\_RNA\_pol; 1.  
 CC DR PFAM: PF00910; RNA\_helicase; 1.  
 CC DR PFAM: PF00073; rlv; 3.  
 CC KM Polypeptide; Coat protein; Core protein; Transferrase;  
 CC RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate;  
 CC 3D-structure.  
 CC FT CHAIN 2 69  
 CC FT CHAIN 70 340  
 CC FT CHAIN 341 578  
 CC FT CHAIN 579 878  
 CC FT CHAIN 879 1027  
 CC FT CHAIN 1028 1124  
 CC FT CHAIN 1125 1453  
 CC FT CHAIN 1454 1540  
 CC FT CHAIN 1541 1562  
 CC FT CHAIN 1563 1745  
 CC FT CHAIN 1746 2206  
 CC  
 CC FT LIPID 2  
 CC FT MYRISTATE.  
 CC RNA-DIRECTED RNA POLYMERASE P3D.

FT ACT SITE 1709 1709 PROTEASE (POTENTIAL).  
 FT ACT SITE 1723 1723 PROTEASE (POTENTIAL).  
 FT VARIANT 431 431 S -> F (IN P3/LEON 12A11B).  
 FT VARIANT 864 864 K -> R (IN P3/LEON 12A11B).  
 FT VARIANT 908 908 T -> A (IN P3/LEON 12A11B).  
 SO SEQUENCE 2206 AA; 246163 MW; 4766B15C861F66D3 CRC64;  
 Query Match 1.6%; Score 7; DB 1; Length 2206;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1271 AKEKENTS 1277  
 1111111  
 Oy 106 AKEKENTS 112  
 RESULT 33  
 ID POLG\_POL2L STANDARD; PRT: 2207 AA.  
 AC P06210;  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEIN VP1 TO VP4; CORE PROTEINS  
 DE P2A TO P2C, P3A; GENOME-LINKED PROTEIN VP6; PICORNAIN 3C  
 DE (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D  
 DE (EC 2.7.7.48)].  
 OS Poliovirus type 2 (strain Lansing).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 RN Enterovirus.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 86115399.  
 RA La Monica N., Meriam C., Racanelli V.R.;  
 RT Mapping of sequences required for mouse neurovirulence of poliovirus  
 RT type 2 Lansing".  
 RL J. Virol. 57:515-525(1986).  
 CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN  
 CC O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.  
 CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,  
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,  
 CC VP3, AND VP4.  
 CC -1- PPM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
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 CC  
 DR EMBL: M12197; AAA46912.1;  
 DR PIR: A29507; GNNY5P.  
 DR HSSP: P03299; IPOV.  
 DR PRAM: PF00548; Cys-protease-3C; 1.  
 DR PRAM: PF00947; Pico\_P2A; 1.  
 DR PRAM: PF01552; Pico\_P2B; 1.  
 DR PRAM: PF00680; RNA\_dep\_RNA\_pol; 1.  
 DR PRAM: PF00910; RNA\_helicase; 1.  
 DR PRAM: PF00073; rhv; 3.  
 KW Polypeptide; Coat protein; Core protein; Transferrase;  
 KM RNA-directed RNA polymerase; Hydrolyase; Thiol protease; Myristate.  
 FT CHAIN 2 69;  
 FT CHAIN 70 340  
 FT CHAIN 341 578  
 FT CHAIN 579 878  
 FT CHAIN 880 1028  
 FT CHAIN 1029 1125  
 FT CHAIN 1126 1454  
 FT CHAIN 1455 1541  
 FT CHAIN 1542 1563  
 FT CHAIN 1564 1746  
 GENOME-LINKED PROTEIN VP6.  
 PICORNAIN 3C.

FT CHAIN 1747 2207 RNA-DIRECTED RNA POLYMERASE 3D.  
 FT LIPID 2 MYRISTATE.  
 FT ACT SITE 1710 1710 PROTEASE (POTENTIAL).  
 FT ACT SITE 1724 1724 PROTEASE (POTENTIAL).  
 SO SEQUENCE 2207 AA; 245829 MW; 2B1E2070BDD4F99 CRC64;  
 Query Match 1.6%; Score 7; DB 1; Length 2207;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1272 AKEKENTS 1278  
 1111111  
 Oy 106 AKEKENTS 112  
 RESULT 34  
 ID POLG\_CXA24 STANDARD; PRT: 2214 AA.  
 AC P36290;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE GENOME POLYPROTEIN [CONTAINS: COAT PROTEIN VP1 TO VP4; CORE PROTEINS  
 DE P2A TO P2C, P3A; GENOME-LINKED PROTEIN VP6; PICORNAIN 3C  
 DE (EC 3.4.22.28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMERASE P3D  
 DE (EC 2.7.7.48)].  
 OS Coxsackievirus A24 (strain EH24/70).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
 RN Enterovirus.  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92271460.  
 RA Supanaranond K., Takeda N., Yamazaki S.;  
 RT "The complete nucleotide sequence of a variant of Coxsackievirus A24,  
 RT an agent causing acute hemorrhagic conjunctivitis".  
 RL Virus Genes 6:149-158(1992).  
 CC -1- FUNCTION: IT IS THOUGHT THAT THE P2C PROTEIN ATTACHES TO VESICULAR  
 CC MEMBRANES AND IS ASSOCIATED WITH VIRAL RNA SYNTHESIS.  
 CC -1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN  
 CC O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.  
 CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,  
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,  
 CC VP3, AND VP4.  
 CC -1- PPM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.  
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 CC  
 DR EMBL: D90457; NOT\_ANNOTATED\_CDS.  
 DR PIR: A48548; A48548.  
 DR HSSP: P03300; IAR8.  
 DR PRAM: PF00548; Cys-protease-3C; 1.  
 DR PRAM: PF00947; Pico\_P2A; 1.  
 DR PRAM: PF01552; Pico\_P2B; 1.  
 DR PRAM: PF00680; RNA\_dep\_RNA\_pol; 1.  
 DR PRAM: PF00910; RNA\_helicase; 1.  
 DR PRAM: PF00073; rhv; 3.  
 KW Polypeptide; Coat protein; Core protein; Transferrase;  
 KM RNA-directed RNA polymerase; Hydrolyase; Thiol protease; Myristate.  
 FT CHAIN 1 59  
 FT CHAIN 70 340  
 FT CHAIN 341 577  
 FT CHAIN 578 888  
 FT CHAIN 889 1035  
 FT CHAIN 1036 1132  
 FT CHAIN 1133 1461  
 FT CHAIN 1462 1548  
 FT CHAIN 1549 1570  
 GENOME-LINKED PROTEIN VP6 (P3B).

FT CHAIN 1571 1753 PICORNAIN 3C.  
 FT CHAIN 1754 2214 RNA-DIRECTED RNA POLYMERASE P3D.  
 FT LIPID 2 MYRISTATE (BY SIMILARITY).  
 FT ACT\_SITE 1717 1717 PROTEASE (POTENTIAL).  
 FT ACT\_SITE 1731 1731 PROTEASE (POTENTIAL).  
 SQ SEQUENCE 2214 AA; 247212 MW; EDD074569E1B22B8 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 2214;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1279 AERENTS 1285  
 1111111  
 Oy 106 AERENTS 112

RESULT 35  
 ID YHP\_YEAST STANDARD; PRT; 3744 AA.  
 AC P38811;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DE 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE HYPOTHETICAL 433.2 KDA PROTEIN IN HXT5-NRK1 INTERGENIC REGION.  
 GN YHR099W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;  
 OC Saccharomycetaceae; Saccharomycetes.

RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C / AB972;  
 RX MEDLINE: 94378003.

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,  
 Du Z., Faveille A., Fulton T., Gattung S., Giesel C., Kirsten J.,  
 Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,  
 Latteille P., Louis E.J., Macri C., Mardis E., Menzes S., Mouser L.,  
 Nham M., Rifkin L., Riles L., St Peter H., Trevisan E., Vaughan K.,  
 Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,  
 Vaudin M.;  
 RA "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome  
 VII.";  
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome  
 VII.";  
 RL Science 265:2077-2082(1994).  
 CC -1- SIMILARITY: STRONG, TO S. POMBE SPAC1P5.11C.  
 CC -1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.

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CC EMBL: 000060; AAB68923.1;  
 DR EMBL: 000060; AAB68923.1;  
 DR PIR: S46715; S46715;  
 KW Hypothetical protein; Transferase; Kinase.  
 FT DOMAIN 3414 3744 P13K/P14K.  
 SQ SEQUENCE 3744 AA; 433171 MW; AE3588676F5D5777 CRC64;

Query Match 1.6%; Score 7; DB 1; Length 3744;  
 Best Local Similarity 100.0%; Pred. No. 1.63e+00;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 654 KLSPEPT 660  
 1111111  
 Oy 191 KLSPEPT 197

RESULT 36  
 ID RUBR\_PYRFU STANDARD; PRT; 53 AA.  
 AC P24297;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE RUBREDOXIN (RD).  
 OS Pyrococcus furiosus.  
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN-DSM 3638;  
 RX MEDLINE: 92031546.  
 RA Blake P.R., Park J.-B., Bryant F.O., Aono S., Magnuson J.K.,  
 Eccleston E., Howard J.B., Summers M.F., Adams M.W.W.;  
 RT "Determinants of protein hyperthermostability: purification and amino  
 acid sequence of rubredoxin from the hyperthermophilic  
 archaeobacterium Pyrococcus furiosus and secondary structure of the  
 zinc adduct by NMR.";  
 RL Biochemistry 30:10885-10895(1991).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  
 RX MEDLINE: 93271899.  
 RA Day M.W., Hsu B.T., Joshua-Tor L., Park J.-B., Zhou Z.H.,  
 Adams M.W.W., Rees D.C.;  
 RT "X-ray crystal structures of the oxidized and reduced forms of the  
 rubredoxin from the marine hyperthermophilic archaeobacterium  
 Pyrococcus furiosus.";  
 RL Protein Sci. 1:1494-1507(1992).  
 RN [3]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE: 93271900.  
 RA Blake P.R., Park J.-B., Zhou Z.H., Hare D.R., Adams M.W.W.,  
 Summers M.F.;  
 RT "Solution-state structure by NMR of zinc-substituted rubredoxin from  
 the marine hyperthermophilic archaeobacterium Pyrococcus furiosus.";  
 RL Protein Sci. 1:1508-1521(1992).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY, AND STRUCTURE BY NMR.  
 RX MEDLINE: 93271901.  
 RA Blake P.R., Day M.W., Hsu B.T., Joshua-Tor L., Park J.-B., Hare D.R.,  
 Adams M.W.W., Rees D.C., Summers M.F.;  
 RT "Comparison of the X-ray structure of native rubredoxin from  
 Pyrococcus furiosus with the NMR structure of the zinc-substituted  
 protein.";  
 RL Protein Sci. 1:1522-1525(1992).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).  
 RA Bau R., Rees D.C., Kirtz D.M., Scott R.A., Huang H., Adams M.W.W.,  
 Eldenese M.K.;  
 RT "Crystal structure of rubredoxin from Pyrococcus furiosus at 0.95-A  
 resolution.";  
 RL J. Biol. Inorg. Chem. 0:0-0(1998).  
 RN [6]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE: 93299375.  
 RA Wampler J.E., Bradley E.A., Stewart D.E., Adams M.W.W.;  
 RT "Modeling the structure of pyrococcus furiosus rubredoxin by homology  
 to other X-ray structures.";  
 RL Protein Sci. 2:640-649(1993).  
 CC -1- FUNCTION: RUBREDOXIN IS A SMALL NONHEME, IRON PROTEIN LACKING  
 ACID-LABILE SULFIDE. ITS SINGLE FE, CHELATED TO 4CYTS, FUNCTIONS  
 AS AN ELECTRON ACCEPTOR AND MAY ALSO STABILIZE THE CONFORMATION  
 OF THE MOLECULE.  
 CC -1- MISCELLANEOUS: EXTREMELY THERMOSTABLE. BEING UNAFFECTED AFTER  
 INCUBATION FOR 24H AT 95 DEGREES CELSIUS.  
 CC -1- SIMILARITY: BELONGS TO THE RUBREDOXIN FAMILY.  
 CC PIR: A41189; A41189.  
 DR PDB: 1CA4; 30-APR-94.  
 DR PDB: 1C9A; 30-APR-94.  
 DR PDB: 1ZRP; 31-OCT-93.  
 DR PDB: 1B08; 26-AUG-98.  
 DR PDB: 1B09; 26-AUG-98.  
 DR PDB: 1BRF; 02-SEP-98.  
 DR PDB: 1PFA; 02-SEP-98.  
 DR PRINTS: PR00163; RUBREDOXIN; 1.  
 DR PROSITE: PS00202; RUBREDOXIN; 1.  
 KW Electron transport; Iron; Metal-binding; 3D-structure.  
 FT METAL 5 5 IRON (BY SIMILARITY).



FT METAL 8 8 IRON (BY SIMILARITY)  
 FT METAL 38 38 IRON (BT SIMILARITY)  
 FT METAL 41 41 IRON (BT SIMILARITY)  
 FT STRAND 2 5  
 FT TURN 6 8  
 FT STRAND 11 13  
 FT TURN 14 16  
 FT STRAND 18 18  
 FT HELIX 19 21  
 FT TURN 22 22  
 FT STRAND 23 23  
 FT TURN 25 26  
 FT HELIX 29 31  
 FT TURN 34 35  
 FT STRAND 37 37  
 FT TURN 39 41  
 FT STRAND 44 44  
 FT HELIX 45 47  
 FT STRAND 48 50  
 SQ SEQUENCE 53 AA; 5895 MW; 9CCCBBA4A381EC1E CRC64;

Query Match 1.4%; Score 6; DB 1; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 1.07e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 23 ISPGTK 28  
 111111  
 146 ISPGTK 151

RESULT 37  
 ID YC61\_PORPU STANDARD; PRT; 75 AA.

AC P51376;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE HYPOTHETICAL 8.7 KDA PROTEIN YC61 (ORF75).  
 GN YC61.  
 OS Porphyra purpurea.  
 OG Chloroplast.  
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RA STRAIN-AVONPORT.  
 RA Reith M.E., Munro J.,  
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast  
 genome."  
 RL Plant Mol. Biol. Rep. 13:333-335(1995).  
 CC -1- SIMILARITY: BELONGS TO THE YC61 FAMILY.

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CC EMBL: U38804; AAC08262.1;  
 KM Hypothetical protein; Chloroplast;  
 SQ SEQUENCE 75 AA; 8742 MW; 21E2375D9DE3B19B CRC64;

Query Match 1.4%; Score 6; DB 1; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 1.07e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 45 VDIIDD 50  
 111111  
 38 VDIIDD 43

RESULT 38  
 ID LEPA\_NPPOP STANDARD; PRT; 80 AA.

AC O10311;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE LATE EXPRESSION FACTOR 10.  
 GN LEF-10.  
 OS Orygia pseudotsugata multicapsid polyhedrosis virus (OPMVV).  
 CC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 CC Neolepoptodovirus.  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RA MEDLINE; 97271300.  
 RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,  
 RA Rohmann G.F.;  
 RT "The sequence of the Orygia pseudotsugata multinnucleocapsid nuclear  
 RT polyhedrosis virus genome."  
 RL Virology 229:381-399(1997).  
 CC -1- FUNCTION: INVOLVED IN LATE/VERY LATE GENE ACTIVATION (BY  
 CC SIMILARITY).

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DR EMBL: U75930; AAC59056.1;  
 KM Transcription regulation.  
 SQ SEQUENCE 80 AA; 8255 MW; 07AC5B3BAC095658 CRC64;

Query Match 1.4%; Score 6; DB 1; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 1.07e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 VLSAAA 9  
 111111  
 20 VLSAAA 25

RESULT 39  
 ID TYRO\_FELCA STANDARD; PRT; 80 AA.

AC P55033;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE TYROSINASE (EC 1.14.18.1) (MONOPHENOL MONOOXYGENASE) (FRAGMENT).  
 GN TYR.  
 OS Felis silvestris catus (Cat).  
 CC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RA STRAIN-EUROPEAN SHORTHAIR; TISSUE-MELANOMA;  
 RA Vander Velde D., de Weger R.A., de Wit M.L., Garderen E.,  
 RT Submitted (MAR-1996) to the EMBL/GenBank/DBS databases.

CC -1- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN  
 CC THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC  
 CC COMPOUNDS. CATALYZES THE RATE-LIMITING CONVERSIONS OF TYROSINE TO  
 CC DOPA, DOPA TO DOPA-QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO  
 CC INDOLE-5,6 QUINONE.  
 CC CATALYTIC ACTIVITY: L-TYROSINE + L-DOPA + O(2) -> L-DOPA +  
 CC DOPACQUINONE + H(2)O.  
 CC COFACTOR: BINDS TWO COPPER IONS.  
 CC SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MELANOSOMAL.  
 CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.

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DR EMBL: U40716; AAB08729.1; -  
DR PFAM: PF00264; tyrosinase.1.  
DR PROSITE: PS00497; TYROSINASE\_1; PARTIAL.  
DR PROSITE: PS00498; TYROSINASE\_2; PARTIAL.  
KW Oxidoreductase; Monooxygenase; Copper; Glycoprotein; Transmembrane;  
KW Melanin biosynthesis.  
FT NON\_TER 1  
FT CARBOHYD 59  
FT METAL 80  
FT NON\_TER 80  
SQ SEQUENCE 80 AA; 8633 MW; 926D7C99D49B74D3 CRC64;

Query Match 1.4%; Score 6; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 1.07e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 RNF6NH 26  
IIIIII  
QY 268 RNF6NH 273

RESULT 40  
ID DMP\_BPT5 STANDARD; PRT; 84 AA.  
AC Q38167;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE DMP PROTEIN (FRAGMENT).  
GN DMP.  
OS Bacteriophage T5.  
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.  
RN [1].

RP SEQUENCE FROM N.A.  
RA MEDLINE; 94335651.  
RA Decker K., Krauel V., Meesmann A., Heller K.J.  
RT "Lytic conversion of Escherichia coli by bacteriophage T5: blocking  
RT of the phua receptor protein by a lipoprotein expressed early during  
RT infection."  
RL Mol. Microbiol. 12:321-332(1994).

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DR EMBL: X75923; CAA53525.1; -  
DR NON\_TER 1  
FT SEQUENCE 84 AA; 9408 MW; E3D0C184A8271A6D CRC64;

Query Match 1.4%; Score 6; DB 1; Length 84;  
Best Local Similarity 100.0%; Pred. No. 1.07e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 VLSAAA 10  
IIIIII  
QY 20 VLSAAA 25

RESULT 41  
ID CYC6\_PLEBO STANDARD; PRT; 85 AA.  
AC P00117;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-MAR-1989 (Rel. 10, Last annotation update)  
DE CYTOCHROME C6 (SOLUBLE CYTOCHROME F) (CYTOCHROME C553).  
OS Plectonema boryanum.  
CC Bacteria; Cyanobacteria; Oscillatoriales; Plectonema.

RN [1]  
SEQUENCE:  
RP STRAIN-CCAP 1462/2;  
RC MEDLINE; 78023897.  
RA Alken A.;  
RT "Purification and primary structure of cytochrome f from the  
RT cyanobacterium, Plectonema boryanum."  
RL Eur. J. Biochem. 78:273-279(1977).

CC -1- FUNCTION: CYTOCHROME C6 IS A MONOHEME MONOMER. IT FUNCTIONS AS AN  
CC ELECTRON CARRIER BETWEEN MEMBRANE-BOUND CYTOCHROME F AND P700 IN  
CC THE PHOTOPHOSPHORYLATION CHAIN IN CHLOROPLASTS AND ALGAE. IT  
CC SUBSTITUTES FOR PLASTOCYANIN IN COPPER-DEFICIENT BLUE-GREEN ALGAE  
CC AND IN THE CHLOROPLASTS OF SOME EUKARYOTE ALGAE.  
CC PIR; A00109; CCPB6.  
DR HSSP; P56534; 1C6S.  
DR PFAM; PF00034; cytochrome\_c\_1.  
DR PRINTS; PR00605; CYTOCHROME\_C1.  
DR PROSITE; PS00190; CYTOCHROME\_C\_1.

KW Electron transport; Photosynthesis; Heme.  
FT BINDING 14  
FT BINDING 17  
FT METAL 18  
FT METAL 58  
SQ SEQUENCE 85 AA; 8576 MW; B9C0E4042A505B4 CRC64;

Query Match 1.4%; Score 6; DB 1; Length 85;  
Best Local Similarity 100.0%; Pred. No. 1.07e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 AAGGK 8  
IIIIII  
QY 23 AAGGK 28

RESULT 42  
ID CYC6\_ANAVA STANDARD; PRT; 86 AA.  
AC P00113;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CYTOCHROME C6 (SOLUBLE CYTOCHROME F) (CYTOCHROME C553).  
GN PCTJ.  
OS Anabaena variabilis.  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.

RP SEQUENCE [1].  
RA MEDLINE; 82265568.  
RA Beecher J., Margolish E.;  
RT unpublished results, cited by:  
RL Ulrich E.L., Krogmann D.W., Marley J.L.;  
RL J. Biol. Chem. 257:9356-9364(1982).

RN [2]  
RP SEQUENCE OF 1-22; 30-39 AND 56-86.  
RA MEDLINE; 77056395.  
RA Alken A.

RT "Protein evolution in cyanobacteria."  
RT Nature 263:793-796(1976).  
CC -1- FUNCTION: CYTOCHROME C6 IS A MONOHEME MONOMER. IT FUNCTIONS AS AN  
CC ELECTRON CARRIER BETWEEN MEMBRANE-BOUND CYTOCHROME F AND P700 IN  
CC THE PHOTOPHOSPHORYLATION CHAIN IN CHLOROPLASTS AND ALGAE. IT  
CC SUBSTITUTES FOR PLASTOCYANIN IN COPPER-DEFICIENT BLUE-GREEN ALGAE  
CC AND IN THE CHLOROPLASTS OF SOME EUKARYOTE ALGAE.  
CC PIR; A00105; CCA16.  
DR HSSP; P56534; 1C6S.  
DR PFAM; PF00034; cytochrome\_c\_1.  
DR PRINTS; PR00605; CYTOCHROME\_C1.  
DR PROSITE; PS00190; CYTOCHROME\_C\_1.

KW Electron transport; Photosynthesis; Heme.  
FT BINDING 14  
FT BINDING 17  
FT METAL 18  
FT METAL 58  
SQ SEQUENCE 82  
CONFLICT 82  
E -> D (IN REF. 2).

FT CONFLICT 84 84 E -> D (IN REF. 2).  
 SO SEQUENCE 86 AA; 8973 MW; 427099FBBCLF7442 CRC64;  
 Query Match  
 Best Local Similarity 100.0%; Score 6; DB 1; Length 86;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 19 AGKNL 24  
 |||||  
 OY 25 AGKNL 30

RESULT 43  
 ID CERA\_CERCE STANDARD; PRT; 98 AA.  
 AC P81038; 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE CERASTOTIN (EC 3.4.21.-) (FRAGMENTS).  
 OS Cerastes cerastes (horned desert viper).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
 CC Viperidae; Viperinae; Cerastes.  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-VENOM;  
 RX MEDLINE; 97390078.  
 RA Marrakchi N., Barbouche R., Guermazi S., Karoui H., Bon C.,  
 RA el Ayebl M.;  
 RT platelet-aggregating and agglutinating properties.";  
 RL Eur. J. Biochem. 247:121-128(1997).  
 CC -1- FUNCTION: THROMBIN-LIKE SNAKE VENOM SERINE PROTEASE. POSSESSES  
 CC ESTERASE AND AMIDOLYTIC ACTIVITIES. CLOTS HUMAN PLASMA AND  
 CC PREFERENTIALLY CLEAVES THE ALPHA CHAIN OF FIBRINOGEN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 CC TRYPSIN FAMILY. SNAKE VENOM SUBFAMILY.  
 DR HSSP; P00761; 1EPT.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; PARTIAL.  
 KW Hydrolyase; Serine protease; Venom; Glycoprotein.  
 FT ACT\_SITE 41 41 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT CABOARD 94 85 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT NON\_TER 98 98 POTENTIAL.  
 SO SEQUENCE 98 AA; 11156 MW; 36AF696ABF074012 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 6; DB 1; Length 98;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 35 WLSNA 40  
 |||||  
 OY 19 WLSNA 24

RESULT 44  
 ID NPM\_BOVIN STANDARD; PRT; 105 AA.  
 AC Q02379;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE NADH-UBIQUINONE OXIDOREDUCTASE 15 KDA SUBUNIT (EC 1.6.5.3)  
 DE (EC 1.6.99.3) (COMPLEX I-15 KDA) (CI-15 KDA).  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-22.  
 RC TISSUE-HEART;  
 RX MEDLINE; 92389317.

RA Walker J.E., Arizmendi J.M., Dupuis A., Fearney I.M., Finel M.,  
 RA Medd S.M., Pilkington S.J., Runswick M.J., Skehel J.M.;  
 RT Sequences of 20 subunits of NADH:ubiquinone oxidoreductase from  
 RT bovine heart mitochondria. Application of a novel strategy for  
 RT sequencing proteins using the polymerase chain reaction.";  
 RL J. Mol. Biol. 226:1051-1072(1992).  
 CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
 CC TO BE UBIQUINONE. THIS IS A COMPONENT OF THE IRON-SULFUR (1P)  
 CC FRAGMENT OF THE ENZYME.  
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.  
 CC -1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE; MATRIX SIDE.  
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DR EMBL; X63220; CAA44905.1;  
 DR PIR; S28239; S28239.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.  
 FT INIT\_MET 0  
 SQ SEQUENCE 105 AA; 12536 MW; 97D4971CE32662D1 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 6; DB 1; Length 105;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 49 IRAKE 54  
 |||||  
 OY 104 IRAKE 109

RESULT 45  
 ID YCXL\_CHLPP STANDARD; PRT; 110 AA.  
 AC P05720;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE HYPOTHETICAL 12.7 KDA PROTEIN IN 16S-23S DNA SPACER.  
 OS Chlorella pyrenoidosa.  
 CC Chloroplast  
 CC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;  
 CC Chlorellaceae; Chlorella.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 86232622.  
 RA Yamada T., Shimaji M.;  
 RT "Peculiar feature of the organization of rRNA genes of the Chlorella  
 RT chloroplast DNA.";  
 RL Nucleic Acids Res. 14:3827-3839(1986).  
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DR EMBL; X03848; CAA27477.1;  
 DR PIR; A24444; A24444.  
 KW Chloroplast; Hypothetical protein.  
 SQ SEQUENCE 110 AA; 12782 MW; 1F58A6055A1A377 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 6; DB 1; Length 110;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Aug 22 08:32:29 2000

US-09-240-675-2.rsp

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Db 95 IENIYS 100  
| | | | |  
QY 180 IENIYS 185

Search completed: Mon Aug 21 10:32:48 2000  
Job time : 51 secs.

